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| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20252 | 50620 | A | 20368 | 341 | 2239 | LCASSCPFICPPIRPSVCPAAPL LLGCRAMARGYGATVSLVLLG LGLALAVIVLAVVLSRHQAPCG PQAFAHAAVAADSKVCSDIGR AILQQQGGSPVDATIAALVCTSV VNPQSMGLGGGVIFTIYNVTTG AQWIGVPGELRGYAEAHRRHG RLPWAQLFQPTIALLRGGHVVA PVLSRFLHNSILRPSLQASTLRQ LFFNGTEPLRPQDPLPWPALAT TLETVATEGVEVFYTGRLGQM LVEDIAKEGSQLTLQDLAKFQP EVVDALEVPLGDYTLYSPPPPA GGAILSFILNVLRGFNFSTESMA RPEGRVNVYHHLVETLKFAKG QRWRLGDPRSHPKLQNASRDL LGETLAQLIRQQIDGRGDHQLS HYS LAEAWGHGTGTSHVSVLG EDGSAVAATSTIYTPFGAMVYS PRTGIILNNELLDLCERCPRGSG TTPSPV/SGDRVGGAPGRCWPP VPGERSPSSMVPSILINKAQGSK LVIGGAGGELIISAVAQAIMSKL WLGFDLRAAIAAPILHVNSKGC VEYEPNFS/QETVSCFVALAVL KLLASSDPATLAPKWRL*EVQ RGLQD\RGQNPDEGPFFLDVV PACV/SQEGACV*RPSRT*RKSG EAAGLLKTLLCPELEVLAPP |
| 20253 | 50621 | A | 20369 | 203 | 1518 | RCYLQFLALLTSTSARAAAAI AAAEPPAGSPSMTRAGDHNR QRGCCGSLADYLSSAKFHL*LG HSLSTWGD RMWHFAVS VFLVE LYGNSLLLTAVYGLVVAGSVL VLGAIIGDWVDKNARLKVAQT SLVVQNVSVILCGIILMMVFLH KHELLTMYHGWVLTSCYILIITI ANIANLASTATAITIQRDWIVV VAGEDRSKLANMNATIRRIDQL TNILAPMAVGQIMTFGSPVIGC GFISGWNLVSMCVEYVLLWKV YQKTPALAVKAGLKEEETELK QLNLHKDTEPKPLEGTHLMGV KDSNIHELEHEQEPTCASQMAE PFRTFRDGVVSYYNQPVF/LGW HGSCFPLYDCPGL*LHHHRVRL HSGTEWFHPQYFDGSISYNWN NGNCSFYLATSKMWFGSDRSD LRIGTAFLFDLVCDLCIHAWKP |
| 20254 | 50622 | A | 20370 | 1 | 497 | |
| 20255 | 50623 | A | 20371 | 1 | 1575 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20256 | 50624 | A | 20372 | 251 | 1351 | SLKSTDGVKCGLSINIFHKRREN ILFGMGNPLLDISAVVDKDFLD KYSCLKPNDQILAEDKHKELFDE LVKKFKVEYHAGGSTQNSIKV AQWMIQQPHKAATFFGCIGIDK FGEILKRKAAEAHVDAHYEQ NEOPTGTCAACITGDNRS LIAN LAAANCYKKEKHL DLEKNWM LVEKARVCYIAGFFLHVSPESV LKVAHHASENNRIFTLNL SAPFI SQFYKESLMKVMPYVDILFGK* DRSWPTFAREQGFETKDIKEIA QKDTSPCPKMNSKGQRIRDLHP KGRDDT\IMATESEVTAFAGLGI KTQKE\IDTNEAGDAFVGGFLS QL\VSDKPLTECIRAGHYAASIII RRTGCTFPEKPDFH |
| 20257 | 50625 | A | 20373 | 1 | 201 | |
| 20258 | 50626 | A | 20374 | 15 | 304 | |
| 20259 | 50627 | A | 20375 | 51 | 283 | TWVKEAQNDGLVCYIFIFNCQ MTGLDIEKDAQIEMACLITDSD LNILAEVRDAHVIQSYFLKGTG NITIIFSSFFI |
| 20260 | 50628 | A | 20376 | 2 | 520 | QRRLRDWGRGCWSRVMLGGS LGSRLLRGVGGSHGRFGARGV REGGAAMAAGESMAQRMVW VDLEMTGLDIEKDAQIEMACLIT DSDLNILAE/GNSVHEDKKFLD KYMPQFMKHLHYRIIDVSTVKE LCRRWYPEEYEFAPKKAASHR ALDDISESIKELQFYRNNIFKKK |
| 20261 | 50629 | A | 20377 | 2 | 206 | EFGTRRHVPPCLINFFKDQGSP* LARLVSNWPQVIHPPWPPTVL GLRGVGHCPWPRLGNSSVWV GGH |

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| 20262 | 50630 | A | 20378 | 1 | 1401 | MRSQKTSLYFSLEAKFYCSLRN ERIASCDIINDAGIQTKTLMKRS HVAYALKKKPVEQGDSEFELESK GFMAITIAVCIEQNLRHSSSLFIC MSSTGQSGTTNNASSLIPSYVFT PPHFNLLDKQGRTAGKSHCGE DRKEHNNACHQEEEEAPDVNPL HGLQASGSPGKTQRIKSQALEG TRL YSHSEETRSGLIRLLRLRQR RLRDWGRGCWSRDM LGGSLG SR\LLRGVGGSHGRFGARGVRK RGAAMAA\GESMAQRMVWVD LEITGLDI*KVQIEMACITDSD LIILAEGPNLI\KQPDELLDSMS\ DWCK\EHHGKSGLTAKVKEST NYHCQQA E\YEFALWYDQPD SLPGLCPTCQEIKFHE\DKKFP* QNTCPQFMKHLHYRI\DVSHC* KELCQTAGYP EYEFA\PKKAA FSIGPLDD\ISENL\KKVPFFPEN NHLPRKKIRMKRKEGKL*KMG ENEKTVS |
| 20263 | 50631 | C | 20379 | 180 | 248 | |
| 20264 | 50632 | A | 20380 | 455 | 1133 | GIEGWRGEADTLPAEGQDGG RVSKGDI FSGGAETAQGWGVM GPFQAAPSKRAGREHRGGQRR VQHV GWYPRPGSDKGHGKGT QDSRVPQLPPHPPIHLVSRHRG KLRHGFLRPMPEPRGLESKGTG NCFGELQH/RTSP*GRSGPREGG PRNIAQQGGCRGSACGRRSH\E ALRPRVWCGEGPQWTW\CAVC P\NRSAPGAGLAD\RQHPGESRA WGETRLGEAGGAE |
| 20265 | 50633 | A | 20381 | 214 | 412 | |
| 20266 | 50634 | A | 20382 | 3 | 257 | PATVIITVNTTWSAALISRESAL RSFPVKAAALSPSREGGSVTAT PNVRSMTSAVPIMRVSVQSKR *PEEQN*QETYPQTTSR |
| 20267 | 50635 | A | 20383 | 1 | 1569 | |
| 20268 | 50636 | B | 20384 | 15 | 1744 | |

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| 20269 | 50637 | A | 20385 | 2 | 7205 | QASGSCWSSPFFSASTPSAAAT GVPGPTDMAAVLQQVLERTEL NKLPKSVQNKLEKFLADQQSEI DGLKGRHEKFKVESEQQYFEIE KRLSHSQERLVNETRECQSLRL ELEKLNNQLKALTEKNKELEIA QDRNIAIQSQFTRTKEELEAEKR DLIRTNERLSQELEYLTEDVKR LNEKLKESNTTKGELQLKLDEL QASDVSVKYREKRLEQEKELL HSQNTWLNTELKTKTDELLAL GREKGNEILELKCNI |
| 20270 | 50638 | A | 20386 | 120 | 7384 | GWTRFPRVPPRESPAGGRARAT ERGDRGGGPGVWVLLVFAFL RFYPVGRCHWGPWAPPTWAA VLQQVLAERTELNKL\PKSVQNK LEKFLADQQ\SEIDGP*RGGHGE I*RWESQYFEIEKRLSHSQER LVNETRECQSLRLELEKLNNQL KA\LPEKNKELEIA\QDRNIA\IQ SQFTRTKEELEAEKRDILRTNE RLSQELEYLTEDVKRLNEKLKE SNTTKGELQLKLDELQASDVSV KYREKRLEQE |
| 20271 | 50639 | A | 20387 | 2 | 433 | |
| 20272 | 50640 | A | 20388 | 2 | 181 | GFRRVSLEF*FPGVRWGMRLK GAPDLAPFSQM*SGGRAPCVAS *PPCRGLRLMRTGSRR |

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| 20273 | 50641 | A | 20389 | 1 | 2422 | MAGALAGLAAGLQVPRVAPSP DSDSDTDEPSLRRSAGGLLR SQVIHSGHFMVSSPHSDSLPRRR DQEGSVGPSDFGPRSIDPTLTRL FECLSLAYSGKLVSPKWKNFK GLKLLCRDKIRLNNAIWRAWYI QYVKRRKSPVCGFVTPLQGPEA DAHRKPEAVVLEGNYWKRRIE VVMREYHKWRIYYKKRVSGG GPGRPQSFPPAAAGYRPPRKIPG KGILTPELAPLGPSIQSRADSAT VWPQRLLAASLPRGRLRKPSRE DDLLAPKQAEGRWPPPEQWCK QLFSSVVPVLLGDPEEEPPGGRQ LLDLNCFSLSDISDTLFTMTQSGP SPLQLPPEDAYVGNADMIQPD TLPQLPSLDDFMDISDFFTNSRLP QPPMPSNFPEPPSPVVDLSLFSS GTLGPEVPPASSAMTHLSGHSR LQARNSCPGPLDSSAFLSSDFLL PEDPKPRLPPPVPPPLLHYPPP AKQETVPEFPCTFLPPTPAPTPP RPPPGPATLAPSRPLLVKAERL SPPAPSGSERRLSGDLSSMPGPG TLSVRVSPQPILSRGRPD SNKA LLGSFLGSPNSLLPETENRRITHI SAEQKRRFNKLGFDTLHGLVS TLAQPSLKVSKATTLQKTA EY ILML\QKERAGLQEEAQQLR\DE IEEL\NAAINLCQQQLPATGVPI\ THQRFQDMRDMFD\DYVRTRT LHNW\KFWVSSLKPMAGGLQ |
| 20274 | 50642 | A | 20390 | 315 | 387 | |
| 20275 | 50643 | A | 20391 | 570 | 1017 | FCLHILQVPHTLAGHSPCAHG/R PPLPRF/HDRLPEEIQQQIVRETF HLVLKRDDNICNFLEGGSLIGG SDYKLIYRHYATLYFVFCVDSS ESELGILDLIQLEQFKKDNEETG FGSGTRALEQALEKTKANIKW VKENKEVVLQWFTENSK |
| 20276 | 50644 | A | 20392 | 1 | 1128 | |
| 20277 | 50645 | B | 20393 | 62 | 130 | |

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| 20278 | 50646 | A | 20394 | 99 | 718 | ENRGWQSMIQAILVVNNHGKP RLVRFYQRFPEEVIQQIVRETF HLVLKRDDN\CNFLEGGSL*L GGSDYKLIYRHYATLYFVFCV DSSESELG\LDLIQVFVGNWSWIS CFENVV*IWI*TFHMDK\VHYIL QEVVMGGMVLETNMNEIVAQ IEAPNRLEKSEG\GLSAAPARA VSAVKNNINLPEIPRNINIGDLNIK VPNLSQFV |
| 20279 | 50647 | A | 20395 | 3 | 370 | SLHLAAILGETSTVEKL/YAAGA GLCVAERRGHTA/LHLACRVG AHACARAL/LQPRRRPREAPD TYLA/QGPDRTPDTNHTPVAL/Y PDSdleKEEEEESHTPLHVAVIH K/DVEMVRLLRDAGADLDK |
| 20280 | 50648 | A | 20396 | 2 | 1097 | SRQSPATGGRLRWAPDAALAM AVVACLGQAADSDKWGDSRLS SLGPDAAAPGGPGLGAELGPGL SWAPLVFGYVTEdGDTFSAGT EYMDLQNDLRQVSHEGWCR WGP GFPV*LPTACPLLLQTALH LAAILGETSTVEKLYAAGAGLC VAERRGHTALHLACRVGAHAC ARALLQPRRRPREAPDTYLAQ GPDRTPDTNHTPVALYPDSdle KEEEESEEDWKLQLEVENYEG HTPLHVAVIHKDVEMVRLLRD AGA\DLDKPEPTCGRSPLHLAV EGPRQADVLELLLRAGANPA A\RM YGGRTPLGSAMLRPNPVI LAR\LLRA\HGAPEPEGEDEKSG P\CSSSSDSDSRLSPSAWSPLPPG |
| 20281 | 50649 | A | 20397 | 47 | 478 | LRLRKLKAIMLAfGRGKTRNSE ESSDSQEVWIKDTWMFTALGH CGISMFGLDRELTLTNYELFIS SSPTPS*VPQRLCYVVSTFLMYL SLDHLYTGEMKAFLHVLDTQS VNSDFAFFVRLSFQYFYKLLCV LWQGTVNKEFI |

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| 20282 | 50650 | A | 20398 | 1 | 1992 | METFVIGWQPAVTVWTIGVAP PPTLEITSQHEIWVAQHPNYIIS VKQESPAPMPWTAVALDSHRS MNTIVNCAREGSTLHAPYESLM PDDLRWNSFILKSSPSPHSRSM KLSSMKLVPGAKYIRDHCLVK EALTIHKSPILLAAIDLLGNLSG FTDYQSYVIHGCLENNPTLERSI ALFNGISKWVQLMVLSKPTPQ QRAEVITKFINVAKGATAELNL WQHPKIIMLSQVVPGVFSQEHS LIRSLHANLHFTVCFPEDPLAM VAGMVQESTCPCEILQLPTTGQ LANWNEMTELVSNGNYCNYS KPFPTCDGLKIPILGVHLKDWA VHVNFDPWTEEIKVNIVKMHQ LSVTLSELVSLQNASHHLEPNM DLINLLTV/DGLQPADLMHAISL FRTSHRPQGLFL*IKGTSPAHS DRSCQHFRV*KCSSWESWHGG/ WLSLEE*MSSFLLRSF*KI/YCSR KNVACQTRAVCTNLDALLSS QMSNNHHPFSLPAQDEVFEFPG VTAGHRDLDSRAITLVGTSSRK ISVRLQRATTSTQATQTEPVWSE AGWGDSGSHTFPKMKSKFHDK AAKDKGFAKWENKPRVHAG VDVVDRGTEFELDQDEGEETR QDGEPAAVSVGAVAAPGMSE KELLQVDGRTPTRVLRMADLV GISEFRGEPFV |
| 20283 | 50651 | A | 20400 | 1 | 417 | |
| 20284 | 50652 | A | 20401 | 2 | 94 | |

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| 20285 | 50653 | A | 20402 | 190 | 2189 | AFCPAGTRSAPCPRPRTMTMTL HTKASGMALLHQIQGNELEPLN RPQLKIPLERPLGEVYLDSSKPA VYNYPEGAAAYEFNAAAAANA QVYGQTGLPYGPGSEAAAFGS NGLGGFPPLNSVSPSPLMLLHPP PQLSPFLQPHGQQVPYYLENEP SGYTVREAGPPAFYRPNSDNRR QGGRERLASTNDKGSMAEMESA KETRYCAVCNDYASGYHYGV WSCEGCKAFFKRSIQELPTLC*I GWYWYQNRDIDQWNRTEPSEI IPHIYNHLIFDKRDKNKKWGKD SLFNK*CWENWLAICRKLKLD HFLTPTYTKINSRWIKDLNVRTK TIKTLEENLGNTIQDIGMGKDF MSKTPKAMATKAKIDKWDLIK LKSFCSSLGYLKTENTAKETTIR LNRQPTWEKIFAIYSSDKGLIS RIYKELKQIYKKK/GNPINKWV KDMNRHFSKEDIYAANRHMKK CSSSLAIREMQIKTTMRYHLTP VRMVIIRKSGNDRCWRCGEIG TLLHCWWDCCLVQPLWKTWV RFLRDLQLEIPFDPAIPLLGIYPK DYKSCCYKDTCTRMFIAALFTI AKTWNQPKYPTTIG*IKKMWHI YTMEYYAAIKKDEFI/SLVGTW MKLETIILSKLTQEQTCKHHMF SFITGSRTMRTHGCREGNITHW GLLRDSVNMVTQAH |
| 20286 | 50654 | A | 20403 | 2 | 907 | RVPAMATSSFALPRILGAGARA PSRWLGFLGKATPRPARPSRRT LGSATALMIRESEDSTDFNDKIL NEPLKHSDFFNVKELFSVRSLF DARVHLGHKAGCRHRFMEPYI FGSRLADHDIIDL\EQTATHLQLA LNFTAHMAYRKGIIIFISNRNQF SYLIENMARDCE\YAHTRYFM GGMLTNARLLYGPTVRLPDL/I FLHTLNNIFEPHVAVRDAAKM NIPTVGIVDTNCNPCLITYPVP NDDSPHAVHLYCRLFQTAITRA KEKRQQVEALYRLQGQKEPGD QGPAHPPGADMSHSL |
| 20287 | 50655 | B | 20404 | 70 | 1477 | |

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| 20288 | 50656 | A | 20405 | 153 | 688 | AHPLLRSPEETSRSRKPRCATT NGFLRIPEKTPPWSPEVAIHRNR \ITPNKPPTVKSLEKVFC*LDKE AQKEKESQK*KGPVRMPTKT\L RITTARKTP\CGE\GSKDRWDRF\ QIEISQSR LH*LCTSPF*DLFKQI TFHQYLSPGV*GEKSPFADALS QISIHTIDDQFVKKKKKKKKW |
| 20289 | 50657 | A | 20406 | 26 | 603 | RPRGTLREYKVVGRCPAHSHK CHTPPL\YR\MRNFAP\NHVVA KS/RAFWYFVSQKKDEESLPG EIVYCGQGV*ESSPCGSKNFGI WLR\DSRSG\THN\MYRE*PGP *PTAGGCSPSCYPRHGVARHAG PEAHFHFRIERLEEIAGQQNC RRPGCSKQFPRISRKFPLAPPG SLRRQDKPRF\TTKRPNTFF |
| 20290 | 50658 | A | 20407 | 161 | 418 | |
| 20291 | 50659 | A | 20408 | 1 | 2580 | |
| 20292 | 50660 | A | 20409 | 3 | 264 | |
| 20293 | 50661 | A | 20410 | 3 | 302 | ALALLSPWVVDGTRHRGAGGG AHPGGSGRTGAHRGGGRLRHG GLQVPSAPREGS*GPARNRAQ RRAVDR TQ*ECSSKEVYT*RLV PPPPLGSHSSPE |
| 20294 | 50662 | A | 20411 | 2 | 415 | |
| 20295 | 50663 | C | 20412 | 1 | 1230 | |
| 20296 | 50664 | A | 20413 | 238 | 1765 | VTAYHAATMNEVSVIKEGWLH KRGEYIKTWRPRYFLLKSDGSF IGYKERPEAPDQTLPLNNFSV AECQL\MKTERPRPNTFVIPCP QLTNIIRGTL/HTLVSPNQRE\EW NPPYQVVPQQPSRGGPKARTP WNNKCGSPK*LSHD*ENGSGGS ASHG/RKVTMNDSTYLNLLGK GTFGKV\ILFRKKATGR*FA\MK \IFRKKVINAKD*VAHNIQPRAG VLPEHPGNPFLQLR*KYAFDPD TTRPVPL*MEYA\NGGELFF\HL S\ RERV\FTEERA\RIFYGAEIVSA SEVTWHSRGRGNTRDNQSWKT LMLEQKMAHIK\ITDFGL\CKRG ASSDGAT\MKTCETPEYLAHE \LEDNDYGRAVDWWGLGVVM YEMMCGRLPFYNQDHERLFELI LMEEIRFPRTLSP EAKSLLAGLL *\KDPKQRLG\GGPSDAKEVME HRFFLSINWQDVVQKLLPPFK PQVTSEVDTRYFDDEFTAQSITI TPPDYDSLGLLEAGPADPASP QFSYSASIRE |

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| 20297 | 50665 | A | 20414 | 192 | 866 | LSCRMRLVLGQNPTLDSIDRS GVRSKRIFNKLRESFHYNSE LTISVNMSYNCCSGNFSSRSCG DYLRYPASSRGFSYPSNLVYST DLCSPSTCQLGSSLYRGCQEIC WEPTSCQTSYVEVQAPAKTSC YRPKNLPCSASPCKTTYSLGSLG FGSSSRSLGYG*GSCYSVGCG SSGFRSLGYGGCGFPSLGYGVG FCRPTYLASRSCQSSCYRPTCGS |
| 20298 | 50666 | A | 20415 | 312 | 1420 | RSHSNAVPSVWNLTLPLDSGPH QSPASTTGPTNTERSSVPMSCS PPACPTQCVLCSCTEGQIYCG TTCPEPGCPAPLPLPDSCCQACK DEASEQSDDEDSVQPLHVVHRP QDPCSSDAGRKRGPPTAPTGL SAPLSFIPRHFPRPKGAGSTTVKI VLKEKHKKACVHGGKTYSHGE VWHPAFRAFGPLPCILCTCEDG RQDCQRVTCPTIYPCIRHPREK WPGKCKICKPEDKADPGHSEIS STRCPKAPGRVLVHTSVSPSPD NLRRFALEHEASDLVEIYLWKL VKDEET*GSGEVKYLAQGHTA RIFHLTQIKKVRKQDFPERGTA LPTARWPPRRSLERLPSDPGAE GHGQSRQSDQDITKT |
| 20299 | 50667 | A | 20416 | 17 | 1008 | KSGARSLQPQFLRAPEDGGPLS LPNAAMARGPKKHLKRVAAP KHWMLDKLTGVFAPRPSTGPH KLARECLPLIIFLKDQTLNALT GD\EVKKI\CMQRFIKIDGKVRT DITYPAGFMDV\SIDKTGREFP VL/YLIDTQGVRFCL*HRIYTLR EGQSTSLCKVRKILLWAPKGIP HL\VTH\ DAR\TIR\YDPDPLIQGE MNTHSRLI*KTGKI*FPSKFDH LVTCVMVT\GGA\NLGRNWVLI TQQRSTLGSF*PLVHVK\ DAN GNKLLATSDFSNI/VVIGKGNK PW\ISL\PRGKGIPPHHLEERDK RLAAKQSSWVKWGPWVTWSD |
| 20300 | 50668 | A | 20417 | 1 | 1377 | |
| 20301 | 50669 | A | 20418 | 1 | 2178 | |
| 20302 | 50670 | A | 20419 | 158 | 250 | |

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| 20303 | 50671 | A | 20420 | 1 | 860 | MDQTVKSLMASEEEEYSTKEEK YEKEMKLLEEKLKEAETRAEF VERSVAKLEKTTDDLEETLASA KEETWRFIRPGTRPYWNSATCF LLPGHKMAAEVHKLNPNVSEH DQERWHDAFGNGGADNHSL QASTRRGGPLSQELLQSLAASL AAGGLTALSAEFTIGKGELMAH DVLWGCAPDEYDDLISGTCSHL PKGKTHDVLTGSDDGHSNTS LAWGAGVQFNPTESVAIDIAYE GPGSGDWRTDGFIVGGLFCGV NMAVKIS\GVLKDG TGKPVQN* TIQLKAKRNSTTVVNTLASEN PDEAGRYSMDVEYGQYSVILL VEGFPPSHAGTITVYEDSQPGTL NDFLCAMTES\ DARPEALGRFG LYWWKEVARNAS\AVGQNTA AAKKSASDASTSAREAAATHAV DAGGFKNAQARTSSPDKAGSA GFKQGFPRGGNGINKRAT*RIK KVACR*SLMASEEEEYSTKEEKY EKEMKLLEEKLKEAETRAEFVE RSVAKLEKTTDDLEETLASAKE ETWRFIRPGTRPYWNSATCFLL PGHKMAAEVHKLNPNVSEHDQ ERWHDAFGNGGADNHSLQA STRRGGPLSQELLQSLAASLAA GGLTALSAEFTIGKGELMAHDV LWGCAPDEYDDLISGTCSHLPK GKTHDVLTGSDDGHSNTSLA WGAGVQFNPTESVAIDIAYEGP |
| 20304 | 50672 | B | 20421 | 34 | 800 | |
| 20305 | 50673 | A | 20422 | 130 | 368 | RQVITTL YIPYRRRHLSPPDPEQ PLNHKQNRKVNHGGTEFQVVV LPFPKMKINCYRRNQFFLFFFST VKVPVGWSMVPLQAATAGAR L*NSDISPLKSQQTQDKFPSSKP PHIYIKK |
| 20306 | 50674 | A | 20423 | 1 | 57 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20307 | 50675 | A | 20424 | 85 | 874 | GPRGLVSMAGGSVEVTPSTFTC YLRPPSASPPTPPSHPGLLPRSPA LCSLHTGARTLPLFGGRCSSA VLPPRPGP/RAGSGSGQRERFHR FQPTYPYLQHEIDLPTISLSDG EEPPP*QVPCHLQVR\DPKQQL\ ELNRE\SVGAPPNRTIFDSLMD SARLGGPCPPSSNSG/ISAPTCYG \SGGRMEGPPP\TYSEVIGHLPG GPSFQH\Q\QSSGPPSLLEGTR\ HPHTHSRP*RSAAIWSKEKDKQ KGHPSLGSPGGPGLGLRR |
| 20308 | 50676 | A | 20425 | 3 | 250 | ESVSATEDLAPDAAQGEDNSEI KELL\RENEPLPACNGPAQAQPS PTTERAKSQEEVLPSSTTPSPGG ALSPSGQPSSSVDA |
| 20309 | 50677 | A | 20426 | 2 | 393 | |
| 20310 | 50678 | A | 20427 | 1066 | 1824 | |
| 20311 | 50679 | A | 20428 | 3 | 902 | |
| 20312 | 50680 | A | 20429 | 1 | 2163 | |
| 20313 | 50681 | A | 20430 | 1 | 1890 | |
| 20314 | 50682 | A | 20431 | 1 | 2882 | MKQQLPVSYLQVIFNHWASRIS GARGAGWGPVRLGRLCADRAL DGESRPGGGGQSGVPASEASQ KAAHGRRLPVPARLLRCAHSA LEPGRGSASSPRNSTTSDNDQPP DYSFSKRCDSHSLGFSLVWESR NLTLPPTSKLLHFSAFHFFIYKC RAEGHKLYKDLKNFLSAVKVM HESSKRVSETLQFIYYSEWYGH EELKAIVWNNDLLWEDYEEKL ADQAVRTMEIYVAQFSEIKERI AKRGRKLVDYDSARH |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20315 | 50683 | A | 20432 | 1 | 1791 | MPGARTSSSGASENHRARGQG GGPQGVGRMAEGKAGGAAGL FAKQVQKKFSRAQEKVLQKLG KAVETKDERFEQSANNFYQQQ AEGHKLKDKLKNFLSAVKVMH ESSKRVSETLQEIYSSEWDGHE ELKAIVWNNDLLWEDYEEKL\ ADQAVRTMEIYVAQFSEIKE\RI AKRGRKLVDYDSARHHLEAVQ NAKKKDEAKTAKAEFEFNKAQ TVFEDLNQELLEELPILYNSRIG CYVTIFQNISNLRDVFYREMSK LNHNLYEVMKLEKQHSNKVF VVKGLSSSSRRSLVISPPVRTAT VSSPLTSPTSPSTLSLKSESESVS ATEDLAPDAAQGEDNSEIKELL EEEEIEKEGSEASSSEDEPLPA CNGPAQAQPSPTTERAK\SQEE VLPSTTTPSPGGALSPSGQLSSS ATEVVLRTRTASEGSE\RPKKT ASIQRTSAPRRPPPPRATASPRP CSGNIPSSPTASGGGSA\TSRAS LGTGTASPRTSLEI*PNPE\PEK PVRTPEAKENENIHQNPEELC TSPTLMTSQVASEPGEAKKME DKEKDNKLISADSSEGQDQLQV SMVPENNNLTAPEPQEEVSTSE |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20316 | 50684 | A | 20433 | 158 | 1830 | QLQSKMKLFWLLFTIGFCWAQ YSSNTQ/SKGRTSIVHLFEWRW VDIALECERYLAPKGFGGVQVS PPNENVAIYNPFRPWWERYQPI VSYKLCSTRSG\NEDEFNMVTR CNNV\GVRI\YVDAVINHMCN\N AVSAGTSSTCGSYFNPWKLRTF PAIPYPGWDFNDGKC\KTGSGD IENYNDATQVRDCARLTGLLDL ALEKDY\VRSKIA\EYMNHL\DI GVAGFRLDASKHM\WPGDIKAI LDKLN\LNNSNWFAGSKPFI\F QEVIDLRVGEPNLKASDYFGNG RVTEFKYGA KLGTVIRKWDGE KMSYLKKWG\EGWGF\MPSDR ALVFVDNHDNQRG\HGAGGASI LTFW\ DARLYKMA\VGFM LAHP YGFTRVM\SSYR\WAKHSFKKG NDVNDW\VGPTQINNG\VIKEV TINPRH*L VGND\WV\CEH\RWR \QIRNM\VNFRNGSGMAQPFLQ NWYDNGSNQVAF\GRGNR\GFI VFNK*WPVIFI*LCKPGLPAGSY CDVISGDKVIGNCSAIKIPVSVD GKAHFSMSNSAEDPFLAIHAES KIVKFKIKCKSAKQKKKKKKG RPF |
| 20317 | 50685 | A | 20434 | 3 | 383 | |
| 20318 | 50686 | A | 20435 | 1 | 378 | CASGSSGWRPVLWAGAFTMAS AELDYTIEIPDQPCWSQKNSPSP GGKEAETRQPVVILLGWGG\SK DKNLVKYS AIYHKRKLLELLFD YEIEKEPPAFSLSSATVASCCTA TCWSSCRPVASAACV |
| 20319 | 50687 | A | 20436 | 1 | 558 | CASGSSGWRPVLWAGAFTMAS AELDYTIEIPDQPCWSQKNSPSP GGKEAETRQPVVILLGWGGCK DKNLAKYS AIYHKRG CIVIRYT APWHMVFFSES LGIPSLRVLAQ KLELLFDYEIEKEPLL FHVFSN G\VRHAVPLTCWELLQTRRFCR LRVVG TIFDSAPGDSNLVGGSA GLGSHPGARG |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20320 | 50688 | A | 20437 | 78 | 1237 | CWSHSDTYWPRTPRPPPPGRPG PVVHLAQPV LHPEAGIPEFWES GSPGQTRGAALVLT VHICVSEN SPSPGGKEAETRQPVVILLGWG GCKDKNLAKYSAIYHKRNTAT LQPPLTYMRGWGLFLT GAPAD QYLIQIKRISQWLRGCIVIRYTA PWHMVFFSESLGIPSLRVLAQK LLELLFDYEIEKEPLL FHVFSNG GVMLYRYVLELLQTRRFCRLR VVGTFIDSAPG*QQPG*GL\SGP GQPSWERRARPMLRLLLLVAF ALGGSSCFHVLLAPITALFHTHF YGQAYRTRALAWPELYLYSRA DEVVLARDIERMVEARLARRV LARSVDFVSSAHVSHLRDYPY YTSLLCRTSMRKLRLPKAIAPS HLCSQKINALKPSP |
| 20321 | 50689 | A | 20438 | 3 | 427 | |
| 20322 | 50690 | B | 20439 | 101 | 1099 | |
| 20323 | 50691 | A | 20440 | 733 | 2228 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20324 | 50692 | A | 20441 | 582 | 2595 | PPPVRRRDPGPAVRPAGAMA KKSAENGIYSVSGDEKKGPLIA PGPDGAPAKGDGPVGLGTPGG RLAVPPR\ETWTRQMDFMSCV GFAVGLG\NVWRFPPYLCYKNG GGVFLIPYVLIALVGGIPIFFLEIS LGQFMKAGSINVWNICPLFKGL GYASMVIVFYCNTYYIMVLAW GFYYLVKSF\TSTLPWATCGNY/ TWKHSPTCVEIFRHEDCANAS LANLTCDQLANR\RS\VIEFWE NKVLKLSGGLE\VP GALNWE\V TLGLLACWVLVYFCVWKGVK STGK\IVYFTA/THYPYVVLVVL LVRGVLLPGALDGIIYYLKPDW SKLGSPQVWIDAGTQIFFSYAIG LGALTVLGSYNRFNNNCYKDA IILALINSGTSFFAGFVVSILGF MAAEQGVHISKVAESGPGLAFI AYPRAVTLMPVAPI\WAALFFF MLLLLGLDSQFVGVEGFITGLL DLLPASYYFRFQREISVALCCA LCFVIDLFMG\TDGGMVVFQLF DYYSASGTTLWQA\FWECVV VAWVYGADRFMDDIACMIGY RPCPWMKR\CWSFFTPLVCMGI FILNVVYYEPLVYKQN/TYVYP WWGE\AMG\WPFALS\SM LFVP L\HLLGLPSLRAGHPWLKRW QH\LTQPIWGLHPL/EELPRFRD ADVQGT LTHP*TPVSESSKVVV |
| 20325 | 50693 | A | 20442 | 1 | 363 | MGKRGLILLIEACIAIAQPLQRW FVVPPRAGMPVTYD/HSNSAAG SPPV*NARLCSPGEKVL CRSQT GNFPHTPQEQA VPSAWNALPV QP*SH/GPSPMLVPCRCVCPMET RVQGSASPGGQG |
| 20326 | 50694 | A | 20443 | 747 | 1389 | LGAVQLCPPPCRPC HRAALPGG LFPPPRPPHSPQAGPLHPQWTQ* PGSVGSPTQLSPEASRPQWPPT A\GSPRAGVHPGHGQA*SADISS AKQWTQVGPAGQGGSKFGKT KVPWQSGPLGWDPGARAGQG VG*ETRGPSLQLAWS DGEGV/P GWRGSYRGHRRGP*PPAPWPW SGGHPGSPMEWPCPGTELQMR NRAGSRDLHSLGRAPPAATAPS |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20327 | 50695 | A | 20444 | 90 | 1181 | RAEPHLQVPGVPGSAQKPQGT QMAPVSPRRGPQRGWHTLGAQ RLLPQAALSSPAFPQHPGGRWA PRRRGQSSQGHSPESLPSERAQP HWNHPQLLSPCTPLSCP*GGPR QA/EQAGDSGSGTWVGLGAAP SERGAPMSARHWLRAPGRRPIF LLSALW*TPAWGGGPAASRSP GGPSSRVVGCPLCPLAPGPVPS VE*RPMSTKDLPPSPR*KP/PA GPAPV*/SPKAVGIPAWERPPT PETEGAGGSCAERLLAPVEMAP VSRGQRRDPEPGSRHG/DPPTDT AALGGPRPPQHLPRTRQHWI* GPGAPPTDTAALGDLRPQSPGL LMELG\PISRDPHGRGPWQGPV GKLWPGGQGSCPQSPPV |
| 20328 | 50696 | A | 20445 | 2 | 957 | IPSRKDHEKAEFEVHEVYAVDV LVSSGEGKVRVPPELAKRGD*E CSPDQMLLKLLFQAKDAGQRT TIYKRDPKQYGLKMKTSRAFF SEVERRFDAMPFTLRY*AMIVL GTSLTHRPYTQEHFFLSLPA*TC SVHVLTPSLSLPISFSLKVM*K NPKHDFCLRVGAILKYEQNGK T*WGVKDTSEYHLPCQAFEDE KKARMGVVECAKHELLQPFNV LYEKEGEFQKELHFGFPDYKISF L*VQKS*V*QRNFLSKHIFIFAIG EFVAQFKFTVLLMPNGPMRITS GPFEPDLYKSEMEVQDAELKA LLQSSASRKT |
| 20329 | 50697 | A | 20446 | 85 | 266 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 20330 | 50698 | A | 20447 | 207 | 1759 | LSQRALRLSPRARSFSLSPACPL PCLLALSLALSSRIEGLTTACG WGRETEAAAAQGKRGCSGGS KMSGEDQQEQTIVD/DSLVT KYKMGGDIANRVLRLSVEASS GVSVLSLCEKGDAMIMEETGKI FKKEKEMKKGIAFPTSISGTIN *PI/CHFSPFERSD\QDYIPPRKGD LVK\IDLGVPCWMGFIANVASH/ SFVVDVAQGTQVTGRK\ADVIK AAHLCAEAA\RLVKPGNQNT QVT\EAWNKVAHSFNCTPI\EG MLSHSLKQHVIDGEKP*FQNPT DKQK\RAHEKADFEV\HEVYAV DVLVKPQERARPKDAGQRTTIY KRDPSKQYGLKMKTSRAFFSE VERRFDAMPFTLRAFEDKKA RMGV\VECA\HELLQPF\NVLY EKEGEFVAQ\FKFTVLLMP\NGP MRITS\GPFEP\DFYK\SEMEV\Q DAELKALLQSSAKSEKPQKKK KK\KASKTAGEWPLVAFSAVLE TFRRKWKLGGLEVGPISPACCS CLHPPSHQTPRLCEVQFFFST |
| 20331 | 50699 | A | 20448 | 1 | 3825 | |
| 20332 | 50700 | A | 20449 | 1084 | 2429 | ARERSLRGSPAREREKERKCTA LSE*GEQMERKTNS*TKQTE*N RNEIGPRGAGPPGDAGSGRQPA LRPHVHKQTEKTTRVRTVLNE KQLHTLRTCYAANPRPDALMK EQLVEMTGLSPRVIRVWFQNK RCKDKKKSILMKQLQQQHS K/SGEQPLGRRLESGGGCASAA VSACPFLGEPWEIQGELGAPDG VCLYLHASKASLGFEASYFVWD RGFSLSQWQPRVAGSGRCAEP KAAWQCAAPASRAGGLCTPSA AAERSPVEKEGSSDAIECAPPR KAMQTLNHSRPGAPVSKVAEK ARPNSSTYCLLLAPQSLQGLTG TPLVAGSPIRHENA VQGS AVEV QTYQPPWKALSEFALQSDLDQP AFQQLGLLSAGGRSPRDTFRLG ARGPGAPARVPLHLPLPGVSAA P\VSFSESGSLGNSSGSDVTSLS QLPDTPNMVPSPVET |
| 20333 | 50701 | A | 20450 | 133 | 276 | |
| 20334 | 50702 | A | 20451 | 2 | 205 | WDTSS*SLRTPRSRQVSTRPRR KKEKLPSKGMFSSVSLPQVLTQ RHQRPTCSWSLCWQPQHLLLR S |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20335 | 50703 | A | 20452 | 182 | 411 | GRAWPAPPTSVTPRLRSPAESP RWPSAEERSSLP/VRGRRPGYG* VSCCGPRAPPGVNGDALRSARP AQLPA*RPQRH |
| 20336 | 50704 | A | 20453 | 786 | 1208 | GVHRGTHGRQKWRPCAPRAQ HSWGPGGRLPAGCRG*AGSCA/ PSLGL*CGAGPQGWRDP*TR RRTPRRPPRGPRPRVWMAPPAR SHPWRAAPRSAGAAPRPLGLG GRSGRETRPAPGGELQRPAAAG PPLMSCGWRVLA |
| 20337 | 50705 | A | 20454 | 385 | 727 | KAMSPVFPRHSHKWDLDLSRPLF TSAALLSACKILKLKVDKNKM VATSGVKKSYI*STV*TTREDW TAGRQRTWRCIYSTTEEKEDSG *SPSKGNGEGRGDAT*TTER*RS DTGL |
| 20338 | 50706 | A | 20455 | 568 | 3382 | HPGWVARGPGAGEGHAAGCG PARCQAGGPLQDGGCGGQGHR FGGGHVPEIKGGGFPHAGACAL EERQPR*QP*GVGKRGGGLFHA SSSPSSGGSRTPEAEG*GGA VCR AGDLGHIDDAGDHGDSGK\KE RVEEEGGKPKHVLSTSGVQSD AREPGEESQKADVLEGTAERLP PIRASGLGADPAQAVVSPGQGD GVPGPAQAFPGHLPPTKVEAK APETPSENLRTGLELAPAPGRV NVVSPSLEVAPGAGQGA |
| 20339 | 50707 | A | 20456 | 762 | 1245 | LRQYSVKMRIVPTILLNFGADP DLRDIRYNTVLHYAVCGQSL\S LVEKL\LEYEADLEAKNKDGYT PLL VARY*QLIPKLVKFLE\KG ADVNASDNYQRTALILAVSGEP PCLVKLLLQQGGEICNEG\MVD SQLRNMFISMVLLHRYPQFTAS HGK\QKHAK |
| 20340 | 50708 | A | 20457 | 346 | 608 | PKRRGAPLPVIPQSAS*KPKLPM GRPPPPVPSVSPGPLPGSLAIAP HSLEPHLVQSSCLVPPKTKQS KRKPGRGAQAPTLPNATEFSVC RNDPKEGRRSP*FPNRLLEPE APPRPSAGESPRPAAA/SPLPCSE EK/PTPQLCARERLAPSAAPPPP PRCGPAPLLEPSAWTPELARRA |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20341 | 50709 | A | 20458 | 340 | 889 | SAPFSSGERTPGCPEASPFPGGG GGNARPSGPAPHPSSAS*KPKL PMGRPPPPVPSVSPGPLPGSLAI APHSPEPQLVQSSCLVVPKTK QSKRKPGRGAQAPTLPNATEFS VCRNDPKEGGRSP*FPNRLLE PEAPPRPSAGESPRPAAA/SPLPC SEEK/PTPQLCARERLAPSAAPP PPPRCGPAPLLEPSA/EAEEGGW GAGPLGRALPPPPPGKGLASGQ PGVRSPDEKGADQRQPSGPRLC SAPAPRRRS/PPRRRRPSNFVPED QPHYVPGSASAGPRRSPRPPRR ELGAPSHLP |
| 20342 | 50710 | A | 20459 | 148 | 397 | GHKELVTGTEAIELAHAYETCH AVPRTIAKLVPKTH\LMSESEW RNLGVQQE/RQGWVH\YMIHEP EP*HFGCSRRLTQGTQRK |
| 20343 | 50711 | A | 20460 | 139 | 272 | VLKPGGSYSFGSPSCNSSH*LIG FQKWKDVPCEDKFSFVCKFKN |
| 20344 | 50712 | A | 20461 | 440 | 1167 | ARDSLQLSMAQTSSYFMLISCL MFLSQSQGQEAQTELPQAR\ISC PEGTNA\RSYCYF*WKTRET W\VDADLYCQNM\NSGKLGVC GSPRAEGCLFWPQLI*GGVGT* WTFNVLDLGLQ*PPKRTRRWH WEQWGPLVSLQSSWGHWEPPS RCLNPGY\CVSLDLQSTRISRN WKDVPFVKDK\FSFVCKVQKT RGQAGKIQCLELTPAITNGVQK LNRTISPTQLNLVTLFSAEFALLI FNSFT |
| 20345 | 50713 | A | 20462 | 3 | 322 | |
| 20346 | 50714 | A | 20463 | 1 | 420 | DLYELVQYAGNIIPRLYLLITVG VVYVKSFPQSRKDILKDLVEMC RGVQHPLRGLFLRN\YLLQCTR NILPDEGEPTDEETGDISDSMD FVLLNFAEMNKLWVRMQHQG HSRDREKRERERQVSW\RCKCG TLQ\QIVLTG |
| 20347 | 50715 | A | 20464 | 1 | 1446 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20348 | 50716 | A | 20465 | 3 | 2564 | LGAGAACCRLWGVAMPTTQQ SPQDEQEKLLEDAIQAVKVQSF QMKR\CLD\KNKRIGVRHKTML RNMLGVELRTSMLSPKSYELY MAISDELHYLEVYLTDEFKGR KVADLYELVQYAG\NIYPQGF YLLVHSLSCNNVKSFPQSR\DI LKDLVEMCRGVQH\PLRGLFLR NYLLQCTRN\LPDEGEPTDEETT GDIRDSMDFVLLNFAEMNKLW VRMQHQGHSRDREKRERERQE LRILVGTNLERLSQVE\WCKCG TLARQIVLTGILEQVVNCRDALA QEYLMECIIQVFPDEFHLQTLNP FLRACAE\HQNVNVKNIIIALID RLALFAHREDGPG\IPADIKLFDI FSQQV\ATVIQSR\QDMPSE\DV VSLQVSL\IN\AMKCYPDRV\DI YV\DKVLGNNSGRIFNKLNLLEHI ATSSAVSKGNFTRLLGKLPVGH FTNNILT\VL\KLKHFHPLFGYFD YESRK\SMSCYVLS\NV\ADYNT EIVSQDQVDSIMNLVSTLIQ\DI P\DIQVDEPDPEDF\ADEPEALV ARFIHLLRSEDPDQQYLILNTAR KHFGAGGNQRIRFTLPPLVFAA YQLAFRYKE\SKVDDKWEKKC QKIFSFCPTKT\I\SALIKAE\AQE LPLRTFSFKGGT*LA\AGELGFG NHG\TVAY\EFMSQGIFSVWKD/ EKSGDFPKAQLGWPFTFGSIGA LFEVVEVLSVEEDSWNPLR\TQ |
| 20349 | 50717 | C | 20466 | 23 | 385 | |
| 20350 | 50718 | C | 20467 | 16 | 435 | |
| 20351 | 50719 | A | 20468 | 1 | 436 | |
| 20352 | 50720 | A | 20469 | 1 | 747 | |
| 20353 | 50721 | A | 20470 | 1 | 864 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20354 | 50722 | A | 20471 | 2 | 2138 | VGRAAAAAA AVAVPLAGGQE GSPGGGRRGSRGTTMVKKRKG RVVIDSDTEDSGSDENLDQELL SLAKRKRSDSEEKEPPVSQPAA\ SSDSETSDDDEWTFGSHKHKK KGQARTLEQKGTMMKKQANKT ASSGSSD/RTDSSAESSAP\EEGE VSDSDSNSSSSSSSDSDSSSEDEE FHDGYGEDLMGDEEDRARLEQ MTEKEREQELFNRIEKREVLKR RFEIKKKLKTANKKEKKEKKK* QEEEQEKKKLTQIQESQVTSN KERRSKRDEKLDKKSQAMEEL KAEREKRKNRTAELLAKKQPL KTSEVYSDDDEEEEDDKSSEKS DRSSRTSSSDEEEEEKIEPPKSQP VSLPEELNRVRLSRHKLERWCH MFAFFAKTVTGCFVRIGIGNHNS KPVYRVAEITGVVETAKVYQL GGTRTNKGLQLRHGNDQRVFR LEFVSNQEFTSEFMKWKEAM FSAGMQLPTLDEINKKELSIKEA LNYKFNDQDIEEIVKEKERFRK APPNYAMKKKTQLLKEKAMAE DLG\DQDKAKQIQDQLNELEE RAEALDRQRTKNISAISYINQRN REWNIVESEKALVAESHNMKN QQMDPFTRRQCKPTIVSNSRDP AVQAAILAQLNAKYGSGVLPD APKEMSKASVGQGKDKDLNSK SASDLSE\DLFKVHDFDVKIDLQ VPSSSESKALAITSKAPPAKDGAP |
| 20355 | 50723 | A | 20472 | 438 | 709 | FLSQSWIFKQIRASRTLFLVAFS SNTFTSCRSFCSSEAMGAGSG RSPQLQPRRRNRKPRAEPSNR AQTPTRTS/LRRCSLRPHRPCAR SR |
| 20356 | 50724 | A | 20473 | 2 | 1315 | ILQKRIGGFLDALVRNSQPARYI NDYQLSNYGLDMLGPSLDPAP MASEELQKDLEEVKVLLEKAT RKTEKSKIETIKNKLQQKSQK KAELLDNEKPAAVVAPITTYT KGGGGEERGGEAPTSNEAQAT EVRGGAGGGKDKDDGDRER\P RKTRGGRARTE*NNRHEQ*IQI KKRRETEKERRNEKGRRRHKT ATQKRREERRARRVGEGTRK REQPAHEQEHAATTTHTRPPAP/R RTRKTQTHNRKERKKEE |
| 20357 | 50725 | C | 20474 | 43 | 162 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20358 | 50726 | A | 20475 | 2 | 363 | YEPLDSNKRIGHTSSSSYVLCLCS SLAIFSNFMGNLLSFCGVLKLLK SLACIH*RFFFN*A**VFIHSSRE Q*FINVCSSCPAFFNPERRNELY ASLLSFVPSALVPIFEDNVSYLF VKSF |
| 20359 | 50727 | A | 20476 | 505 | 2294 | VYSDAKSIYCLLFAHSQRPPCV FNENDPQNSGTVHTVFLVGLTD HRHARAKIESWAGEAAPFTLV AASADKLFGDLHISKYCGRIAV SVFQFQQYCGLCDSTS/SLQQY CGLCGST*HSGSTVASVAGLHI VAVPWPLWQDFTLWQYRGLC/ AQDFTLWQYHGLCGRTSRVAV PWPLWQYFTLWQYCGLCGRTS HC/GQYRGLCGRTSHCGSTVAS VAGLHVWQYCGLCGSTSRC/E QYHGLCGRTS/RLWQYHGLCG RTSYC/EQYRGLCGSTSRCG/MY RGLCGRTSH/WWQYCGLCSSSTS YCSRTVA\LWQYFIL\CASTY/W QQYHGLCGNTSYCGIL\QLQQY SGLCSSTSYWGSTVASVAVLHI AAVLWPLRQYFILQQNRGFCG NTSYCG/SYFILWQYHGLCGST SYCG/SYFILQQYHGLCGSTSYC /EQYRGLCGSTSYC/TQYCGLCG SSSYC/AQNCGFCGNTSYCGSTS /VLQQYHGLCGSTSYCGRTV/V FCGSTSYWGSTSYCGSTVASLA VLHIVAVLCPL*QYFTTNKTKN KTKPGSCHLTYPGGAAGGPSL* APGGVAGTVGSASRSASWGLP EWICCLRDPKSLSPFYWGFVW |
| 20360 | 50728 | A | 20477 | 2 | 554 | LSSTGGLHAGRLCCSPCLLVIPL KSSQHIF\RVL\NTNIRLGRRKNS PLPITAHLRVWARRYA\HV\VL KADIDLT\K\RAGEL\TEDE\VER VITH/ILQNPRQYKDPKTGFFEQ DKKDVK\DGKYSQVPSQLVWD NKLP*KTWEPTERRFRAH*/RGL RHFLGAFRVRGQAHQEPLGRR GRHRWVCPRRK |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20361 | 50729 | A | 20478 | 50 | 774 | LFGVVYTGFC LGVW TAGVGGV PGPNFPRPILTLVRGP*GKGVG WVAGPGQLRPTGPWSI*VSHPT PPGPLSISYRAQAAGGQGPAPV THPQGRQEP*RQLPPGGPLA/RH PPKAPDPARPHP/RQHRGPS/ST APKGRCWQH KQEPSGHPAGHT PGRPG/PPQAPRPS PWVGPGPQ TPTPCP*DEPHRPPGLQWRPFS PLAMAPMGRLQALPGLDQRGQ TVSPLRLLGALES LAWLP SAFIA |
| 20362 | 50730 | C | 20479 | 156 | 908 | |
| 20363 | 50731 | B | 20480 | 1 | 804 | |
| 20364 | 50732 | C | 20481 | 278 | 551 | |
| 20365 | 50733 | A | 20482 | 169 | 1144 | INYSLEKHV GALGRVL FSL*RA GCPGMGSTRERGLYL GKHRGS GGIW*ALAGP*KSRGDSVSLTQ GH THVCSRSPR*ADSPPG/SHLS PVPHSVEVAGHVLPATRAAV PCSASAGA*QSTYRTGVHQGNP TV*TK/PSRRPSGGVAK*FLPSA VRGEPGAKPLVDDLLPGWSLA THGQPPLVAAPGSGLWGRPAD A*GCETAGGSPCPRSTSRPSGPS GVQGCPLG*AGSGASASRSEPP GSTSCCPRAP/T*PAAPCVDPWP AGDQWRSHGYLPPSREL*G/W MPPSRPATLPQLAFARQRQGNR FDAAFESSGEDFHQM PRVGRM |
| 20366 | 50734 | C | 20483 | 31 | 90 | |
| 20367 | 50735 | B | 20484 | 48 | 197 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20368 | 50736 | A | 20485 | 5447 | 5642 | PRDMESCYNPGLDGIIEYDDFK LNSSIVEPKEPAPETADGPYLVI VEQPKQRGFRFRYGCEGSPHGG LPGASSEKGRKTYPTVKICNYE GPAKIEVDLVTHSDPPRAHVAHS LVGKQCSKLGICAVSVGPKNM TAQFNNLGVLHVTKKNMMGT MIQKLQRQLRSRPQGLTEAEQ RELEQEAKELKKVMDLSIVRLR FSAFLRASDGSFSLPLKPVTSQP IHDSKSPGASNLKISRMDKTAG SVRGGDEVYLLCDKVQKDDIE VRFYEDDENGWQAFGDFSPTD VHKQYAIVFRTPPYHKMKIERP VTVFLQLKRKRGGDVSDSKQF TYYPLVEDKEEVQRKRRKALP TFSQPFGGGSHMGGGSGGAAG GYGGAGGGGSLGFFPSSLAYSP YQSGAGPMRCYPGGGGAQM AATVPSRDSGEEAAEPSAPSRT PQCEPQAPE\MLQRAREYNARL FGLAQRSARALLDYGVTDARR ALLAGQRHLLTAQDENGDTPL HLAIIHGQTSVIEQIVYVIHHAQ DLGVVNLTNHLHQTPHLAVIT GQTSVVSFLLRVGADPALLDRH GDSAMHLALRAGAGAPELLRA LLQSGAPAVPQLLHMPDFEGLY PVHLAVRARSPECLDLLVDSGA EVEATERQGGRTALHLATEME ELGLVTHLVTKLRANVNARTF AGNTPLHLAAGLGYPTRLRL |
| 20369 | 50737 | A | 20486 | 3 | 346 | PQTITDELWVTLTVEVWDIST/ LFPGN*SHA/TLPSH*NLITLTP NANI/AIPQHALKGLKPVITRL QHGLLKPINSPYNPILPVQKLD KSYRLVQNLRLINKIVSPIHPV PN |
| 20370 | 50738 | A | 20487 | 1 | 808 | YGTSLLLPWQLITCPLPSH*NL ITLTPNANI/AIPQHALKGLKPV ITRLQHGLLKPINSPYNPILPV QKLDKSYRLVQNLRLINKIVSP HPVVPNPPAFTSQITQAVSQAL GIQWNLHIPYHPQSSGKVERTN GLLKVHLTKLSLQLKDWTVL LPLALLRIRACPRDATGYSRFEL LYGRTFLLGPNLIPDTSPLGDYL PVLQQAQAANLLLPTDPQPH EDTLAGRSVLVKNLTPQTLQPR WTGPHFIISTPTAVCLQDPPH |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20371 | 50739 | A | 20488 | 2 | 513 | CCPIASEAQ*TITDAELWVTLTV EAQSLLRVFLSYLPTLTHKYGT SLLLPWQPITCPLPSR*NLITLTP LN/GQYPIPQHALKGLKPVITRL LQHGLLPINSPYHSPILPVLKP DKAYKLVQNLRLIYQIVLPIHP VVPNPYTLSSVPPSTTHYSVL DLKHAFFTIPLQP |
| 20372 | 50740 | A | 20489 | 1 | 1893 | |
| 20373 | 50741 | C | 20490 | 1 | 1806 | |
| 20374 | 50742 | A | 20491 | 1 | 645 | MTSGPQINQPKKHLTNFKSEPS DL/FPSSPGCSLPAED*RCPIALE AP*TITQARVTLIVEGKSVPLV NTEATQSTLPSFQGPVSLASITV VGIDGQASKPLKTPLLWCQLG QHSFMHSFLVIPTCPVLLGRDI LTKLSASLTIPGLQPHLIATLLP NPKPPSCLPLSPHLNPQVWDIS TSLATDHMPITIRLKPNHPYPAQ RQYPIPQHAKD |
| 20375 | 50743 | A | 20492 | 113 | 328 | LGSGAWGGGDLPWEINPLSSCS LLREKDLLTTS GPQTTS PRNISP ILNRDPTVQLTWQPLPELELW PKAL |
| 20376 | 50744 | C | 20493 | 183 | 254 | |
| 20377 | 50745 | A | 20494 | 1 | 511 | MWKGPGLDMYGKSSVSPKTS DILGRDTLLLALKVQTVVLQTA CGEGHVAGNCGRPLETEGSLQ LTATKKLRDSVLQPKSPEFCQQ FTRAWNRTQVPDETEAPAGTY AAQSGDLPWEINPLSSCSLLHE KDPPTASGPQTTS PRNISPILNR VSEVSDHAGTPALVLHP |
| 20378 | 50746 | A | 20495 | 1 | 1108 | MWESLELPGNIFNGFDQNADN DMDDEIQAEVISDGDDEFVGN WNKPRDLVPCILATLALTKRGQ DTAQTMASEGARPKHWQLPGG VGPVGAQKSRIEVWEPLPIFRR MYGKACMSRQKFAAGAGFSW YVPVAVVGAKVHDVNLHMLS FPSKWKLHTCMKFGAVTQIVTS LGRSSCSLLEKDPPMVL RPTSP RNISPISNLTKETRFIRGPKTPAP VTDWEGSLPLVFNHCRDASLII HPGFRGVRPRRDACLSPSPLAN LINLTFKVYNNRKKLQFLAFTV RQTSAMSPA HKNFQTPEPQRPG IPPEPPPPGACYKC/HEIRPPGQG MPAAQDSS*ATS/LSVRDPTGN WTVQLTWHPLPELELWPKAL |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20379 | 50747 | A | 20496 | 128 | 302 | TAAARHSSRTSSPRSLQVLEI WPSGQGMPAAWDSS*AASHL WQPLPEPLELWPKAL |
| 20380 | 50748 | C | 20497 | 80 | 106 | |
| 20381 | 50749 | A | 20498 | 196 | 575 | |
| 20382 | 50750 | A | 20499 | 1 | 505 | TKETRFIRGPKTPAPVTDWEGS LPLVFNHCRDASLIHHPGFRGVR PRRDACLSPLANLINLTFKVY NNRKKLQFLAFTVRQTSAMSP AHKNFQTPEPQRPGIPPEPPPPG ACYKC/HEIRPPGQGMPPAAQDS S*ATS/LSVRDPTGNWTVQLTW HPLPEPLELWPKAL |
| 20383 | 50751 | A | 20500 | 372 | 563 | LRSADLPWEINPLSSCSLLHEKD PPTSSGPQT/TSRPNISPILN/PEK KETRFIRGPKTPAPVMD |
| 20384 | 50752 | A | 20501 | 96 | 505 | WS*QP*GLGSHRHHRRRHHRSS SSSSSSSSSSSKSNSDWQPLPEPL ELWPKAL |
| 20385 | 50753 | A | 20502 | 79 | 207 | |
| 20386 | 50754 | A | 20503 | 583 | 736 | |
| 20387 | 50755 | A | 20504 | 99 | 246 | DLIFHQRHSVSAESLTMHGLNN *QTSKRVRVQGTWQPLPEPLE LWPKAL |
| 20388 | 50756 | A | 20505 | 654 | 719 | |
| 20389 | 50757 | A | 20506 | 71 | 951 | LRSGDLPWEI/NPLSSCSLLREK DPPTTSGPQT/TSRPNISPISNPR/ PKETRFIRGPKTPAPVTDWEGS LPLVFNHSRDTSLIHPGFRGVR PRRDACLGPSPLAASPTFLGKG PAAPRQTELGPNSSASAPPPYN PFIASPPHTWSGLQFPSMTSPPP PAQQFTLKKVAGAKGIVKDLIN LTFKVYNNRKKLQFLASTVRQ TPATSPAHNKFNFTPELQQPGVP PEPPPRGACYKFQKSGHRAKEC LQPRIPKPHPICVGPVHWKSDCP THLAATPRAPGTLAQGSLLTPSQI |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|---|
| 20390 | 50758 | A | 20507 | 1 | 1010 | CSEYEDSSPAPVPATDLSSTLSS SVPQPQDTGTSQQLHPLDPWHE LLRAQELQGATNHKGYSHAEH EHAGLVQGGNGALAFSNSGH RHAVPTISSGTGRRRTPSSSAFG LLNLHQWFVSGFQAFSDRLKA ALSASLLLRFGDSDWLPSSSAC KCLMLGLHFVIVGNICATLKEK YSSMLHLDVTMKNKEKRTRL QKRKKGMPPHPAYEDLNIAAIT LPANVVLHQPSGFRITSGQLDPV WWSLDTDAHEIWCQDPGLGSG DFPWEITPLSSYSLLHEKDPPTT SGPQTTSRNPISPNRQRRQV LSMDPKLRHRSRTGKAAPWC LIIAGTPL |
| 20391 | 50759 | A | 20508 | 3 | 539 | IVDDCGGAFTMGVIGGGVFQAI KGFRNAPVCRLLEAPLFIYSCS RSVSPTVNVSSERAESRPTLFM AVSLHMAWCLAHIGIRHRLRG SANAVRIRAPQIGGSFAVWGGL FSTIDCGLVRLRGKEDPWNISIT GA\LTGAVL\AARSAPLAM\VGS AMMGILL\ALIEGVSILL/TR*T ATV |
| 20392 | 50760 | A | 20509 | 3 | 778 | GEQRAALPPAPKECTHPNVTNT LVQAESSDAGVRLRWGRGLTA RPDASAMEEYAREPCPWRIVD DCGGAFTMGVIGGGVFQAIKG FRNAPVGIRHRLRGSANAVRIR APSTTGSAFVWGGLFSTIDCGL VRLRGKEDPWNISIT\SGA\LTGA VL\AAP\SGPLAMGGLQQ*WGG ILSAPHLRAFGILL/TR*TA\QQF RKWAPNSLEDPA\SQLPPKDVTP APGYPA\SYQQYHLRKPLATMGA TSSVFPDGGSTLKGAGFGPG |
| 20393 | 50761 | A | 20510 | 1 | 231 | LRWRVWSLSLLMFRCVRSFFLL VGSWSRWFRSEAADLCGECYS S*GSTSGVVRFSRWACGLAGLR SEAADLAPPTSC |
| 20394 | 50762 | A | 20511 | 318 | 494 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20395 | 50763 | A | 20512 | 1 | 1234 | MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKET GVSHITRHDMQLQIPKQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPQQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNISIDSWKNAGR VFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGSLLRSQM PCADLSILKEAAETLDSTSTRNS AFLGNTHDEAPIVHVFIPLAYS TNIWSLIFNPTTMIMMCSRDLW SSCENKRVDLAFGLVYSGTPVQ KLEQMKFSPQLGCNHFESKDR NDFLFAPEEIEKDPQGESLLCDF MTKTPKAMATKAKIDKWDLIK LKSFCTAKETTIRVKNQPTWE KNFAIYPYDKGLISRIYKELKQI YEKKIKQPHQKVDERLLNLT DRLTGEKAYRFIKVQVLRVTQ GMKIQRARRSKELQGDGDEIQR WKRLHSPRLLGEEPRIIFKLD SANDMHKSAPFSSLQSPLWHQP VMQEVERQYKEKKDLVREGG KCRCQGRPGKVVLTELSLEAR GGWMEDIPSRRTSKCGPWELV SHCVQNWWVLGLTDFKNEAS DPRGVKLQFTTVSVTALKAAAR LELLVLPGLLVVSLASGVKLQT FAVSVTAHKRSVDPKTEGAGS GLGQPRKGLSQCSSGPKG*YPE STKNLNKFTRKKSNNPIKRLMK |
| 20396 | 50764 | B | 20513 | 1 | 531 | |
| 20397 | 50765 | A | 20514 | 1139 | 1562 | GALQPTAALWEPLSGLAKARA GTLSLQGSVEGVA*AGTGAAC GACGPDGVPGGRLGGPRTGS SRPALSHFITEEDKDQRVQDQL GGVWHRMEIHEQHVGKQQUEE GDVEDHIPGEDHEGGGEERHIV PKQLLVLDVDRFLPK |
| 20398 | 50766 | A | 20515 | 1 | 1597 | |
| 20399 | 50767 | A | 20516 | 461 | 1601 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20400 | 50768 | A | 20517 | 1 | 914 | MNNLRRAALRAVTLTAKVCSF TPEPARPQTHQKEETPNTSEHQ KEQTPDTPPLRTVTLTARVHGF LEVSETKNPPIPDTPATREAEG RSRLAVYSTRDSPCVACSGSYT QAQGSGLGRKFQDPVSLFEDLTK NTPEPNLRPITSKPVLVQETLSN FALFLKESNGP\VKVWGS\H\KG LT*KALHGF\H\H\EF\G\DN\TAR LYQVQGP\H\N\PLSQK\TTVGPK\ DEESH*\DLGQCDCLTKNGVA DVSI*\R\FCESHSSGDH\CIIG\RTL VVPWKKPDDFGQRVGNE\ESSK TGNAGKSVWPCGVNWIAQ |
| 20401 | 50769 | B | 20518 | 8 | 173 | |
| 20402 | 50770 | C | 20519 | 13 | 180 | |
| 20403 | 50771 | A | 20520 | 3 | 486 | VTETWKCAGIPHRYRSFESC/IW NPVINSRMDYAGPVC\FKNADI GRCAHEKLRED*\DGAAPGEIGI QPEADATPYFATPTPVLT\HG PCAAESEPALLIGSKQFGLSRNSHI AIAFDDTKVKNRLTIELEV\RT EAEFRLLFYMARINHADFATVQL RNLGPY |
| 20404 | 50772 | A | 20521 | 1 | 459 | |
| 20405 | 50773 | A | 20522 | 2 | 239 | SDSSGSREVDPAATTMPGAA GVLLLLLLSGGLGGVQAQR PQQRQSQAHHQQRGLFPAVLNLA SNALITTNATCGEKGPEMYCKL VEHVPGQPVRNPQCRICNQNSS NPNQRHPITNAIDGKNTWWQS PSIKNGIEYHYVTITLDLQQV FQIA YVIVKAANSRPGNWILERSL DDV\EYKAWQ*\H\AVT\DT EALTP*PN*SPELGHRQNAQD*\EVI CTSFYSKIHPLNGEIHISLINGR PSADDPSPELLE |
| 20406 | 50774 | A | 20523 | 2 | 445 | |
| 20407 | 50775 | A | 20524 | 1 | 2765 | MGRRRLLVWLCABAALLSGA QARGTP\PWGRGLR/LPGASRYSL YTTGWRPRLRPGPHKALCAYV VHRNVTICILQEGAESYVKA EYRQCRWGPKCPGTVTYRTVLRP KYKVG YKTVTDLAWRCCPGFT GKRCPEHLTDHGAASPLEPEP QIPSGQLDPGPRPPSYSRAAPSP HGRKGPGLFGERLERLEGDVQ RLAQTYGTL SGLVASHEDPNR MTGGPRAPAVPVGFGVIEGLV GPGDRARGPLTPPLDEILS |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20408 | 50776 | A | 20525 | 2 | 363 | RFTKVEMKEK\MLSAAREKGR VTHKGKPISLKADLSAETLQAR REWGPIFNILKEKNFQPRISYPA KLSFISEQEIKYFTDKQMLRDFV ITRPALKELLKEALNMERNNW YQPLQKHAKL |
| 20409 | 50777 | A | 20526 | 1 | 1566 | |
| 20410 | 50778 | A | 20527 | 1 | 1604 | MAILFEMRLGQQSSAKFPGFQS SFFPVI PVNKPSPGKFKRDRAHFS STRLLWPDCQISQLWGGYLRK KGSSPSQGLIDKTPSPWKKAPR ERGGCGRSFSRFKHPCLTALKR AADLPAQHSSSAKDTSQKGPTD TSYRRALAGIWQVPPLGRSFQK KDQAAIFAVVQPLQVIPRQTGS GVDLQQTSADWQQRGLTVRR KTNKQKGIACSLKDPIRGHQHQ RPKDHNFSPAREQNWTENEFD KLTEVGFRRWVITNSSELKKHV LTQCKDAKNLERSLEELLTRIPS VEKNINDLMELKNTARELREA YTSFNSPIDQAEERISVIEDQFN KINREDKIREKRIKRNKQSLQEI WDYVVRPNLQLIGVPESDKEN GTKLENTLQNIHQENFPNLAREA NIQIEI\QRTQPQRYSLRRATPRH IISV/RFTKVEMKEK\MLKAVRE KGR\VTHKGKPIRLTTADLSAET LQARRQSGGQYFNIL*RKGFQPR R\ISYPAKLSFISEGEIKYFIDK\Q MLRDF\VTTRDWPALKEHQAC |
| 20411 | 50779 | A | 20528 | 58 | 1081 | SSMAKPC\GVRLSGEARKQVEV FRQNLFQEA E\EFLLR\FLPQKII Y\LNPA SFQEDFPFNVA*/LLNLS SGAPLGHPPIRPLHPKDDME TDKAGRRKEVP*SVGFFPWGN* GKFL\SLVCPGLKPE\WDFSKR NCILGDLHWIQTDPSPRFEDGN DFGGSQSRKKVLEKG*MPVKT KV EAF\QTTISKY/FSSERGDAC GPRPPKETHVMDYRALVHERD EAAYGELRAMVLDLRAFYAEI VKSSGIGAHVSFKVQNIHSSYC SGPTVSPTCVTGLPASQSPDSG AQLASSSGSHTCAAGGAACQS RALRLHSSALGWSMGLGTVEQ GAALIEEVQAAQEPTG |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20412 | 50780 | A | 20529 | 1632 | 1932 | KEGCELCRCCCRPGPPASSHGQ PHHVFPF/VLSMASPWAVSPSS VNVSQFFIC/TCQDAKTEWLDC KHVVFGKVKDGMNIVEVMEH LGSKNGKISNQQEDHHC |
| 20413 | 50781 | A | 20530 | 245 | 740 | GAWKARSDCSSNP*NYVNRLE LFADKVPKTAEF\QALSTGEK GFGYKGS\AFHRIIPGF\TCQSGD FTRPYSIGGKSHLPGRNLMTRT FILKHTGPGILSMANAGPSVNV SQFF\CPAKMPRTEWLDCKHV VFGKVKDGMNIVEVMEHLGSK NGKISNQQEDHHC |
| 20414 | 50782 | A | 20531 | 135 | 1427 | GKPTFASRQQPLAECEPASSAL QRRWLWRWRWWLRRRRRQR RSSGSCQGPAGPLGGPPANRG AAPQGSAMNYNNAKDEV DGG PPCAPGGTAKTRRPDNTAFKQQ RLPAWQPILTAGTVLPIFFIIGLI FIPIGIGIFVTSNNIREIEIDYTG EPSSPCNKCLSPDVTPCFCTINF TLEKSFEGNVFMYGSLNFIYQ NHRRYVKSRDDSQLNGDSSAL LNPSKECEPYRRNEDKPIAPCG AIANSMFNDTLELFLIGNDSYPI PIALKKKGIAWWTDKNVKFRN PPGGDNLEERFKGTTKPVNWL KPVYMLDSDPDA*WIHK\DDFI VWMRTAALPTFRKLNRLIQRK SDLHPTLPAGRYSLNV\NAYYP VHYFDARKRMIMSAISWMGGK NPFLGMAYFAVGAI SFHLGVAL LGINHKYRNSNTADITI |
| 20415 | 50783 | A | 20532 | 1 | 370 | |
| 20416 | 50784 | A | 20533 | 1 | 1104 | LREFANFDFDIWRKKYMRWM NHKKSVMDFFRIDKDQDQK ITRQEFIDGILSSKFPTSRLMSA VADIFDRDGDGYIDYYEFVAAL HPNKDAYKPITDADKIEDEVTR QVAKCKCAKRFQVEQIGDNKY RFGDSQQRLRLVRILRSTVMVRV GGGWMALDEFLVKNDPCRAK GRTNMELREKFILADGASQGM AAFRPRGRRSRPSSRGASPNRST SVSSQAAQAA\SPQVPATTPK GTPIQGSKLRLPGYLSGKGFHS GEDSGLITAAARVRTQF\ADS KEGLPSRPGSSSLEAKFGSR\AS SRRGSDASDFDISEIQSVCS DVE TVPQTHRPTPRAGSRPSTAKPS KIPTPQRKSPASKLDKSSKR |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20417 | 50785 | B | 20534 | 527 | 4627 | |
| 20418 | 50786 | A | 20535 | 37 | 315 | |
| 20419 | 50787 | A | 20536 | 1314 | 1577 | HGSGSAPTCRWPRTOGRCREIC ADGFSGVMRNCTG*EAASGR* CKSFVHVYLQLRCACSVCHSA GSDSFQLQRSPTHTPSTCTHALV |
| 20420 | 50788 | A | 20537 | 1 | 1652 | MQATKTESGRNGKPGQPSNRC HYLLNQGWVANSGKGGRTNIP DKELKSGDDPENVHITSFQYLA LAAFPRGRARDLQLAMTEPPHP SVGSCAARASLTSAAPCSTAPSP INHPKAEECGCTARDWQAAPP AARVRDPLGEASWAPESYVC NCSVVGSLNVNRCNQTTGQCE CRPGYQGLHCETCKEGFYLN TSGLCQPCDCSPHGALSIPCNSS GKCQCKVGVIGSICDRCQDGY YGFSKNGCLPCQCNMRSARCD ALTGACLNCHENSKGNHCEEC KEGFYHSPDATKECLRCPCSAV TSTGSCSIKSSELEPECDCEDG YISPNCNKCENGYYNFDISCRK CQCHGHVYLISTPKICKPESGEC INCLHNTTGFWCENCL*GYVH DLEGNCIKKEVILPTPEGSTILVS NASLTTSVPTPVINSTFTPTTL* TIFSVSTSENSTALADVSWTQF NIIILTVIIIGVVLLMGFEGAGY MYRENQNRKLNAPFWTIELKE DNISFSSYHDSIPNADVSGLVED DGNEVAPNGQMTLTTPIHNYK |
| 20421 | 50789 | A | 20538 | 1 | 177 | |
| 20422 | 50790 | A | 20539 | 1 | 480 | |
| 20423 | 50791 | A | 20540 | 410 | 896 | FSCLKRMHIKAMPEDAKGQDW IALVKAAAAAAKNKTGSKPR TSANSNKDKDKDERKWFKVPS KKEETSTCIATPDVEKKEDLPTS SETFGLHVENVPKMVFPPPEST LSNKRKNNQGNFQAKRARLN KITGLLASKAVGVDGAEEKED YNETAPMLEQV |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20424 | 50792 | A | 20541 | 1 | 1526 | LKDEEDFFDFKAGEEVLARWT DCRYYPKIEAINKEGTFVQF YDGVIRCLKRMHIKAMPEDAK GQVKSQHPLSWCCPIDPAGSCN QSMGSEDWIALVKAAAAAAA KNKTGSKPRTSANSNKDKDKD ERKWFKVPSKKEETFNLLLATP DVE/RRKEDLPTSS/EKHL*GLH VRRNVPKMVFPQPESTLSNKRK NNQGN\FQAKRARLNKITGLL ASKAVGVDGAEEKEDYNETVA PMLEQA\ISPKPQSQKKNEADIS SSANTQKPALLSSTLSSGKARS KKCKHESGDSSGCIPPKSPLSP ELIQ\VEDLTLVSQLSSSVINKTS PPQPVNPPRPF\KH\SERRRRSQR LGTLP\MPDDSVKVVSSPLSSPL D/EGKVFS/LSSSSKISQESSS/IPE VPDVA/HICPLEKLGPCLP\LDLS RGSEVTAPVAS\SSYRNECPRA EKEDTQMLPNPSSKAIADGRGA PAAAGISKTEKKVKLEDKSSTA FGIRSWDFSALLMKIPSYSPISLS GLPES |
| 20425 | 50793 | A | 20542 | 363 | 1187 | FHITMCGICCSVNFSAEHFSQDL KEDLLYNLQKRGPNSSKQLLKS DVNYQCLFSAHVLHLRGVLT QPVEDERGNVFLWNGEIFSGIK VEAEENDTQILFNYLSSCKNES EILSLFSEVQGPWAFIYYQASS HYLWFGRDFFGRRSLLWHFSN LGKSFCLSSVGHPIWNWQISG KKFQHLDFFRIDLKSTVISRCIIL QLYPWKYISRENIIEENVNSLSQ ISADLPAFVSVGSQMEGQTVSL EKPVVPLNMDVATSWHWETH AVFFPCATYR |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20426 | 50794 | A | 20543 | 1140 | 2372 | CCHKLHWRLIAVIFPMCHLQER YFKSFLLMYT*KEVIQQFIDVLS VAVKKRVLCLPRDENLDSQME VLENV**GKANVGNPVFWGGL D/CPWLLATLLDRHIPLDEPLVL LNVAFAIEEKTMPPTTFNREGNK QKNKCEIPYPKNFSKDVA ADSPNKTCQCAPDRITGRAGLK ELQAVSPSRIWNFVEINVS MEE LQKLRRTRICHLIRPLD TVLDDSIGCAVWFASRGIGW LVAQEGV KSYQSNAKVVLT GIGCRWSNL QGYSPSSVS AFKSHGLGRIGIKE IMMEL GRISSEILGRDDRIVIG DHGKEARFPFLG*/RMLSP FLNS SARFGEKANLDFTPR GIGELPF NALQPVELGALT ASALLPKRAM QVFGSRIAK MEKINEKASDKCG RLQIM SLENLSIEKGTKL |
| 20427 | 50795 | B | 20544 | 70 | 464 | |
| 20428 | 50796 | A | 20545 | 18 | 552 | |
| 20429 | 50797 | A | 20546 | 1 | 1257 | |
| 20430 | 50798 | B | 20547 | 223 | 342 | |
| 20431 | 50799 | A | 20548 | 9 | 5293 | KIHRHRLSPATEKGAASSGEGD KDPPPPAHEDIAVKGTATAAGT GPGTGAAAAAAAAAAVPPHPNI RALQTQAPQQIPRGVPVQQPLED RIFTPAVSAVYSTVTQVARQPG TPTSPYSAHEINKGHPNLAATP PGHASSPGLSQTTPYPSGQNAGP TTLVYPQTPQTMNSQPQTRSPF FPKGLKIQPPARATIPNSKSFPFV PGAQTPTAVYQG*FRHIMMV NHLPLPYPVPQGPQYCIPQYRH SGPPYVGPPQ |
| 20432 | 50800 | A | 20549 | 1 | 78 | |
| 20433 | 50801 | A | 20550 | 1 | 2805 | MAKGFYISKSLGILGILLGVAA VCTIIALSVVYSQEKNKNANSS PVASTTPSASATTNPASATTL D QSKAWNRYRLPNTLKPDSYRV TLRPYLTPNDRGLYVFKGSSTV RFTCKEATDVIIHSHKKNLTLS/ QGHRVVL RPPDIDKTELVEPTE YLVVHLKGS LVKDSQYEMDSE FEGELADDLAGFYRSEYMEGN VRKV VATTQMQAADARKSFPC FDEPAMKAEFNITLIHPKDLTAL SNMLPKGPSTPLP |
| 20434 | 50802 | A | 20551 | 1 | 239 | |
| 20435 | 50803 | A | 20552 | 1 | 654 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20436 | 50804 | A | 20553 | 161 | 3193 | GSLSRLLPTITMAKGFYISKSLGI LGILLGVA AVCTIIALS VVYSQE KNKNANSSPVASTTPSASATTN PASATTL DQSKA WNRYPNT LKPDSYQVTLRPYLT PNDRLY VFKGSSTVRFTCKEATDVIIIHS KKLNFP\LSQGH RVVLRGVGGS QPPDIDKTELVEPTEYLVVHLK GSLVKDSQYEMDSEFEGELAD DLAGFYRSEYMEGNVRKV VVAT TQMQAADARKSFPCFDEPAMK ARF\NITLIPPQGT |
| 20437 | 50805 | A | 20554 | 3 | 429 | |
| 20438 | 50806 | A | 20555 | 3568 | 4012 | VLSTSPFGTELNPPI SPLAVNSTE LLKGELSLSSLGVLSLSDTSVPN SVSNSFLLGLRRLGRGVGISCS NALSALDLAACNFSLMRPLME NSAKPVLEVEGIGG/TAFDAGA GIALSDHFIKLISWYDNEFGYSN RVVDLMAHMASKE |
| 20439 | 50807 | A | 20556 | 1 | 1211 | QTAASSFASPGEPHRSNTMGKV KALVNGFDRIGRLVTRAAFNSG KGDIVAINDPFIDLNYMVYMFQ YDSTHGKFHGTVKAENGKLV NGNPITIFQ\ERDPSKIKWG*H\G AEYVV\ESTG\VF TTM\EKAGAH FAGGSQKGHSSFAPSTEAIMFM MKVNYEKYDNLKII SNASCTT NCLAPLAKVIHDNSGIVERLMI TVHVITTTQKTVDGPCRKL RPD GHRALQNIIPASTSTAKAMVKV IPELNK KLTGMASHVPTAKVLV VDPTCH/LGKPAKY YDIKMM KQASEDPIKGILGYTEHQIVSSD FNSDTQSSTFDAGAGITLNDHF VK\LISWYDNEFGYSNSVVDLM AHVASKELSGYSLKVSFAVQK LFSLIRS NLIIAFDAIVFGVFVM KSLPV SICRM |
| 20440 | 50808 | A | 20557 | 1 | 300 | PTANVSVDLTCL* KPAKYD DIKKVVKQASEGPLKGILGYTE HQVVSSDFNSDTHSSTFDAGAG IALNDHFVKLISWYDNEFGYSN RVVDLMAHMASKE |
| 20441 | 50809 | A | 20558 | 1 | 3399 | |
| 20442 | 50810 | A | 20559 | 1 | 3126 | |
| 20443 | 50811 | C | 20560 | 298 | 435 | |
| 20444 | 50812 | A | 20561 | 1 | 888 | |
| 20445 | 50813 | B | 20562 | 1 | 4536 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20446 | 50814 | A | 20563 | 37 | 3900 | LGLGLSMLVGQGAGPLGPAVV TAAVVLLLSGVGPAHGSEDIVV GCGGFVKSDVEINYSLEIKLYT KHGTLKYQTDCAPNNGYFMIP LYDKGDFILKIEPPLGWSFEPTT VELHVDGVSDICTKGGDINFVF TGFSVNGKVL SKGQPLGPAGV QVSLRNTGTEAKIQATATQPG GKFAFFKVLPGDYEILATHPTW ALKEASTTVSVTNSNANAASPL IVAGYNVSGSVRS DGEPMKGV KFLLFSSLVTKED\A |
| 20447 | 50815 | A | 20564 | 1 | 310 | EEETVPTTAGASPGPPRNKKNR ELRPQRPKNAYILKKS RISKKPQ VPKKPREWK NPEPSAAAS*GGE GQA HGGPAICPGQICALSQTPG LPGNSLSPRSPVGK |
| 20448 | 50816 | A | 20565 | 3 | 267 | |
| 20449 | 50817 | B | 20566 | 267 | 560 | |
| 20450 | 50818 | A | 20567 | 1 | 429 | LIGLDPEPLAEVDVISLEQGRRK QIERLGYPDQAKAPFQPKPKQK GRSSTASLVKRKRKVMDEE\NR VK*TIGNGPGLPKGCTLPACAL CPCQPAHFLTLCVSLPSPVPQD KVRQSLQQQHHKEAK/APKPTG ARPSALDRFVR |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20451 | 50819 | A | 20568 | 2 | 1951 | FKPTVWQLRGVLHVDRLFVWA SMETAPKPGKDVLSKKDKLQT KRKKP\RRYWEEETVPTTAGAS PGPPRNKKNRELRPQRPKNAYI LKKSRIKKPQVPKKPREWKNP ESQRGLSGAQDPFPGPAPVPVE VVQKFCRIDKSRKLPHSKAKTR SRLEVAEAEETSIQSLLRSEL LLAEEP\GFLEGEDGEDTAKICQ ADIVEAVDIASAAKHFDLNLRQ FGPYRLNYSRTGRHLAFGGRRG HVAALDWVTKKLMCEINVME AVRDIRFLHSEALLAVAQNRW LHIYDNQGIELHCIRRCRDRTRL EFLPFHLLDASETGFLTYLDV SVGKIVAALNARAG\RLDVMSQ NPYN\VIHIGHSNG\TASLWESS YGREPLAK\ILC\HRGLGSGAVA \VDSYRHVTWATSGP*DHQLED LDFARGRY\QPLEHSGPCPMG AGHLAFSQRELL/VLAGLGDVV NIWAGQGKASPP\SLDRPYFTH RV*GPVHGLQFCPFEDVLGVG HT*G\ITSML\VPGAGEPNFDGL\ ESNP\YRSRKQRQ\EWVKALL EKVPAELICLDPRALAEVDVISL ETGKRRKQIERLGYPDQ\AKAP F\QPKPKQKGRSSKA\TLVKRK RKVMIEDHKG/DKVRQSLQQQ HHKEAK\AKPTG\ARPSALDRF |
| 20452 | 50820 | A | 20569 | 1 | 437 | |
| 20453 | 50821 | A | 20570 | 157 | 425 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20454 | 50822 | A | 20571 | 207 | 1562 | LVIVFFYPQHTAPGPPLTVLNQ AMHARGPHGQLSPALPLASSVL MLLMNLAHLGQPWMLGPLTW HISPFSLPVHRLALTHALGHTALP GLLLSLLLPTVGWQQECHLGT LRFLHASALLALASGLLAVLLA GLGLSSAAGSCGYMPVHLAML AGEGHRPRRPRGALPPWLSPW LLLALTPLLSSEPPFLQLLCGLL AGLACILCLSPGPVGMCGFCG WVPGKEVAQRGEGPSNTKEPC THIAWPVAWAHPWLLLVLDR PPCPGQTDAAGAFRWLEPSERR LQVLQEGVLCRTLAG\GMPVQ VVGTVAGLPVRPSSLP/SSSRPPI PGPPYVASPDLWSHWEDSALPP PSLRPVQPTWEGSSEAGLDWA GASFSPGTPMWAALDEQMLQE GIQASEVGSPGIGAGVALTLPTS PPTPNRLQQLERMGFPTEQAVV ALAATGRVEGAVSLLVGGQ |
| 20455 | 50823 | A | 20572 | 460 | 916 | AHSPRDHPWTVLNQAMHARGP \HGQ\SPALPL\ASSVLMMLMST LWLVGAGPGLVLAPELLLDPW QVHRLALTHALGHTALPGL\LLS LLLPTVGWQQECHLGTLRFLH ASALLALASGLLAVLLAGLGLS SAAGSCGYMPVHLAMLAGEG HRPRRPRGALPPWLSPWLLLAL TPLLSSEPPFLQLLCGLLAGLAY AAGAFRWLEPSERRLQV\QEG VLCRTLAGCWPLRLLATPGSLA ELPVTHPAGVRPPIPGPPYVASP DLWSHWEDSALPPSLRPVQPT WEGSSEAGLDWAGASFSPGTP MWAALDEQMLQEGIQ\SL\LD GPAQEPQSAPWLS\KSSVS*MR LQQLERMGFP/TTEAAVVALA\ ATGRVEGA\VSLLVGGQSGTET LVTHGKGGPAHSEGP\GPPWAN CPQHCLLASSVLMMLMSTLWL VGAGPGLVLAPELLLDPWQVH RLLALTHALGHTALPGLAPEPAAP AHCGLAAGVPPGHAEIPACLS ARPGFWAAGSAAGRPWAVQCS RQLWIHACPPGHAGWGRTTP |
| 20456 | 50824 | A | 20573 | 174 | 401 | CTVVFSVLAELSCTSRFCPNMW TPLREPMTENGRWGLSVRVLE HGGNQSNSACGPEPPEGEMGS* LEED*LPALIP |

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|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 20457 | 50825 | A | 20574 | 450 | 1029 | ATQLPPQPWQTPAALGWAAAT SLMPYRAPSPPARAQHPPALCL APPPPLWLQLPHLEASHSLVEA RPNPPVSTLAQQGIQPSRHLPR CPSLRPRQQPPQQVP/PQPAAPT PTATITSTGPSLFASIATAPTSSA TTGLSLCTPVTTAGAPTAGTQG FSLKAPGAA\APPQQHPLPPP PPPPPPAAAPPALP |
| 20458 | 50826 | C | 20575 | 115 | 276 | |
| 20459 | 50827 | A | 20576 | 3 | 307 | ASRLGPREGGARKNPGGPCSAT QYISVPSPGAASFPVLGSQSLLT TVSPPLPA*/LAMAL*PRPLCA PGSPSRSPRLRSPLPPSFFSRGRR RLSLLQPWSE |
| 20460 | 50828 | A | 20577 | 2 | 388 | |
| 20461 | 50829 | C | 20578 | 244 | 487 | |
| 20462 | 50830 | B | 20579 | 5 | 569 | |
| 20463 | 50831 | A | 20580 | 204 | 676 | RTDQYPQRGETEELEGQLLPH RQLPGGLGAHRGPDACGLRD SSRGVPLAGSPLRVR*GRGHDL RQSGGVRPGGGSNRGLVVAGD ARGRAAPLAGGVPAADRSL PGVPAAREPHGPTAPDPDSAA EPGAVSTLRAEPTQPVVSTGC CSSTWN |
| 20464 | 50832 | B | 20581 | 1 | 1413 | |
| 20465 | 50833 | B | 20582 | 60 | 224 | |
| 20466 | 50834 | B | 20583 | 8 | 2469 | |
| 20467 | 50835 | A | 20584 | 841 | 1436 | HHQVPLPVGRERGGKRGPGSW ETCLSVLGPAPPSEPWPVSPSW VHSLVPGEQALPLICSQPPMAP QWPETGPGPHLVHRTCRCVCLN WQGMTRTRGYQAGPSSRRTIPT PAQLPAPLASLPPRQDPPSSPAE PPSGRFSMEPWWEARHPGSP AAPCSSHRIT/APPTPSLAAQPG/ PVGSNPPLSPEGLCLAGTPACG W |
| 20468 | 50836 | A | 20585 | 1799 | 5195 | SKGNNGSPSTTQTQTPRAAPDGS LSEETPAGPPTCSVPASALPRQ QYAKSLPVSVPVWGFKEKRTE ARSSDEENGPKPKPASVDANTK LTRSLPCQGS�KRATSCERAGK AVGEEVSGYSLHGCSEKERRRRP RLKKEGGSGEPGVGYLFISVLV NSNSELIRLINNAIKNDLASRNP TFMCLALHCIANVGSREMGEA FAADIPRILVAGDSMDSVKQSA ALCLLRLYKASPDLVPMGEWT ARVVHLLNDQHMGV |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20469 | 50837 | A | 20586 | 8 | 268 | SRSSRTWSPPIPEKEKTKLQKQREDELIQKIHKL VQKRDFLVDDAEVERLREQEEDKEMADFLRIKLKPLDKVTKSPPI*QSQAHL |
| 20470 | 50838 | C | 20587 | 50 | 196 | |
| 20471 | 50839 | A | 20588 | 16 | 1263 | SLSSRCMMVAEQGCALEPCQGLSHGAALGVLMVVFP/VSSLQQDQLDIIS\MAETT\MMP\EEIELEMAKIQRLREVLVRRESELRFMSFEEQYNEDHKKGVIDLFTADSLKTMTRLVTGVWLAATASNPLQEGEHAGEQIGAGGCRSRLEGGALTWDPVLLPPVRISRMLLL LIPGELPGIAFKLMNPTKAEPMHMFIILEPFDLRKLMDDIQLCKDIMDLKQELQNLVAIPGCTRSMMLVSAQLLEGLRKLIIAEDKGADMSRAQSRKRPPKMLICLLVDVFFPEKEKTKL\QKQREG*ANPRRFHKL VQKRDFLV\DDAEVERL\REQ\EDKEMADFLRIK\VKPLDKVTKSPASSRAEKKAEPPI\S KPTVAKTGLALIKDCCGATQCNHVSHPVGCPCGPWGPPTLLS |
| 20472 | 50840 | A | 20589 | 31 | 339 | |
| 20473 | 50841 | A | 20590 | 1 | 1179 | |
| 20474 | 50842 | A | 20591 | 1 | 1167 | PARSMAATSLMSALAARLLQPAHSCSLRLRPFHLAAV/RGNLSLQQVGVCNHNHGLLQ*PPGLK*SSHLSLNEAVVISGRKLAQQIKQEVQRQVEEWVASGNKRPHLSVILVGENPASHSYVLNKTRAAAVVGINSETIMKPASISE\EELLNLINKL\NDDNVDGLLVQLPLPEHIDERRICNAVSPDKDVGDFHVINVGRMCLDQYSMLPATPWGVWEIIKRTGIPTLGKNVVVAGRSKNVGMPIAMLLHTDGAHERPGDATVTISHRYTPKEQLKKHTILADIVISAAGIPNLITADMIKEGAAVIDVGINRVHDPVTAGVPGLVGNVDFEGVRQKAGYITVPVPGVVGPMTVAMLMKNITIAAKKGAEA*RSEKVLKSKELGVATN |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20475 | 50843 | A | 20592 | 1 | 1963 | MAASDVNCGACFAELQGNATA NTPGGTSHHHLAIHGSCDHSQ AKEAGRKRQWPWPPDGRSEPAP DSHPHLSPEALGYFRRALSALK EAPETGEERDLMVHNIMKEVE TQALALSTNRTGSEMLQELLGF SPLKPLCRVWAALRSNLRTVAC HRCGVHVLQSALLQLPRLGSA AEEEEEEEDGKDGPTELEEL VLGLAAEVCDDFLVYCGDTHG SFVVRTLLQVLGGTILESERARP RGSQSSEAQKTPAQECKPADFE VPETFLNRLQDLSSSLFKDIAVF ITDKISSFCLQVALQVLHRKLA QFCAHICNAVIGYLSARGSSVD GKPLLLFLRDQTSFRLLEQVLL VLEPPRLQSLFEEHLQGQLQTL AAHPIANFPLQRLDAVTTPEL LSPVFEELSPVLEAVLAQGHGP VVIALVGACRRVGAYQAKVLQ LLLEAFHCAEPSSRQVACVPLF ATLMAYEVYYGLTEEGAVPA EHQVAMAAARALGDVTVLGSL LLQHLLHFSTPGLVLRSLGALT GPQLLSLAQSPAGSHVLDAILTS PSVTSPSCAAVCLQNLKGTNIVA LACKSP*QPRVLKCHLEWSSLE GP/RRKIAAELGEQNQELKEPP FGHHVARNVALTTFLKRREAW EQQQGAVAKRRRALNSILED |
| 20476 | 50844 | A | 20593 | 55 | 393 | |
| 20477 | 50845 | A | 20594 | 150 | 379 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20478 | 50846 | A | 20595 | 1 | 2408 | MGVWGIRTPFMVVGLESPVGS SPRGQGSCVRLPQRRPDKSHAG ARTGPETLRERAQQSNKLPEW AEKGSHPARWSPNRGGRWTLT TARERRPSRALKARAAGRRQA KVADFRLPAAAPPEGAAQLRLE SERLPHQDEKEPSSYRGSCGSCP VTLRKMPYLGSEDVVKELKKA LCNPHIQADRLRYRNVIQRVIR YMTQGLDMSGVFMEMVKASA TVDIVQKKLVLYLMCTYAPLK PDLALLAINTLCKDCSDPNPMV RGLALRSMCSLRMSKLDQWQG AEVLNFLRLRYQPRSEELFDILN LLDSFLKSSSPGVVMGATKFLFI LAKMFPHVQTDVLVRVKGPLL AACSSERELCFVALCHVRQIL HSLPGHFSSHYKKFFCSYSEPH YIKLQKVEVLCELVDENVQQ VLEELRGYCTDVSADFAQAAIF AIGGIARTYTDQCVQILTELLGL RQEHITTVVVQTFRDLVWLCPQ CTEAVCQALPGCEENIQDSEGK QALIWLLGVHGERIPNAPYVLE DFVENVKSETFPAVKMELLTAL LRLFLSRPAECQDMLGRLLYYC IEEEKDMAVRDRGLFYRLLLV GIDEVKRILCSPKSDPTLGLLAE PAERPVNWSWDFNTLVPVYG KAHWATISKCQGAERCDPKLP KTSSFAASGPLIPEENKERVQEL PDGALMLVPCRQLTADYFEK |
| 20479 | 50847 | B | 20596 | 330 | 2458 | |
| 20480 | 50848 | A | 20597 | 2 | 171 | |
| 20481 | 50849 | A | 20598 | 32 | 1040 | LQLAKLGDWRMQUALRHVHCR FTEG*FMYSL*LTFPAGYQVT GVFMKNWDSLADHGVCTAD K\DCEDA\YRVCQILADIPFHQV SYGTEVIFFYSSDFLNEYEKGR PNPDIVCNKHIKFSS*SLCSKNL TGADAIATGHYARTSLEDEEVF EQKHVKKPEGPASWRNCLSVG WFLYTLGQRANIGGLREPWYV VEASPPSHSILQAPRTDHPALYR DLLRTSRVHWIAEPPAALVRD KMMECPPPRAPLFYPVPCVLT NQDGTWVVTAVTPDARVSPLQ FAVFYKGDDECLSGSKILRLGPS AYTLQKGQRRAGMATESPSDS PEDGPGLSPLL |
| 20482 | 50850 | A | 20599 | 12 | 432 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20483 | 50851 | A | 20600 | 2 | 509 | RLHSLLDGYYQAIKVLNIDLS TKSMYSRVPEC\QVTTYYYVGF AYSMRCYQDAIRVFASILLYI HRTNSMFQRTKYKYEMIIMLN EQMHALLAIALTMYPMRI\DESI YLHLREKYVDKMLRMQNGDL QVYEELFRYSCTKFL*PVPPNY DTVHAHYHTESFLQSLRR |
| 20484 | 50852 | B | 20601 | 8 | 1188 | |
| 20485 | 50853 | A | 20602 | 1 | 257 | |
| 20486 | 50854 | B | 20603 | 210 | 312 | |
| 20487 | 50855 | C | 20604 | 49 | 288 | |
| 20488 | 50856 | A | 20605 | 13 | 446 | IPVRPTRPADDDYEEAAYDPYA YPSDYDMHTGDPKQDLAYERQ YEQQTYQVIPEVIKNFIQYFHKT VSDLIDQKVYELQASRVSSDVI DQKVYEIQDIYEN\DAVFLILYK ELYRHIYAKVSFQSFSQYRCK TAKKSEEEIDFL |
| 20489 | 50857 | B | 20606 | 77 | 611 | |
| 20490 | 50858 | A | 20607 | 1 | 1956 | SLVDPRVRPRVRLASEAAMS YPAD\DYEEAAYDPYA\YPSD YDMHTGDPKQ\DLAYE\RQYEQ \QTYQVIPEVIKNFIQYFHKTVS DLIDQK\VDELQASPCQLQVIVID QERLYEDSRTIY*EQA WTKL\TE RFF\KNTWPWGGWKPLVPQGLA MDA\VSFLDFYPKNYTYRHIYA KVSGGPSLAEQRFESYYNYCNL FNYILNADGSRSPNYPNQW\W WGYSMEFIYPVFSHF\SQYRW *DLPKKSEEE\DFLRSNPKIW\N VHSVNLNVL\HSLVDKSNINRQL GGYTQACGDP*ECGWGSMGR HSLYMM\LHYFSLVR/GFSRLHS LLG\DYQAIKVLNIELNKK MYSRVPRVPRSPITY\YYVGFAY LMMRRY\QDAIRVFANILLYIQ RTKSMF\QRT\TYKYEMI\NKQIE QMHAL\LAIALTMYPMRI\DESI HLQLREKYG\DK\MLRMQK\GD PQVYE*LF\SYSCP\RFLAA\VP TYDNVHPN\YHKEP\FLQ\QLKG VFLDEVQ\QQGPAFKPIRSFLKL\ YTTHALLAKPGLASLDPHRGRE FRDPRFLCLSNHGG*RNVLVGP AGISSPWIGEISVSPQRVDLPTL NKDMIPHRGTPKVPQAVMGDF LHPVRSHKFGGA*SEPLKEGWG QRPWMIFTTHFREPVFDVIIGQG |
| 20491 | 50859 | A | 20608 | 2 | 413 | |

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|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 20492 | 50860 | A | 20609 | 232 | 621 | |
| 20493 | 50861 | A | 20610 | 1 | 3590 | MAPRKRGGRGISFIFCCFRNND HPEITYRLRND SNFALQTM E PA LPMPPVEELDV MFSELVDEL DL TDK HREAMFALPAEKKWQIYC SKKKDQEENKGATSWPEFYID QLNSMAAGILEGVFVHIVITHC LQNQQQLLHDKQGNRH FICCL RSHQH PMLPACSNVHLSSFDRK TLCKDALCPLPASHVSRYL RKS LLALEKEEE EERSKTIESLKTAL RTKPMRFVTRFIDL DGLSCILNF LKTMDYETSESRIH |
| 20494 | 50862 | A | 20611 | 203 | 3480 | SHQEIEQNSAMAPRKRGGV RGI AFIFCCLRNNDHPEITYRLRND S NFALQTM EPALPMPPVEELDV MFSELVDEL \DL PDKHREAMFA LPAEKKWQIYCSKKKDQEENK GATSWPEFYIDQLNSMAARKSL LALEKEEE EERSKTIESLKTALR TKPMRFVTRFIDL DGLSCILNFL KTMDYETSESRIHTSLIGCIKAL MNNSQGRAHVLAHSESIN VIAQ SLSTENIKTKVAVLEILGAVCLV PGGHKKVLQA |
| 20495 | 50863 | A | 20612 | 1 | 338 | PGGALRVPDAPAGAEGQELCR SDFPVGGAGVGDEEGVQCPAP AAHRDDTDLRGAH*EVQDAAG RRKQPDREQPAGAE EGAPHLPE RVPPG*RHGTCTDRGQARACG GPLAPE |
| 20496 | 50864 | B | 20613 | 610 | 6429 | |
| 20497 | 50865 | B | 20614 | 28 | 280 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20498 | 50866 | A | 20615 | 160 | 1397 | VKMSAQESCLRLIKDFLFVFNLF FFALGSLIFCFGIWILDKTSFL SFVGL/AAFVPLQIWSKVLAIS GNLSPWGIALLGLCWGALKVEL RCLLG\LYFG\MLLLLFATQITL KSSSSNQRAQLERSLR\DVVGK TI\QKYGINPEETAPEEN\WDYV QSNLRWCGWHYGRDWFKVFIL RGNGSEAH\RVTRS*YNFMAT* NSTILNKVIVHQLTRLEHLARS HSAD\ICAVPAESHITRKGCAQ GIQK\WLHNTLIFP*WAICLGVG LLE\LGFM\TLNIPVEETVDHGL PTGSARYRLGPAPPQSRAPPVS VRWALPVLVPVNICLIPRLAVEPS GVHISPGD\TTWLRAPAAVTSPT GPGAFVHSFLSPSVGLPPPTRLF FTQTSNKPPAFLVNDHKKGGRS KKALEGPNVTRA |
| 20499 | 50867 | A | 20616 | 290 | 492 | |
| 20500 | 50868 | A | 20617 | 1164 | 2134 | NNYNHHHHHHHHHHHDYYNHH/ HHYHHHHHHHHHNYNHHHHHDH HHNYKHHHHHHYHQHHHNYNH HHHHHHSYNHHHHHHHHHHN YNHYHHHHHHHHHHHREYHH HH/HHHHYHHHHHHHNYNYHH HYHHHHHQHYHHNHHHHNHH YNHHYHHNQYHYHHYHHHD YYHHH/HYHHHNYYYLYNRYH HYHHYHQSNNHYRHHHHHHQY HHN/HEPFA/HHT*ILFCS*KQDR NLHCAWPFFFPFNCHHHCHH HHQQQQHSGVKTKQSRPESLLP ERCILYHQHHPLHRPGAPQHQ KTASWRGQAREAAGSSPGSLSS HTADHEVEAFKRCFYSRF |
| 20501 | 50869 | B | 20618 | 164 | 1526 | |
| 20502 | 50870 | A | 20619 | 1 | 762 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20503 | 50871 | A | 20620 | 69 | 1054 | AISCHVVHAGHQQTQITGNDPF PVVTYSKGP NLQSSRSDMDDST EREQSRLT SCLKKREEMKLKEC VSILPRKESPSVRSYKDGKLLA ATLLLALHACCLTEVSFYQVAA LQGD LASLRAELQGHHA EKLP AGAGAPKAGLGGSSSCSPRDLK IF*TTSSREKAIP/GSEQQK*GVP FQGPEETVTQDCLQLIADSETPT IQKGSYTFVPWLLSFKRGSAL E EKENKILVKETGYFFIYGQVLY TDKTY\AMGH LIQRKKVHVFG DELS\LVTLFR\CIQNMPETLPNN SCYSAGIAKLEEGDELQLAIPRE NAQISLDGDVTFFGALKLL |
| 20504 | 50872 | A | 20621 | 3 | 855 | LQNSHGHTMIRTL LSTLVAGA LSCGDPTYP PYVTRVVGGEAR PNSWPWQVSLQYSSNGK WYHT CGGSLIANSWVLT A\AHCIS S\ R TYRVGLGRHNL YV A\ESGSLA/ MSSVSKIVVHKD\WNFNQISKG\ NDI\ALLKLANPVSLTDKIQ\LA\ CFPPAGTILPN\NY\PC*VTGLGE SCR TNG\AVPDVL\QQGR\LLAV DYATCS\SSA\WWGSSVKTSMIC A\GGDGVISSCNGDSGGPLNCQ A\SDALWQVHGIVSFGSRLGCN YYHKPSVFTRVSNYIDWINSVI AYN |
| 20505 | 50873 | A | 20622 | 19 | 414 | SVCWEDRYLKARMEESPLSRA PSRGGVNFLNVARTYIPNTKVE CHYTLPPGTMP SASDWIGIFKP/ GYLPKPGAQLYQFRYVNRQQQ VCGQSPPFQFREPRPMDELVT L EEADGGSDILLVVPKATVLQNQ |
| 20506 | 50874 | A | 20623 | 1 | 393 | AKSWQEEQSAQAQRLKDKVA QMKDTL GQAQQRV VSEAPWQ QETGNSKGKL*RSLRV*REGER HG*RLNNTTPSPNAVEWRER/IT SLADE*FTRNCDLHLLLSPEAEL EPLKEQLRGAQELAASSQQKAT LY |
| 20507 | 50875 | A | 20624 | 56 | 416 | NRPLLALVASDTQPLH THTHTH TPLSDAPKPIPGA/HLP/CSYLEF PLTSVPHPSLFHNL RYSVWRGF LYF*GFLYSVSSPRISSHGKK*CI CAFCEEWGEQVVP GIPISKAPLP LQVPPQQ |
| 20508 | 50876 | A | 20625 | 115 | 392 | |
| 20509 | 50877 | B | 20626 | 1 | 3388 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20510 | 50878 | A | 20627 | 3 | 1889 | SSPREKTSDDSHRPSRHGFLFLR LVGLSPFSYLCVPPSRPVPGSPR SLSAMRLLPLAPGRLRRGSPRH LPSCSPALLLLVLGGCLGVFGV AAGTRRPNVVLLLTDDQDEVL GGMTPLKKTKALIGEMGMTFS SAYVPSALCCPSRASILTGKYPH NHHVVNNTLEGNCSSKSWQKI QEPNTFPAILRSMCGYQTFFCR GNI*MKYGAPDAGGLG\HVPL GLGVTWYALEKNS\KYNYTL FYSMGKARKHGENY\SDYLT DVLANVSLDF\LDYKSNF*PFF MMIATPAPHSPWTAAPQYQKA FQNVFAPRNKNFNIHGTNKH LIRQAKTPMTNSSIQFLDNAFR KRWQTLLSVDDLVEKLVKRLE FTGELNNTYIFYTSDNGYHTGQ FSLPIDKRQLYEFDIKVPLLVRG PGIKPNQTSKMLVANIDLGPIL DIAGYDLNKTQMDGMSLLPILR GASNLTWRSDVLVEYQGEGRN VTDPTCPSLSPGVSQCFPDCVCE DAYNNTYACVRTMSALWNLQ YCEFDDQEVFVEVYNLTADPD QITNIAKTFDP\ELLGKMNYRL MMLQSCSGPTCRTPGVFDPGY RFDPRLMF\SNRGSVRTRRFSQT SSCSDPHTASADGSLHALFLMK |
| 20511 | 50879 | A | 20628 | 132 | 253 | |
| 20512 | 50880 | A | 20629 | 1 | 1269 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20513 | 50881 | A | 20630 | 1 | 1920 | MDEAEFSSFVVRTNTCGELRSS HLGQEVTLCGWIQYRRQNTFL VLRDFDGLVQVIIPQDEVLENFL LLSKSFFDAIAGSAASVKKILCE APVESVVQVSGTVISRPAGQEN PKMPTGEIEIKVKTAELLNACK KLPFEIKNFVKKTEALRLQYRY LDLRSFQMQYNLRLRSQVMVK MREYLCNLHGFVDIETPTLFRK TPGGAKEFLVPSREPGKFYSLP QSPQQFKQLLMVGGILDYFQV ARCYRDEGSRPDRQPEFTQIDIE MSFVDQTGIQSLIEGLLQYSWP NDKDPVVVPFPTMTFAEV\RPP YGTDKPDTRFGMKIIDISDVFR NTEIGFLQDALSKPHGTVKAICI PEGAKYLKRKDIGSIRNFAADH FNQEILPVFLNANRNWNSPVAN FIMESQRLELIRLMETQEEDVV LLTAGEHNKACSLLGK\LRGTN VAGPSRKQEGVVLDRDPTLFSFL WVVDPLFPQRRKIQUESWDR GQHPFTAPHPR*ITLLYTEPKK ARSQHYDLVLNGNEIGGGSIRI HNAELQRYILATLLKEDVKMLS HLLQALDYGA\PPHGGIALGLD RLICLVGTGSPSIRDVIAFPKSFRG HDLMSNTPDSPVPS*GTEALSYP SLQANRLQSRKSSLNHAYHAES |
| 20514 | 50882 | A | 20631 | 1 | 425 | KEPVGCVNNISFLASLAGSTSR NRLQSTRGAGRLQNSGTGLSTN LQHFQEENFRKSSPQLEHT/WSF FGECTTHHLPPVKAPLQTKKKT TNHCFLCGKKTGLASSYECRQ VGELEKLRCFLCDNPAWGLCKI KYLNCLFITS |
| 20515 | 50883 | A | 20632 | 1 | 1647 | |
| 20516 | 50884 | A | 20633 | 1 | 3096 | |
| 20517 | 50885 | A | 20634 | 1 | 419 | |
| 20518 | 50886 | A | 20635 | 558 | 1070 | SFRFGHSHGLWKRKKVA*GSN AIQHNMLQGKQNFHGAALWY KGNSTQSKRPQRAP*ESSTTKR GLQLSRQTLQLDPGGTVPCSEE YCICQ*EGPASRNRYNGVPSHF PSPTCIRESSHSGKILKSRLRCW GWPTDPWSVLPMDPRTSPLCA AGSQAVVAHSGRQKYPAL |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20519 | 50887 | A | 20636 | 3887 | 4573 | KKTTLLTLSKTRNINPFKVVK KKAYGSRKHLRQ/HLAINPAAL LPTAASQISEVKPVLPELAFSS EHRRSHGLESVPVLPGSGEAGV SFDLPAQADTLHSANKSRVKM RGKRRPQTRAARRLAAQESSEA EDMRSPEDPLHSGLMAPFPQM AIGHSSSEQPVEKTALRRPWQLP LHLGKVVLCLEWTQAPLQSLW VIPEGRLTFLILGTFFPRALDLSP WREQNPRQR |
| 20520 | 50888 | A | 20637 | 1 | 2988 | MATAPSPMLTLAPAWLCPAT TTPRDHSEASLEALPGDPPAHP AAAATAAAVIPALEPPHTPVYA IFVNHSLLDLYIDRPLPYLIGSK LFMEQEDVGLGELSSEEGNADE QSSGLEGACKVNLELLLTNAD KGLKAPEQHLKHVAGVLNGES VETSVLNYRELSPHKNRLLSPL RCSAPMSLHNSLVKPERQSKCF EFGKLQPSSSQSLDVQNITDSSF SRTTCFQGVKVDLGLKRSVIS KVEARDITEMTNKA |
| 20521 | 50889 | A | 20638 | 1 | 1176 | |
| 20522 | 50890 | A | 20639 | 2 | 367 | |
| 20523 | 50891 | A | 20640 | 124 | 441 | RYPRVPENRCFSELLFFQAPLG VGMARGNQR\ELARQKNLKET\ QE\SRGKGKEDSLTALSRKQRD S*IIAKKQKAA\NEKKS\MQTRE NVMTGYLENPGATAQLGVS |
| 20524 | 50892 | A | 20641 | 32 | 232 | |
| 20525 | 50893 | A | 20642 | 1 | 256 | |
| 20526 | 50894 | C | 20643 | 133 | 509 | |
| 20527 | 50895 | A | 20644 | 88 | 685 | QKRGRLFkihLVVLYLMKVIVI HRKMFQRAQELRWRAEDYHK CKAFSDHPLCKKASLQLGQNG GSGASSFFRIALLALPHS*NFKK QDGPPATSSNSTTFYN**LPEPQ DTSRMSSYSLSLSSSTLRG**S QDSSLSYSGGRGRKITETQEAE VE*AENRSLHSSLGNKKKSVSG TKEKNQKTKQNPHSKNKLTKN |
| 20528 | 50896 | A | 20645 | 42 | 946 | |
| 20529 | 50897 | C | 20646 | 1 | 453 | |
| 20530 | 50898 | C | 20647 | 771 | 1223 | |
| 20531 | 50899 | C | 20648 | 324 | 659 | |
| 20532 | 50900 | C | 20649 | 427 | 654 | |
| 20533 | 50901 | B | 20650 | 343 | 1774 | |
| 20534 | 50902 | B | 20651 | 23 | 525 | |
| 20535 | 50903 | B | 20652 | 2354 | 5689 | |
| 20536 | 50904 | B | 20653 | 448 | 3506 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20537 | 50905 | B | 20654 | 12 | 182 | |
| 20538 | 50906 | C | 20655 | 210 | 422 | |
| 20539 | 50907 | C | 20656 | 145 | 357 | |
| 20540 | 50908 | B | 20657 | 1 | 327 | |
| 20541 | 50909 | B | 20658 | 1 | 2595 | |
| 20542 | 50910 | B | 20659 | 122 | 472 | |
| 20543 | 50911 | B | 20660 | 163 | 418 | |
| 20544 | 50912 | C | 20661 | 86 | 517 | |
| 20545 | 50913 | B | 20662 | 334 | 2946 | |
| 20546 | 50914 | B | 20663 | 11 | 700 | |
| 20547 | 50915 | B | 20664 | 184 | 2372 | |
| 20548 | 50916 | C | 20665 | 267 | 467 | |
| 20549 | 50917 | B | 20666 | 131 | 268 | |
| 20550 | 50918 | B | 20667 | 18 | 255 | |
| 20551 | 50919 | B | 20668 | 100 | 356 | |
| 20552 | 50920 | B | 20669 | 120 | 839 | |
| 20553 | 50921 | B | 20670 | 355 | 504 | |
| 20554 | 50922 | B | 20671 | 1 | 1524 | |
| 20555 | 50923 | B | 20672 | 175 | 366 | |
| 20556 | 50924 | B | 20673 | 436 | 792 | |
| 20557 | 50925 | B | 20674 | 94 | 1347 | |
| 20558 | 50926 | B | 20675 | 865 | 1189 | |
| 20559 | 50927 | B | 20676 | 241 | 423 | |
| 20560 | 50928 | B | 20677 | 124 | 352 | |
| 20561 | 50929 | B | 20678 | 1 | 847 | |
| 20562 | 50930 | B | 20679 | 262 | 4624 | |
| 20563 | 50931 | C | 20680 | 76 | 297 | |
| 20564 | 50932 | B | 20681 | 1 | 702 | |
| 20565 | 50933 | B | 20682 | 1 | 1347 | |
| 20566 | 50934 | B | 20683 | 78 | 2874 | |
| 20567 | 50935 | B | 20684 | 133 | 7317 | |
| 20568 | 50936 | B | 20685 | 294 | 1449 | |
| 20569 | 50937 | C | 20686 | 139 | 367 | |
| 20570 | 50938 | C | 20688 | 154 | 445 | |
| 20571 | 50939 | B | 20689 | 1 | 1086 | |
| 20572 | 50940 | B | 20690 | 111 | 440 | |
| 20573 | 50941 | B | 20691 | 303 | 462 | |
| 20574 | 50942 | B | 20692 | 1 | 2905 | |
| 20575 | 50943 | C | 20693 | 349 | 453 | |
| 20576 | 50944 | C | 20694 | 233 | 376 | |
| 20577 | 50945 | B | 20695 | 1 | 2016 | |
| 20578 | 50946 | B | 20696 | 1464 | 3022 | |
| 20579 | 50947 | B | 20697 | 1 | 1059 | |
| 20580 | 50948 | B | 20698 | 1 | 933 | |
| 20581 | 50949 | B | 20699 | 1 | 930 | |
| 20582 | 50950 | C | 20700 | 129 | 215 | |
| 20583 | 50951 | C | 20701 | 283 | 408 | |
| 20584 | 50952 | B | 20702 | 1 | 1134 | |
| 20585 | 50953 | B | 20703 | 1 | 525 | |
| 20586 | 50954 | B | 20704 | 146 | 556 | |
| 20587 | 50955 | B | 20705 | 1 | 675 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20588 | 50956 | B | 20706 | 1 | 1107 | |
| 20589 | 50957 | B | 20707 | 1 | 774 | |
| 20590 | 50958 | C | 20708 | 52 | 156 | |
| 20591 | 50959 | C | 20709 | 1 | 420 | |
| 20592 | 50960 | B | 20710 | 1 | 1347 | |
| 20593 | 50961 | C | 20711 | 1 | 411 | |
| 20594 | 50962 | B | 20712 | 169 | 248 | |
| 20595 | 50963 | B | 20713 | 63 | 1321 | |
| 20596 | 50964 | B | 20714 | 1 | 359 | |
| 20597 | 50965 | C | 20715 | 1195 | 1674 | |
| 20598 | 50966 | B | 20716 | 964 | 1290 | |
| 20599 | 50967 | B | 20717 | 51 | 389 | |
| 20600 | 50968 | B | 20718 | 108 | 232 | |
| 20601 | 50969 | B | 20719 | 425 | 3545 | |
| 20602 | 50970 | C | 20720 | 35 | 226 | |
| 20603 | 50971 | B | 20721 | 1 | 387 | |
| 20604 | 50972 | B | 20722 | 1 | 1926 | |
| 20605 | 50973 | B | 20723 | 523 | 1242 | |
| 20606 | 50974 | B | 20724 | 42 | 2346 | |
| 20607 | 50975 | B | 20725 | 63 | 287 | |
| 20608 | 50976 | B | 20726 | 59 | 200 | |
| 20609 | 50977 | B | 20727 | 1 | 1176 | |
| 20610 | 50978 | B | 20728 | 1 | 769 | |
| 20611 | 50979 | B | 20729 | 1 | 2009 | |
| 20612 | 50980 | B | 20730 | 219 | 3045 | |
| 20613 | 50981 | B | 20731 | 195 | 1739 | |
| 20614 | 50982 | C | 20732 | 126 | 435 | |
| 20615 | 50983 | B | 20733 | 2752 | 4108 | |
| 20616 | 50984 | B | 20734 | 1 | 1104 | |
| 20617 | 50985 | B | 20735 | 24 | 230 | |
| 20618 | 50986 | B | 20736 | 1 | 1292 | |
| 20619 | 50987 | B | 20737 | 1 | 7977 | |
| 20620 | 50988 | B | 20738 | 157 | 2627 | |
| 20621 | 50989 | C | 20739 | 165 | 533 | |
| 20622 | 50990 | B | 20740 | 35 | 87 | |
| 20623 | 50991 | C | 20741 | 68 | 202 | |
| 20624 | 50992 | B | 20742 | 83 | 2670 | |
| 20625 | 50993 | B | 20743 | 162 | 276 | |
| 20626 | 50994 | B | 20744 | 104 | 245 | |
| 20627 | 50995 | B | 20745 | 66 | 2768 | |
| 20628 | 50996 | B | 20746 | 14 | 3115 | |
| 20629 | 50997 | C | 20747 | 69 | 203 | |
| 20630 | 50998 | B | 20748 | 1 | 2152 | |
| 20631 | 50999 | C | 20749 | 114 | 387 | |
| 20632 | 51000 | C | 20750 | 56 | 250 | |
| 20633 | 51001 | B | 20751 | 53 | 3398 | |
| 20634 | 51002 | B | 20752 | 642 | 2386 | |
| 20635 | 51003 | B | 20753 | 1 | 1242 | |
| 20636 | 51004 | B | 20754 | 51 | 601 | |
| 20637 | 51005 | B | 20755 | 192 | 463 | |
| 20638 | 51006 | B | 20756 | 125 | 1254 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20639 | 51007 | C | 20757 | 208 | 333 | |
| 20640 | 51008 | B | 20758 | 155 | 4443 | |
| 20641 | 51009 | B | 20759 | 1 | 2529 | |
| 20642 | 51010 | B | 20760 | 63 | 321 | |
| 20643 | 51011 | B | 20761 | 226 | 645 | |
| 20644 | 51012 | B | 20762 | 1 | 1395 | |
| 20645 | 51013 | B | 20763 | 258 | 475 | |
| 20646 | 51014 | C | 20764 | 126 | 263 | |
| 20647 | 51015 | B | 20765 | 1 | 1429 | |
| 20648 | 51016 | B | 20766 | 51 | 3256 | |
| 20649 | 51017 | C | 20767 | 83 | 403 | |
| 20650 | 51018 | B | 20768 | 1 | 621 | |
| 20651 | 51019 | B | 20769 | 1 | 463 | |
| 20652 | 51020 | B | 20770 | 1002 | 3594 | |
| 20653 | 51021 | C | 20771 | 107 | 403 | |
| 20654 | 51022 | B | 20772 | 51 | 401 | |
| 20655 | 51023 | C | 20773 | 46 | 398 | |
| 20656 | 51024 | B | 20774 | 1 | 513 | |
| 20657 | 51025 | B | 20775 | 1 | 531 | |
| 20658 | 51026 | C | 20776 | 1 | 423 | |
| 20659 | 51027 | B | 20777 | 52 | 670 | |
| 20660 | 51028 | C | 20778 | 43 | 375 | |
| 20661 | 51029 | B | 20779 | 1 | 1629 | |
| 20662 | 51030 | B | 20780 | 1 | 1713 | |
| 20663 | 51031 | B | 20781 | 1 | 5154 | |
| 20664 | 51032 | B | 20782 | 37 | 585 | |
| 20665 | 51033 | B | 20783 | 1 | 3789 | |
| 20666 | 51034 | C | 20784 | 149 | 367 | |
| 20667 | 51035 | C | 20785 | 89 | 234 | |
| 20668 | 51036 | B | 20786 | 113 | 278 | |
| 20669 | 51037 | B | 20787 | 1 | 1632 | |
| 20670 | 51038 | B | 20788 | 1 | 762 | |
| 20671 | 51039 | B | 20789 | 230 | 3411 | |
| 20672 | 51040 | B | 20790 | 95 | 1150 | |
| 20673 | 51041 | B | 20791 | 1 | 1230 | |
| 20674 | 51042 | B | 20792 | 74 | 3123 | |
| 20675 | 51043 | B | 20793 | 1 | 1719 | |
| 20676 | 51044 | C | 20794 | 206 | 402 | |
| 20677 | 51045 | B | 20795 | 302 | 424 | |
| 20678 | 51046 | B | 20796 | 60 | 80 | |
| 20679 | 51047 | B | 20797 | 1 | 1248 | |
| 20680 | 51048 | B | 20798 | 8 | 1910 | |
| 20681 | 51049 | B | 20799 | 124 | 807 | |
| 20682 | 51050 | B | 20800 | 43 | 618 | |
| 20683 | 51051 | B | 20801 | 7 | 328 | |
| 20684 | 51052 | B | 20802 | 244 | 385 | |
| 20685 | 51053 | B | 20803 | 850 | 970 | |
| 20686 | 51054 | C | 20804 | 97 | 360 | |
| 20687 | 51055 | B | 20805 | 551 | 3159 | |
| 20688 | 51056 | B | 20806 | 861 | 1110 | |
| 20689 | 51057 | B | 20807 | 1 | 876 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20690 | 51058 | B | 20808 | 1 | 849 | |
| 20691 | 51059 | B | 20809 | 1 | 1443 | |
| 20692 | 51060 | B | 20810 | 508 | 2398 | |
| 20693 | 51061 | B | 20811 | 53 | 185 | |
| 20694 | 51062 | B | 20812 | 50 | 633 | |
| 20695 | 51063 | B | 20813 | 1 | 444 | |
| 20696 | 51064 | B | 20814 | 58 | 262 | |
| 20697 | 51065 | B | 20815 | 27 | 1005 | |
| 20698 | 51066 | B | 20816 | 1 | 4860 | |
| 20699 | 51067 | B | 20817 | 1 | 3489 | |
| 20700 | 51068 | C | 20818 | 52 | 363 | |
| 20701 | 51069 | C | 20819 | 347 | 499 | |
| 20702 | 51070 | B | 20820 | 1 | 4140 | |
| 20703 | 51071 | B | 20821 | 85 | 3930 | |
| 20704 | 51072 | B | 20822 | 848 | 3116 | |
| 20705 | 51073 | B | 20823 | 41 | 1211 | |
| 20706 | 51074 | B | 20824 | 248 | 4307 | |
| 20707 | 51075 | B | 20825 | 67 | 3180 | |
| 20708 | 51076 | C | 20826 | 229 | 467 | |
| 20709 | 51077 | B | 20827 | 71 | 1827 | |
| 20710 | 51078 | B | 20828 | 1 | 1045 | |
| 20711 | 51079 | B | 20829 | 1279 | 1479 | |
| 20712 | 51080 | B | 20830 | 1 | 2460 | |
| 20713 | 51081 | B | 20831 | 62 | 3691 | |
| 20714 | 51082 | B | 20832 | 1 | 1062 | |
| 20715 | 51083 | B | 20833 | 1 | 873 | |
| 20716 | 51084 | B | 20834 | 1 | 1041 | |
| 20717 | 51085 | B | 20835 | 161 | 5445 | |
| 20718 | 51086 | B | 20836 | 199 | 343 | |
| 20719 | 51087 | C | 20837 | 86 | 229 | |
| 20720 | 51088 | C | 20838 | 1 | 225 | |
| 20721 | 51089 | C | 20839 | 34 | 165 | |
| 20722 | 51090 | C | 20840 | 238 | 455 | |
| 20723 | 51091 | C | 20841 | 200 | 322 | |
| 20724 | 51092 | B | 20842 | 59 | 164 | |
| 20725 | 51093 | C | 20843 | 1353 | 1793 | |
| 20726 | 51094 | B | 20844 | 1 | 1329 | |
| 20727 | 51095 | C | 20845 | 43 | 324 | |
| 20728 | 51096 | C | 20846 | 223 | 435 | |
| 20729 | 51097 | C | 20847 | 212 | 307 | |
| 20730 | 51098 | C | 20848 | 386 | 529 | |
| 20731 | 51099 | B | 20849 | 300 | 995 | |
| 20732 | 51100 | B | 20850 | 876 | 3312 | |
| 20733 | 51101 | B | 20851 | 153 | 306 | |
| 20734 | 51102 | B | 20852 | 39 | 3131 | |
| 20735 | 51103 | B | 20853 | 29 | 136 | |
| 20736 | 51104 | B | 20854 | 112 | 333 | |
| 20737 | 51105 | B | 20855 | 31 | 474 | |
| 20738 | 51106 | B | 20856 | 26 | 1716 | |
| 20739 | 51107 | B | 20857 | 27 | 1234 | |
| 20740 | 51108 | B | 20858 | 1 | 6390 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20741 | 51109 | B | 20859 | 1 | 1014 | |
| 20742 | 51110 | B | 20860 | 128 | 837 | |
| 20743 | 51111 | B | 20861 | 1 | 931 | |
| 20744 | 51112 | B | 20862 | 357 | 4629 | |
| 20745 | 51113 | B | 20863 | 1 | 1017 | |
| 20746 | 51114 | B | 20864 | 1 | 1908 | |
| 20747 | 51115 | B | 20865 | 224 | 9448 | |
| 20748 | 51116 | B | 20866 | 1 | 1209 | |
| 20749 | 51117 | B | 20867 | 138 | 359 | |
| 20750 | 51118 | B | 20868 | 1 | 1567 | |
| 20751 | 51119 | B | 20869 | 226 | 9033 | |
| 20752 | 51120 | B | 20870 | 20 | 2689 | |
| 20753 | 51121 | B | 20871 | 1602 | 2647 | |
| 20754 | 51122 | C | 20872 | 72 | 452 | |
| 20755 | 51123 | C | 20873 | 64 | 423 | |
| 20756 | 51124 | B | 20874 | 33 | 363 | |
| 20757 | 51125 | B | 20875 | 131 | 1675 | |
| 20758 | 51126 | B | 20876 | 37 | 219 | |
| 20759 | 51127 | B | 20877 | 1 | 564 | |
| 20760 | 51128 | B | 20879 | 1 | 651 | |
| 20761 | 51129 | B | 20880 | 44 | 424 | |
| 20762 | 51130 | B | 20881 | 28 | 202 | |
| 20763 | 51131 | B | 20882 | 1 | 3403 | |
| 20764 | 51132 | B | 20883 | 110 | 970 | |
| 20765 | 51133 | B | 20884 | 70 | 485 | |
| 20766 | 51134 | B | 20885 | 482 | 2943 | |
| 20767 | 51135 | B | 20886 | 469 | 1480 | |
| 20768 | 51136 | B | 20887 | 156 | 308 | |
| 20769 | 51137 | C | 20888 | 218 | 348 | |
| 20770 | 51138 | B | 20889 | 1 | 5130 | |
| 20771 | 51139 | B | 20890 | 21 | 1139 | |
| 20772 | 51140 | B | 20891 | 1 | 1302 | |
| 20773 | 51141 | B | 20892 | 1 | 1028 | |
| 20774 | 51142 | B | 20893 | 1 | 858 | |
| 20775 | 51143 | B | 20894 | 1 | 2001 | |
| 20776 | 51144 | B | 20895 | 1 | 546 | |
| 20777 | 51145 | B | 20896 | 1 | 1167 | |
| 20778 | 51146 | B | 20897 | 1 | 1299 | |
| 20779 | 51147 | B | 20898 | 1 | 1260 | |
| 20780 | 51148 | B | 20899 | 1 | 771 | |
| 20781 | 51149 | C | 20900 | 155 | 337 | |
| 20782 | 51150 | B | 20901 | 1 | 1251 | |
| 20783 | 51151 | B | 20902 | 106 | 543 | |
| 20784 | 51152 | B | 20903 | 57 | 2279 | |
| 20785 | 51153 | B | 20904 | 905 | 1120 | |
| 20786 | 51154 | B | 20905 | 145 | 2277 | |
| 20787 | 51155 | B | 20906 | 1 | 1384 | |
| 20788 | 51156 | B | 20907 | 1 | 4775 | |
| 20789 | 51157 | C | 20908 | 99 | 251 | |
| 20790 | 51158 | B | 20909 | 1 | 693 | |
| 20791 | 51159 | B | 20910 | 77 | 2173 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20792 | 51160 | B | 20911 | 140 | 313 | |
| 20793 | 51161 | B | 20912 | 1 | 392 | |
| 20794 | 51162 | C | 20913 | 1 | 222 | |
| 20795 | 51163 | B | 20914 | 1 | 951 | |
| 20796 | 51164 | B | 20915 | 45 | 1244 | |
| 20797 | 51165 | B | 20916 | 166 | 2544 | |
| 20798 | 51166 | C | 20917 | 279 | 449 | |
| 20799 | 51167 | B | 20918 | 1 | 1250 | |
| 20800 | 51168 | B | 20919 | 229 | 2094 | |
| 20801 | 51169 | B | 20920 | 94 | 434 | |
| 20802 | 51170 | C | 20921 | 253 | 336 | |
| 20803 | 51171 | B | 20922 | 1 | 1314 | |
| 20804 | 51172 | B | 20923 | 6 | 327 | |
| 20805 | 51173 | B | 20924 | 163 | 3060 | |
| 20806 | 51174 | B | 20925 | 20 | 385 | |
| 20807 | 51175 | B | 20926 | 22 | 58 | |
| 20808 | 51176 | C | 20927 | 141 | 287 | |
| 20809 | 51177 | B | 20928 | 37 | 1063 | |
| 20810 | 51178 | C | 20929 | 261 | 401 | |
| 20811 | 51179 | B | 20930 | 66 | 3148 | |
| 20812 | 51180 | B | 20931 | 223 | 4149 | |
| 20813 | 51181 | C | 20932 | 21 | 278 | |
| 20814 | 51182 | B | 20933 | 158 | 1283 | |
| 20815 | 51183 | B | 20934 | 8 | 896 | |
| 20816 | 51184 | B | 20935 | 240 | 387 | |
| 20817 | 51185 | C | 20936 | 312 | 512 | |
| 20818 | 51186 | B | 20937 | 451 | 611 | |
| 20819 | 51187 | C | 20938 | 160 | 428 | |
| 20820 | 51188 | B | 20939 | 110 | 294 | |
| 20821 | 51189 | B | 20940 | 121 | 1764 | |
| 20822 | 51190 | B | 20941 | 1 | 423 | |
| 20823 | 51191 | C | 20942 | 74 | 316 | |
| 20824 | 51192 | C | 20943 | 136 | 255 | |
| 20825 | 51193 | C | 20944 | 79 | 381 | |
| 20826 | 51194 | B | 20945 | 282 | 1180 | |
| 20827 | 51195 | B | 20946 | 63 | 371 | |
| 20828 | 51196 | C | 20947 | 193 | 672 | |
| 20829 | 51197 | B | 20948 | 85 | 898 | |
| 20830 | 51198 | B | 20949 | 35 | 1055 | |
| 20831 | 51199 | B | 20950 | 1 | 870 | |
| 20832 | 51200 | B | 20951 | 103 | 1189 | |
| 20833 | 51201 | B | 20952 | 501 | 594 | |
| 20834 | 51202 | B | 20953 | 39 | 1694 | |
| 20835 | 51203 | B | 20954 | 489 | 4797 | |
| 20836 | 51204 | C | 20955 | 31 | 153 | |
| 20837 | 51205 | B | 20956 | 259 | 699 | |
| 20838 | 51206 | B | 20957 | 4 | 231 | |
| 20839 | 51207 | B | 20958 | 50 | 520 | |
| 20840 | 51208 | C | 20959 | 322 | 456 | |
| 20841 | 51209 | B | 20960 | 163 | 1152 | |
| 20842 | 51210 | B | 20961 | 33 | 745 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20843 | 51211 | B | 20962 | 210 | 3519 | |
| 20844 | 51212 | C | 20963 | 34 | 294 | |
| 20845 | 51213 | C | 20964 | 301 | 381 | |
| 20846 | 51214 | B | 20965 | 71 | 675 | |
| 20847 | 51215 | B | 20966 | 1 | 873 | |
| 20848 | 51216 | B | 20967 | 118 | 1618 | |
| 20849 | 51217 | B | 20968 | 424 | 2415 | |
| 20850 | 51218 | C | 20969 | 106 | 231 | |
| 20851 | 51219 | B | 20970 | 71 | 756 | |
| 20852 | 51220 | B | 20971 | 1 | 1049 | |
| 20853 | 51221 | C | 20972 | 94 | 327 | |
| 20854 | 51222 | B | 20973 | 339 | 2589 | |
| 20855 | 51223 | B | 20974 | 89 | 273 | |
| 20856 | 51224 | B | 20975 | 1 | 2514 | |
| 20857 | 51225 | B | 20976 | 472 | 5831 | |
| 20858 | 51226 | C | 20977 | 247 | 300 | |
| 20859 | 51227 | B | 20978 | 1 | 2487 | |
| 20860 | 51228 | B | 20979 | 55 | 243 | |
| 20861 | 51229 | C | 20980 | 207 | 377 | |
| 20862 | 51230 | B | 20981 | 642 | 4117 | |
| 20863 | 51231 | B | 20982 | 44 | 2127 | |
| 20864 | 51232 | B | 20983 | 48 | 1127 | |
| 20865 | 51233 | B | 20984 | 1 | 3411 | |
| 20866 | 51234 | B | 20985 | 74 | 469 | |
| 20867 | 51235 | B | 20986 | 39 | 1251 | |
| 20868 | 51236 | B | 20987 | 223 | 378 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|---|
| 20869 | 51237 | A | 20988 | 1 | 2577 | MPPNRHRMRGETTLWNP GCDH AGIATQVVVEKKLWREQGLSR HQLGREAF LQEVWKWKEEKG DRIYHQLK\KLGSSLDWDRACF TMDPKLSAAVTEAFVGLHEKG IHYRSTAFVNWPCTLNSAISDIE VDKKELTGR TLLSVPGYKEKV EFGVLVSFA YK\VQGS D*/DDE EVVVANKLGSKTMLGDVAVA VPPPKDTR\YQHL\KGKNVIHP\F LSRSLSP LSSDEFVDMDF\GTGA VKDHPPRHDQNDYEVGQRHGL EASIMDSRGA\PIKCASA FPGPA AGLRPGKRCWWR*RN RGLFRG IEDNPMVVPLCNRSKD VVEPLL RPQWYVRCGEMAQAASAAVT RGDLRILPEAHQRTWHAWMD NIREWCISRQLWWGHRIPAYFV TVSDPAVPPGESEDL SVFYPGT LLETGHDILFFWVARMV MLGL KLTGRLPFREVYLPCPSCENAH GRK\MSKSLGNVIDPLDVHL/Y GISLQGLHNQLLNSNLDPSEVE KAKEGQKADFPAGVPEC GTDA LRFGLCAYMSQGS*K*TWNVN RIMG*RQFCNKLWKCTKFALR GLGKGFVPSDTSNSAGHESLA DR*IRNLLTEAVRLSNQGFQAY DFPAVTTAQYSFWLYELCDVY LECLKPVLNGVDQV/AQAECAR QTLYTLPWTLGLRLLSPFMPFV TEELFQRLPRRMPQAPPSLCVT |
| 20870 | 51238 | A | 20989 | 2 | 4083 | SQRGEHVGAGCRGGDLRELGS PGEPTVSARSTPPPGPLGGSQP RPAPGCEVDSPAQSDHLPVFP LRSDLLITMSTLYVSPHPDAFPS LRALIAARYGEAGEGPGWGGA HPRICLQPPPTSRTSFPPRLPAL EQGPGGLVWVGATAVAQLLW PAGLGPGGSRAAVLVQQWVS YADTELIPAACGATLPALGLRS SAQDPQAVLGALGRALSPLEE WLR LHTYLAGEAPTLADLA AV TALLPFRYVLDPPAR |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20871 | 51239 | A | 20990 | 1 | 756 | MDMGAIKEGESRRPGDRMTVA GTKLLHLQSTHLD FISLSGAPSG ALELSKAQPAHAQDTRVLMKM VIIWDL SQVPLQPGHDGHSFRIH DYLYFQVLSPGDIRYIFTATPAK DFGGIFHTRYEQIHLVPAEPPEA CGELSNGFFIQDQIALVERGGCS FLSKTRVVQEHGGRGGDHL*Q RS*QMTASTW/QMIQDSTQRTA DIPALFLLGRDGYMIRRSLEQH GLPWAII SIPVNVH QHSPPLSCC NRPFLFW |
| 20872 | 51240 | A | 20991 | 2 | 393 | |
| 20873 | 51241 | A | 20992 | 1066 | 1824 | |
| 20874 | 51242 | A | 20993 | 3 | 902 | |
| 20875 | 51243 | A | 20994 | 1 | 2163 | |
| 20876 | 51244 | A | 20995 | 1 | 1890 | |
| 20877 | 51245 | A | 20996 | 1 | 2882 | MKQQLPVSYLQVIFNHWASRIS GARGAGWGPVRLGRLCADRAL DGESRPGGGGQSGVPASEASQ KAAHGRRLPVPARLLRCAHSA LEPGRGSASSPRNSTTSDNDQPP DYSFSKRCDSHSLGFSLVWESR NLTLPTSKLLHFSAFHFFIYKC RAEGHKLYKDLKNFLSAVKVM HESSKRVSETLQFIYYSEWYGH EELKAIVWNNDLLWEDYEEKL ADQAVRTMEIYVAQFSEIKERI AKRGRKLV DYDSARH |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20878 | 51246 | A | 20997 | 1 | 1791 | MPGARTSSSGASENHRARGQG GGPQGVGRMAEGKAGGAAGL FAKQVQKKFSRAQEKVLQKLG KAVETKDERFEQSANNFYQQQ AEGHKLYKDLKNFLSAVKVMH ESSKRVSSETLQEIYSSEWDGHE ELKAIVWNNDLLWEDYEEKL\ ADQAVRTMEIYVAQFSEIKE\RI AKRGRKLV DYDSARHHLEAVQ NAKKKDEAKTAKAEEEFNKAQ TVFEDLNQELLEELPILYNSRIG CYVTIFQNISNLRDVFYREMSK LNHNLYEVM SKLEKQHSNKVF VVKGLSSSSRRSLVISPPVRTAT VSSPLTSPSTLSLKSESESVS ATEDLAPDAAQGEDNSEIKELL EEEEIEKEGSEASSSEDEPLPA CNGPAQAQPSPTTERAK\SQEE VLPSTTPSPGGALSPSGQLSSS ATEVVLRTRTASEGSE\RPKKT ASIQRTSAPPRPPPPRATASPRP CSGNIPSSPTASGGGSA\TSPRAS LGTGTASPRTSLEI*PNPE\PEK PVRTPEAKENENIHNQNPEELC TSPTLMTSQVASEPGEAKKME DKEKDNKLISADSSEGQDQLQV SMVPENNNLTAPEPQEEVSTSE |
| 20879 | 51247 | A | 20998 | 3 | 273 | RRPRQRPTDQTQWFSILPDFSLD LQEGPSVESQTHSDPHIPPVDP TTHLTFNHL SIVCVSLTSLPHL GSPCLWSPALVSQEAASHQDRR |
| 20880 | 51248 | A | 20999 | 309 | 1310 | RHQRAPEQGP DASWKMLDSLL ALGG\LVLL\ARDSVE\WEG\RSLL K\ALVKKSALCGE\QVHILGCE\ VSEKEFREGFDS**STIRLVYHD F\FRDPLNWSKTEEGL\VPGGPL GALRS\MCKR\TDPVPVTIALDS LS\WLLLRLHCT\TLCQALHAV EPSRTLVLGDSSSVGKVSVLGL LHERLPRPAPVVALSSLAQTKV TLGGYHGARPSAHIL\CRRPRQ\ RPN\YQTQWFSILPDFSLGSPRG ALCRVPALIPHITPGGIPHNSF *PFNLHL\SKKEREARDSLILPFQ FSSEKQQA\LLRPRPGQATSHIF YEPDAYDDLDQEDPDDDLNILP |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20881 | 51249 | A | 21000 | 418 | 1304 | GLVMEIGMHHHEHHHLQAPNK EDILKISEDERMELSKSFRVYCH LVKPKDVSLWAAVKETWTKH CDKAEFFSSENVKVFESINMDT NDMWLMMRKAYKYAFDKYR DQYNWFFLARPTTFIENLKY FLLKKDPSQPFYLGHTIKSGDLE YVGMIEGGIVLSVESMKRLNSL LNIPEKCPEQGGMIWKISEDKQ LAVCLKYAGVFAENAEDADGK DVFNSQICWAFY*/R/WQ*LITPN QVVEGCCSDMAVTFNGLTPNQ MHVM MYGVYRLRAFPGPYFSM MHWFSYLQMVLTMTTEKW |
| 20882 | 51250 | A | 21001 | 1 | 1092 | |
| 20883 | 51251 | A | 21002 | 130 | 397 | EGVHSQVNLFPKGNQTHVPAS HGTDSALPPTLQMDYRALVHE PD*AAYGELRAMVLDLRAFYA ELYHIISSNLEKIVNPKGEEKPF |
| 20884 | 51252 | A | 21003 | 11 | 805 | SSMAKPCGVRLSGKGRKQVEV FYRNLFQEAEEFLLR\FLPPESHI P*NRLLEDFFFNVA*/LLNLSS GAPLDIPSPDP\PP\KDDMETD K\QEKKEVPKCDFLP\GNEKCPC PCLPLVKPRSLDLSKEKC\ILVI TWGSRHLDPPRFEDGK*FWG* AIPGEGAWRG*NA\VKDPKWE AFPATPISQVLSSERGDACGPRP PQETHV\MDYRALVHERDEAA YGELRAMVLDLRAFYAELYHII SSNLAEKIV\TPRGEEKPIYVLEP |
| 20885 | 51253 | A | 21004 | 352 | 670 | AKRSRIHVGVIIVDSGAEELGR DAAALSEKPPSLTIGLHMELVG MGGEPAALTATPANCPEYPAKPS SI/EQQ*QSQVQ**Q*QVRHGS PLHRTPRQLFLCSRQFAL |
| 20886 | 51254 | A | 21005 | 3 | 222 | SPEESPPACPRQVFPLYHLQRG QGKRVQVG*GGSLWITTKTRLL PGGVGDNEVAPGSWHLALVFR LLSSGRP |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20887 | 51255 | A | 21006 | 1 | 3639 | MSEETLQSKLAAAKKKIQDILN VLVSDLNRSNGVVLPTLDKWK DAPEAWDLCLALRSICGLAIQL LGAAPLTRAANFSVAEVT DVR DSARRWETRKAPYLSCRJALRM NEAAVFRHLVPGVYFPRCDQG CQLTAALGCGAGVQSHVGPVT VTTGPD SVTAADAAGLCRVLR AVGWGGSECLTPHPYKFHVE PYGGRLVPPRLSVDPGSSRREA TSKVAVDLLVLDAAGADGPVS QSPVWKEAAGVVSQLRGGRQ |
| 20888 | 51256 | A | 21011 | 137 | 944 | KPRCCHSATMFEVPLVQGSILK KVLEALKDLINACWDISSGV NLQSMDS/SHVSLQFTLPSEGF DTYRCD CNLAMGVNLTIMSKIL KCAGNEDIVTLRIEDNVNTLVL VFEASNQEKVSDYEIKLMDLD VEQLGIAEQEYHYVVKMLSGE FASIC*DL SHIGDAVVISGVKDG IIFSASGDLGNKNKLSQTSTVD KEEEAVTMEMNEPVQLTFALR YLNFLT KATPLSSMVT LNMSA DIHLVVDYKIADVGHLYLA PKMEDEEGP |
| 20889 | 51257 | B | 21012 | 205 | 1309 | |
| 20890 | 51258 | A | 21013 | 189 | 410 | |
| 20891 | 51259 | A | 21014 | 1767 | 2158 | RAQPHLYPEAARTGRK*LHFC APSSAPRAPVSERR/CAGRFLSW CPVAAWDPARWARRARRRRR AAARRRRPPRWRRRCLSARGR RRSLNSSKTKNTKCLNSINQRL KILSLQKDL MCGTAGRCKTLTE Q |
| 20892 | 51260 | A | 21015 | 1 | 1710 | |
| 20893 | 51261 | A | 21016 | 132 | 522 | |
| 20894 | 51262 | A | 21017 | 1 | 1386 | |
| 20895 | 51263 | A | 21018 | 331 | 3101 | SFSEANISTAKKTFLYNELYVY NTRKDTWTKVDIPSPPRRCAH QAVVVPQGGGQLWVFGGEFAS PNGEQFYHYKDLWVLHLATKT WEQVKSTGGPSGRSGHRMVA WKRQLILFGGFHESTRDYIYNN DVYAFNLDTFTWSKLSPSGTVP TPRSGCQMSVTPQGGIVVYGG YSKQMPPHSGQSRGRKPGSCLL LLLLLLLLLLLLLLCVLPLGYSL IELSSSYRLHGNEVPATFHGLN SHMGLVATILDNVNP |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20896 | 51264 | A | 21019 | 2 | 2911 | VRGPRARCRRRSSKTEPRKGPS RTSTRKRLELGAGSDSISVRRAP PHEHLFPSGERGPFSLVSRRL GPGKMGKKKGKKEKKGRGAEK TAAKMEKKVSKRSRKEPGVC RRIRPDLGVECSAAAAGFPNR GQFYGLPCARHSSLGFTPHEQE DLEALIAHFQTLDAKRTQTVEV PCPPSPRKCRGSQFVVTEDSVR KGTALRLNASLSVHPEKDELIL FGGEYFNGQKTFLYNELVYVNI RKDTWTKVDIPSP |
| 20897 | 51265 | A | 21020 | 1 | 208 | DGYRHEMLPASLIQAQRDYFG AH/TYELWAKPGQFIH/TNWTG HGGTVSSSSYNALFSVQFFK SVVRDS |
| 20898 | 51266 | A | 21021 | 3 | 316 | |
| 20899 | 51267 | A | 21022 | 2 | 578 | LIGLAVMGQNLILNMNDHGFV TVSKVDDFLANEAKGTKVVGA QSLKEMVSKLKKPRRIILLVKA GQAVDDFIEKLRRCDLKAKGI LFVGSVSGGEEGARYGPSLMP GGNKEAWPHIKTIFQGIAAKVG TGEPCCDWVGDEGAGHFVKM VHNGIEYGDMQLICEAYHLMK DVLGMAQDEMALCPIFCVF |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20900 | 51268 | A | 21023 | 3 | 1758 | AYANLGTRFWREPLRVFPSLVLRASPLFGSALSAMAQADIALI V\LFVMGHNILNMDHGFVC AFNRTVSKVDDFLANEAKGTK VVGAQSLKEMVSKLNKPPRDQ YLLC/VKAGQAVDDFIEKLVPL LDTGDI\IDGGNSEY*GTPQDG CRDLKAKGILFEGS\GVSAGEE GD\RYGP\SLMPGGNK\EA WPHI KTIFQGIA\AKVGTGEPCC\DWV GDEGAGHFVKMVHNGIEYGD MQLICEA YHLMKDVLGMAQD EMAQAFEDWNKTELD SFLIEIT ANILKFQD TDGKHLLPKIQGTS AGARRGNRSGT/WPFSGPGKY GVPV\TLIGEAVFARCLSSLKD ERI\QASKKLKGPQK\FQFDGD* EHSWEDIRKALYASKIISYAQGF MLLRHAA\TEFGWTLNYG\GIA LMWRGGCHRSVFLGKIKDAFD RNP\ELQNLLD\DFFKVQLFEN CQ\DSWR\RAVSTGVQGWAFP MPLFYRLPLSI*TGTSHEMLPAQ PSSRLQRGLLSGAHTL*NSWAK PGAVLFHTNWTG\HGGTVSSSS YQCLDHAAPVTLHDSTVPGHSI GLNGTAHLALCPIFCSVFFKSV |
| 20901 | 51269 | A | 21024 | 317 | 885 | MRWRSKSAWRAEPKSRNTSGT ASNVSPSRPLEC*R/FLRLVSGE LILALIAFICIETIMACSPCEGLY FFEFVSCSAFVVTGVLLIMFSLN LHMRIPQINWNLTDLVNTGLSA FLFFIASIVLAALNHRAGAEIAA VIFGFLATAAYAVNTFLAVQK WRVSVRQQSTNDYIRARTESRD VDSRPEIQRLDT |
| 20902 | 51270 | A | 21025 | 4761 | 5127 | LGSGDLPWEINPLSSCSLLREKD PPTTSGPQT\TSRNPISPISNPHT TSKRLNRSGQAF\QNLLPQELA TSARNLTTRPRNACSPGFLLSR VPSVRDPTGNWTVQLTWQPLS EPELWPKAL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20903 | 51271 | A | 21026 | 174 | 2238 | LRSGDLPWEINPLSSCSLLHEKD PPTTSGPQT\TSPRNISPISNPRQR RHILSMDPKLRRRSWTWVGSPLP LVFNHCRDASLIHPGFRGVRPR RDVCLGPSPLATITDAELYVTL TVEGKSIPFLIDTEATHSTLPSFK GPVALASIHVQNVQIKRDKEGH YIMVKGSIQQEELTILNMYAPN TGAPRFIKQVLNDLQRDLDSHT IIMGDFNTPLSTLDRSTRQKVN KDIQDLNSALHQADLIDIYRTL HTKSTECTFFSAPHRTYSKIDHI VGSKALLSKCKRTEIINCLSDH SAIKLELRRIKLTQNHSTTWKL NNLLLNDYWVHKEMKAEIKM FFEINENKNTTYQNLWDTFKAV CRGKFIALNAYKRKQERSKIDT LTSQLEELEKQEQTRSKASRE EITKIRAELEKETQKTLQKINES RSWFFEKINKIDILLARLIKKR EKNQIDAIKNDKGDIATDPTEIQ TTIREYYKHLCPNKLENLEEMD KFLDTYTLPRLNQEEDESLNRPI TGSEIVAIINSLPTKKSPGPDGFT AKFYQRYKEELVPFLQKYKEEL VPFLLKLFQSIEKEGILPNSFSEA SIILIPKPGRDTTKKENFRPISLM NIDAKILNKILANQIQQHIKKLI HHDQVGFIPGMQGWFNIRKSIN VIQHINRTKDKNHMHSIDA EKA FDKIQQPSC |
| 20904 | 51272 | A | 21027 | 1 | 181 | MEEKEERKRRRKRKRRREEGR DGERKRMEKQKENQDPKDPPT TSGPQT\TSPRNISPISNP |
| 20905 | 51273 | A | 21028 | 167 | 408 | LGSRTFPWEINPPSSCSLLREKD PPTTSGPQT\TRPRNISPISNLVS GLFLLSSPTSLTIPQLSSFNLDL TLQSLPSLNF |
| 20906 | 51274 | A | 21029 | 449 | 663 | LGSGDLPWEINTQSSCSLLCEK DPPTTSGPQT\TSPRNISPISNPDP TGNRTVQLTWQVPPEPELWPKAL |
| 20907 | 51275 | A | 21030 | 79 | 381 | LGSGDLPWEINPLSSCSLLREKE PPTTSGPQT\TRPRNISPISNP TLA GNLATGPRNARSPGFLLSH VLSVWDPTENQTVQLTWQPLP QPLELWPKAL |
| 20908 | 51276 | A | 21031 | 122 | 334 | LRSGDLLWEINPLSS*SLLHEKD PPTTSSPQT\TSPRNISPISNPDP ENQTVQLTWQPLPEPELWPKAL |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 20909 | 51277 | A | 21032 | 109 | 320 | LGSGDLP*EINPPSSCSLLREKD PPTTSGPQTVTSPRNISPISNPDP GNRTVQLTWQPLPQPLELWPK AL |
| 20910 | 51278 | A | 21033 | 620 | 717 | |
| 20911 | 51279 | A | 21034 | 3 | 678 | GGGFSDRDRRTIALQPGQQIWM WGIGKQVGGCGWLRGKNRVV GAAKDQSGTGEKFYFIPKAMG AMEGSGQRRTLPDPAHRNPS GGYSATDCEGSRPAPGEINSHA SHTKPVWWFFTQTRMKFGAVT RIGGLPWEVNPLSSCSLLRE/KD PPTTSGPQSNQPRKHPPISNP VHVPEIWPLGQGMPAARIPPKP RPICVGPH*KSTVQLTWQPLPEP LELWPRLSD |
| 20912 | 51280 | A | 21035 | 339 | 1098 | LGSGDLPWEINPLSSCSLLREKD PPTTSGPPTVTSRNISPISNPGET KETRFIRGPKTPAPVTDWEGSL PLVFNHCRDASLIHPRFKGVRP RRDACLGPSPLAASPTFLGKGQ RLKTDARLPRKPPRPSRTLSFS TAPRILSIVVPGSGHTLAFLDVT RHRLYRESKPVVGEEDYSEW LSDVGKSEWSFSTCASSTSVNK HDTGRRLLGKRGGMESKGL CNFITMTKNIRSLAQMTIWQYL SPCREPV |
| 20913 | 51281 | C | 21036 | 1 | 438 | |
| 20914 | 51282 | A | 21037 | 174 | 483 | LRSGDLPWEINPLSSCSLLHEKD PPTTSGPQTVTSPRNISPISNPQR RHILSMDPKLRRRSWTWVGSPL LVFNHCRDASLIHHPGFRGVRPR RDVCLGPSPLA |
| 20915 | 51283 | A | 21038 | 590 | 824 | PNSSWMRGEPPKDPPTTSGPQTV TSPRNISPISNPGRLSDYSPRFQ RCQTTQGRLPWSFTLSGKSRSFS GEGATWGLKT |
| 20916 | 51284 | B | 21039 | 1 | 1596 | |
| 20917 | 51285 | B | 21040 | 155 | 2206 | |
| 20918 | 51286 | B | 21041 | 1 | 831 | |
| 20919 | 51287 | B | 21042 | 75 | 474 | |
| 20920 | 51288 | B | 21043 | 38 | 1009 | |
| 20921 | 51289 | C | 21044 | 335 | 481 | |
| 20922 | 51290 | B | 21045 | 66 | 652 | |
| 20923 | 51291 | B | 21046 | 1 | 673 | |
| 20924 | 51292 | B | 21047 | 1 | 451 | |
| 20925 | 51293 | B | 21048 | 74 | 3516 | |
| 20926 | 51294 | B | 21049 | 783 | 3463 | |
| 20927 | 51295 | B | 21050 | 1 | 807 | |
| 20928 | 51296 | B | 21051 | 41 | 1700 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20929 | 51297 | C | 21052 | 18 | 381 | |
| 20930 | 51298 | B | 21053 | 1 | 3147 | |
| 20931 | 51299 | B | 21054 | 1 | 2586 | |
| 20932 | 51300 | C | 21055 | 756 | 1403 | |
| 20933 | 51301 | B | 21056 | 42 | 205 | |
| 20934 | 51302 | B | 21057 | 40 | 420 | |
| 20935 | 51303 | B | 21058 | 303 | 1170 | |
| 20936 | 51304 | B | 21059 | 1 | 2631 | |
| 20937 | 51305 | B | 21060 | 19 | 3093 | |
| 20938 | 51306 | B | 21061 | 23 | 241 | |
| 20939 | 51307 | B | 21062 | 84 | 1775 | |
| 20940 | 51308 | B | 21063 | 68 | 1542 | |
| 20941 | 51309 | B | 21064 | 74 | 2566 | |
| 20942 | 51310 | C | 21065 | 730 | 1023 | |
| 20943 | 51311 | B | 21066 | 67 | 1159 | |
| 20944 | 51312 | B | 21067 | 294 | 929 | |
| 20945 | 51313 | B | 21070 | 68 | 336 | |
| 20946 | 51314 | B | 21071 | 1 | 1992 | |
| 20947 | 51315 | B | 21072 | 1 | 4188 | |
| 20948 | 51316 | C | 21073 | 44 | 535 | |
| 20949 | 51317 | B | 21074 | 983 | 2636 | |
| 20950 | 51318 | B | 21076 | 289 | 1693 | |
| 20951 | 51319 | B | 21077 | 364 | 2393 | |
| 20952 | 51320 | B | 21078 | 471 | 590 | |
| 20953 | 51321 | B | 21079 | 1 | 1026 | |
| 20954 | 51322 | B | 21080 | 343 | 4253 | |
| 20955 | 51323 | B | 21081 | 1 | 819 | |
| 20956 | 51324 | B | 21082 | 648 | 894 | |
| 20957 | 51325 | B | 21083 | 1 | 1236 | |
| 20958 | 51326 | B | 21084 | 1 | 822 | |
| 20959 | 51327 | B | 21085 | 211 | 363 | |
| 20960 | 51328 | B | 21086 | 193 | 264 | |
| 20961 | 51329 | B | 21087 | 1 | 1260 | |
| 20962 | 51330 | B | 21088 | 143 | 3158 | |
| 20963 | 51331 | B | 21089 | 85 | 353 | |
| 20964 | 51332 | B | 21090 | 221 | 598 | |
| 20965 | 51333 | B | 21091 | 1 | 4878 | |
| 20966 | 51334 | B | 21092 | 171 | 362 | |
| 20967 | 51335 | C | 21093 | 320 | 408 | |
| 20968 | 51336 | B | 21094 | 1 | 1218 | |
| 20969 | 51337 | B | 21095 | 1 | 1761 | |
| 20970 | 51338 | B | 21096 | 315 | 1224 | |
| 20971 | 51339 | B | 21097 | 526 | 3482 | |
| 20972 | 51340 | B | 21098 | 41 | 4858 | |
| 20973 | 51341 | C | 21099 | 38 | 250 | |
| 20974 | 51342 | C | 21100 | 157 | 225 | |
| 20975 | 51343 | C | 21101 | 191 | 415 | |
| 20976 | 51344 | B | 21102 | 42 | 507 | |
| 20977 | 51345 | C | 21103 | 71 | 367 | |
| 20978 | 51346 | C | 21104 | 231 | 439 | |
| 20979 | 51347 | C | 21105 | 207 | 459 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20980 | 51348 | A | 21106 | 1 | 429 | |
| 20981 | 51349 | A | 21107 | 184 | 544 | VRLLKILQLQRFKMYVQQDL TYFLRKIKCTLENGIVMSNTEA ESGVQLKPGRWGASALYSSHHI IH*A*LLVPR*VSNVCSRNDT* TKNKDTKNRRC*PKSSTRRGK* KRERKEKEVT |
| 20982 | 51350 | A | 21108 | 3 | 1200 | LSQKEEEEDTFIEEQQLEEEKLL ERERQRLHEEWLLREKQAQEE FRIKKEKEEAACKRQEEQERKL KEQWEEQQRKEREEREEQKRQE KKEKEKTFMWKPSVDLFSHLA SLRTPICQDKGNAYQEHFPEK KKKRSSQLAIPGAFGYPHHLL AILGLRCSRKHNFPTSSPTLLIKS MFTTFGMEQCRRDDYDPDASL EYSEEETYYQFLDFYEDVLPF KNVGKVIQF/KGLFEIQQCPRGK HCNFLHVFRNPNEFWANRDI YLSPDRGTSSFGKNSERRERM HDDYYSLRGRNPNPSPDHSY KRNGESERKSSRHRGKKSHKRT SKSRERHNSRSRGRNRDRSRDR SRGRGSRSRSRSRSRSRSRSQ SSSRSRSRGRRRSGNRDRTVQS |
| 20983 | 51351 | A | 21109 | 789 | 907 | |
| 20984 | 51352 | A | 21110 | 236 | 1823 | CPIQRQSPGPAQTGRWEPLPCT VPITLRMSEGGAGKMAALE KMTFPKKMTFPEKPSHKKYRA ALKKEKRKIRRQELARLRDSSL SQKEEEEDTFIEEQQLEEEKLLE RERERLHEEWLLREKQAQEEFR IKKEKEEAACKRQEEQERKLKE QWEEQQRKEREEREEQKRQEK EKEEALQKMLDQAENELENGT TWQNPEPPLDFRVMKDGVN CPFYSKTGACRFGDRCSRKHYP PTS\PTLLIKSMFTTLGMEQCAR RDDYDPDASLEYSEEETYYQFL DFYEDVLPFKNVGKVIQFKVS CNLEPHLRGNIYVQYQSEEEC QAALSLFNGRWYV\AGRQLQC EF*TGDRWKMAICGLFEIQQCP RGKHCNFLHVFRNPNEFWEA NRDIYLSPDRTGSSFGKNSERRE RMGHDDYYSLRGRNPNPSPD HSYKRNGESERKSSRHRGKKSH KRTSKSRERHNSRSRGRNRDRS RDRSRGRGSRSRSRSRSRSRSS RSQSSSRSRGRRRSGNRDRT |
| 20985 | 51353 | A | 21111 | 289 | 366 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 20986 | 51354 | A | 21112 | 1 | 1289 | |
| 20987 | 51355 | A | 21113 | 60 | 367 | EELGYAGRGMGARQPPPPARKA VSPLQERAEPVGSPPG*GWRSRP STHGIASHGGPACSLCSLHFTFF VDFPSLFSPICLPEGWDWQQEQ PCLLYLSSPRCTQA |
| 20988 | 51356 | A | 21114 | 1 | 653 | RRRGSAAAGGRAERKAEVGA MNMAGGKAGKDSGKAKAKA V\RSQR\AGLQFPVGRJHRHLK TRT\TSHGR\VGATAAVYSAAI L\EYLT\AEVLEL\AGYASKDLQ SKSVSLPRHLQLAIPWVIEELDS LIQGLP*AGGGVIPSHPHKSLIG KEGDSKKTALEGMLLTQPLSLP RHLYCNWDKKNNGDMWNFLP PVKWKSIDNYCRHDKRNICMF LDSEV |
| 20989 | 51357 | A | 21115 | 1 | 1019 | SVCWAGGAPRAHSTRTHAWLG RPAMEPGSVENLSIVYRSRDFL VVNKHWDVRIDSKAWRETGRP EP\QVASVEESGSDSGLC/HHSR FCHQLDFSTSGALCVALLVLGG LPGSTGLPRELRAILPLLQLRGH IQESRVSIVRWGGPGPRVSPTNL TPAFCAPGCENPKPSLTGSWSG R*VWIGPAPSLIRHRPHPAGRTH QLRV\HCSALGHPVVGDLTYGE VSGREDRPFMRMLHAFYLRPT DTECVEVCTPDPFLPSL\DACWS PHTLLQSLDQL\AAGLKGQPPD P*TRG*GGPRPGSPSALLPGHGR PPPPTTKPPETEAQRGPCLQWL SEWTLPEDS |
| 20990 | 51358 | A | 21116 | 698 | 1472 | RWAPRRGLSVDLDDGGSSAPLCP PATTARLDAEPHGSLPNSCLWE CSCLLQGIWAAGPSGLSLHYPP LSSPLGSSPPSRPQRLVLIRAGR GGWVGSVGETMTSSYGHVLER QPALGGRLDSPGNLDTLQAKK NFSVSHLLDLEEAGDMVAAQA DENVGE\SSRTRGGGAGLGKGL SGVQTQRASAVWESSRLKMLS RVGRASLGQRMTA*GRLQLYP HAPKSVTDRSPCSSQVTKSWNR GALQHSMIFTKRCLFQTLKE |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 20991 | 51359 | A | 21117 | 50 | 1226 | KMAEEVVVVAKFDYVAQQEQ ELDIKKNERLWLLDDSKSWWR VRNSMNKTGFVPSTYVGR\EN SARKASIVKNLKD TLGIGKVKR KPSVPDSASPADDSFV\DPGERL Y\DLNMPA\YVKFN\YMAERED ELS\LIKG\TKVIVMEKCS\DGW WRGTYNGQVGWFPSNYVTEE\ GESPLGDHVGSLSEKLA AVVN NLNTGQVLHVQALYPFSSSN DEELNFEK\GDVMDVIEKPEN PEWWKCRKINGMVGLVPQKL W*PLLQSIQLTSGLT LTFCG IRPYIPGKFVGNPWYYGKVTRH QAEMALNERGHEGDFLIRDSES SPNDFS VSLKAQGKNKHFKVQ LK\ETVYCIWQRKSCTME*LVE HYK\KAPNFYNVNKGEKLYLV |
| 20992 | 51360 | A | 21118 | 132 | 428 | |
| 20993 | 51361 | A | 21119 | 3 | 337 | AKLAGA AVPVCARGRAAPLAA AALPAARL\PSGAGPAGLVSDV RRRPFARE/PEPRVP/SQPPALSA LGALALKLFSSPPSCWSFSVKT GVLVPWIMCISWPYFLSGNLLT MMW |
| 20994 | 51362 | A | 21120 | 438 | 1066 | LNQKGKGGRGEALKNDLVVAP PPSPRRGVR*EALHVPDTGPFK KPRKRK*NQRQREAERK*TFPR EEEARRETHGPLPAPRPPPLCP/ PAASSAPRPGPKGAR*LSLSAE GRARRRSAGASGGAGAAATAA AAAAP EHPRGSEPRQPASPAPQ RERPRRPAPRLPPQCPRPSKGRA WTLQTTTGQKVCTGAGTRRA WRRAGAVRRFAWA |
| 20995 | 51363 | A | 21121 | 1 | 924 | |
| 20996 | 51364 | A | 21122 | 1 | 435 | |
| 20997 | 51365 | A | 21123 | 1 | 524 | |
| 20998 | 51366 | A | 21124 | 1 | 602 | MGKGSPAHAQGP GSFLHGGAG DQGRGRPITLYEDRGFQGRHY ECSSDHPNLQAYLSRCNSVRVD SGCWVLYEQPNYSGLQ*FLRR GDYADHQQWMGLSDSVRSCR LIP\HASSHRLRIYEREDYRGQM VEITEDCSSLHDRFHLSEIHSFN VLEGSWVLYELPNYQGRQYLL RPGDCRWQDWDGATDARVGS LRRAVELY |
| 20999 | 51367 | A | 21125 | 1 | 1239 | |
| 21000 | 51368 | A | 21126 | 298 | 408 | |
| 21001 | 51369 | C | 21127 | 92 | 241 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21002 | 51370 | A | 21128 | 33 | 191 | RDDPRVRPPPNST*PQQEPGL* LIKCTSPQAPAPRTVHGPYFY MRLIKMF |
| 21003 | 51371 | A | 21129 | 3 | 1285 | |
| 21004 | 51372 | A | 21130 | 3 | 3468 | QPGHTIYLLPTVVICNLLPCELD FYVKGMPINGTLKPGKEAALH TADTSQNIELGVLENFPLCKEL LIPPGTQNYMVRMRLYDVNRR QLNLTIRIVCRAEGSLKIFISAPY WLINKTGLPLIFRQDNAKTDA GQFEEHELARSLSPLLFCYADK EQPNLCTMRIGRGHPEGMPGW CQGFSLDGGSGVRALKVIQGG NRPGLIYNIGIDVKKGRGRYIDT CMVIFAPRYLLDNKSSHLAFA QREFARGQGT |
| 21005 | 51373 | A | 21131 | 3 | 451 | |
| 21006 | 51374 | A | 21132 | 2 | 107 | LEGLEES/VRDRCKKEFTDLMIE MDSRLLGPTSKVK |
| 21007 | 51375 | A | 21133 | 2 | 158 | PGIPVL/DYRTYTDGFFSLPSKD GDKDVMITGKLDILKPQNQHR VFTVESRVI |
| 21008 | 51376 | A | 21134 | 2 | 5632 | FVRRTCRESRCWPGAETELDH WSLGEGVRGAMALQLWALT LGLLGAGASLRPRKLDFFRSEK ELNHLAVDEASGVVYLGAVNA LYQLDAKLQLEQQVATGPALD NKKCTPPIEAS\QCHEAEMTDN VNPLLLVDPPRKRLVECGQLLK G\ICALRALSNI SLRLFYEDGSG EKS FVASNDEGVATVGLV SSTG PGGDRVLFVGKGNGPHDNGIIV STRLLDRTDSREAFEAYTDHAT YKAGYLSTNTQQFVA AF |
| 21009 | 51377 | A | 21135 | 168 | 5568 | AREKCGGAMGAGSSTEQRSPE QPPEGSSTPAEPEPSGGGPSAEA APDTTADPAIAASDPATKLLQK NGQLSTINGVAEQDELSLQEGD LNGQKGALNGQGALNSQEEEE VIVRQVDHIDSEDVSDRDSDE MTTKSAVVHDITDDGQEETPDI IEQIPSESNEELTQPTESQAND IGFKKVFKFVGFKFTVKKDKTE KPDVTQQLTVKKDEGEAAGA GDHQDPSLGAGEAASKESEPK QSTEKPEETLKREQ |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21010 | 51378 | A | 21136 | 807 | 1162 | ISYHGGRRRRPQ/PVGPLGSCRS *SSRRWSTTGRITFRAGWKSCS TPPSTSSLPTSTGTW*GPGTSAL LPPTPLPPPRAAATPCACACASE SRMPAARALGLRVRRRLLEGRS GKDTQG |
| 21011 | 51379 | A | 21137 | 1 | 562 | |
| 21012 | 51380 | A | 21138 | 1 | 423 | |
| 21013 | 51381 | A | 21139 | 1 | 1871 | MTTFKEAMTFKDVAVVFTEEE LGLLDLAQRKLYRDVMLENFR NLLSVGHQAHRDTHFLREEK IWMMKTAIQREGNSGDKIQTE METVSEAGTHQEWFSQQIWEKI ASDLTRSQDLVINSSQFSKEGDF PCQTE/ARTICNSHKTEI/FPRA/I GYKPSFSDVSHFDHFQQLHSGE KSHTCDECGKNFCYISALRIHQ RVHMGEKCYKCDVCGKEFSQS SHLQTHQRVHTGEKPFKCVCEC GKGFSRRSALNVHH |
| 21014 | 51382 | A | 21140 | 1056 | 2988 | FCILIGDKIQTEMETVSEAGTHQ EWSFQQIWEKIASDLTRSQDLV INSSQFSKEGDFPCQTEARTICN SHKTEIFPRAIGYKPSFSDVSLF DFHQQQLHSGEKSHTCDECGKN FCYISALHMHQRVHMGEKCYK CDVCGKEFSQSSHLQTHQRVH TVEKPFKCVCECGKFSRRSALN VHHKLHTGEKPYNCEECGKAFI HDSQLQEHQRIHTGEKPFKCDI CGKSFCGRSRLNRHSMVHTAE KPFRCDTCDKSFRQRSALNSHR MIHTGEKPYKCEECGKGFIARR DLYTHHMHVHTGEKPYNCKECC KSFRWASCLLKTSSSESHSGVEKP FKC\EECGKGFYTISQCYSHQR SHSGEKPYKCVCECGKGYKRRRL DLDFHQRVHTGEKLYNCKECC KSFSRAPCLLKHERLHSGEKP QCEECGRFTQNSHLHSHQRI/V HTGEKPYKCEKCGKGYNSKFI YMHQRVHTGERPYNCKECCGK SFGWASCLLKHQRLHSGENPFK CEECGRFTQNSQLHSHQRVH TGEKPYKCDCECGKGFSSSTR LTHQR\RH\SRETPLKCEQHGK NIV\QNSFS/EKLPEKVHQC*KK PYKCEDL/CGKGYNRRL*IL\DM HQR\VHMGEKTVKCRECDMCF \SQAS\SLRLHQNVHVGEKP |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21015 | 51383 | A | 21141 | 154 | 1470 | KDGDHMGYTYKVIERILEIGAF RPHMSLGQLQSARGVACLGCK GTCSGFEPHSWRKICKSC\NAA KRTTA*HLT*KNDRKLGRWLR DSKYSTLHLLG*KAGTASGFYK RNP\MI\LTNPIATGKDPTFDTIT YEWGSPWEFTQETGDCSYMGA HSPREEGSQLTGHQRGAFYRA ARPAHAPGLPIYD\QDPLALPVD FWRNELKTEWKEFVK\KYKSE GPSALGEVALPGQGWLAPRKE GE/GSRKKPEGGRP/PAATTNG SLSDPSKEVEYVCELCKGAAPP DSPVVY\SDRAGYNKQWHPTCF VCAKCSEPL\DLIYFWKDGAP WCGRHYCESLRPR/CAPACDEI\ IFAEDYQRVEDLAWHRKHFVC EGCEQLLSGLGVHRHPGVQLL VPQLAASPKRSLKGCPTPQPESP GIPTEKDKPGCARDPSLRVPDV TSKPSEINQ |
| 21016 | 51384 | A | 21142 | 1 | 1332 | |
| 21017 | 51385 | C | 21143 | 147 | 272 | |
| 21018 | 51386 | A | 21144 | 160 | 374 | ETPVSSRCEKHVSSPHLCPGIHR AVSLSSH\STCGRSWRSELHGPO STNLSGNTLPLHFLFGAWQTG VFKM |
| 21019 | 51387 | A | 21145 | 3 | 4366 | LGAQQRELQEALGARAALAL LGRLQAERRGLDAAHERDVRE LRARAASLTMHFRARATGPAA PPRLREVHDSYALLVAESWRE TVQLYEDEVRELEEALRRGQES RLQAEETRLCAQEAELRREA LGLEQLRARLEDALLRMREEY GIQAEERQRAIDCLEDEKATLT LAMADWLRDYQDLLQVKTGL SLEVATYRALLEGESNPEIWIW AEHVENMPSEFRNKYYHYTDS LLQRENEWNLFSRQKAPLAS |
| 21020 | 51388 | A | 21146 | 1 | 4617 | RVIDCLEDEKATLTAMADWL RDYQDLLQVKTGLSLEVATYRI VEHVAVEGVSKLWKPLWQKS QSLVISSGVSTGGRLNLERLRR GPTPLASTESVKQVLVNNRMII DDEMVKTLAMSRTCSAPNPLT ADVKTWSRSYSEDAATGPVL GVASTVALLEGESNPEIWIWAE HVENMPSEFRNKSYHYTDSLL QRE\NERNLFS\RQKAPLASFNH SSALYSNLSGHRGSQTGTSIGG DARRGFLGSGYSSATT |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21021 | 51389 | A | 21147 | 2 | 435 | |
| 21022 | 51390 | A | 21148 | 1 | 1233 | MCEEETALVCDNGSGLCKAG FAGDDAPRAVFPSIVGRPRHQG VMVGMGQKDSYVGDEAQSQR GILTLKYPIEHGIITNWDDMEK KKEAEELARNMAIQQELEKEK QRVAQQKQQQLEQEQFHAFEE MIRNQELEKERLKI VQEF GKVD PGLGGPLVPD/SGEALLRCVPHL NSLIHTAFRLSHNCKAS*ATCG GQVLETWSTEQLRKYSHNRWI APCGGAWAAVPTVSPVSQCQH CPGSGDMWNSLWKTDEE*1YH YPCSHPPQAKCWV*LLQHRERR RTFPHTGSAGPHHTGLDSCQF *AVREHGVR\GIHETTYNSIMKC DIDIRKDL YANNVLSGGTTMYP GIADRMQKEITALAPSTMKIKII APPERKYSVWIGGSILASLSTFQ QMWISKPEYDEAGPSIVHRKCF |
| 21023 | 51391 | A | 21149 | 2 | 1273 | PRVRPRVRPRVRS LGEEPLIPSV LRSPAHSATHMCEEETALVC DNGSGLCKAGFAGDDAPRAVF PSIVGRPRHQGVMVGMGQKDS YVGDEAQSQRGILTLKYPIEHG IITNWDDMEKI WAPLLTMEI RVSTWKRHPTLLTEAPLNPKAN REKMTQIMFETFNVPAMYVAI QAVLSLYASGRTTGIVLDSD GVTHNVPIYEGYALPHAIMRLD LAG\RDLDYLMKIL/AKRGGY SFVTTAEREIVRDIKEKLCYVAL DFEK* \MATAASSSSLE\KSYELP DGAGLSPIGWTL\CPETLFQP YFISNGVPLEFNDDNLTIPSMK\ CDIDIP*GLICPTMFLSGGTTHV PWALLDRIQKENPSPGPPGTMK IKNIAPPEREVTSVWD/LGGSILA SLSTFQAMWISKPEYDDAGPSI VHRKCF |
| 21024 | 51392 | A | 21150 | 95 | 674 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21025 | 51393 | A | 21151 | 1 | 1536 | MGGGEQGTLRTAENQGLQVCP GEAGSSLGFSGNTPTNGLPARG DQTSYRDFWSGPQFPDTSRLTA APGAREQCGTHGEGSTLEGSR PDVPQDLFSPTLGFYGSTYPELE QGMLGGH*G/PAENQGLQVCP GEAGSSLGFSGNTPTNGLPARG DQTSYRDFWSGPQFPDTSRLTA APGAREQCGTHGEGSTLEGSR PDVPQDLFSPTLGFYGSTYPELE QGMLGGHVEASREYQMLSHV GNPDYPHALATEQATSPSTESG SAGFKGVALAMLSKITMCVRIG ILVFQQDQGSMDKAFSTTGMM LVTYLLTCRAWRLQCGASYR AHDVNVLPGCSGPAALLLGDW FSLHSSDAVLPAQQGQMLSQ EADACITLPHLFPSREVVFLLGL EAGGLIPGAEGPPEDMGLVRGP PAVAAGPPPRWLSPEFCLLQYS EEEGCKEPLWLKVEAEVSTLYR FMPTGFTRGPFNIEHREWGNTT ATWTRMISNHNKHSQRGRKMT ARLPCGGAPHFSDRTDDKWRR SSLLTRSGCQTERLLTSQTEPLP AGGSPHFSNGETGQRRSSPPQR GCDRPQALLTSKTEQQRKSASH ISYDERPGKDAPHFLDGMVAG KRRSSLSRLGSQA |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|---|
| 21026 | 51394 | A | 21152 | 689 | 2176 | PATSPTSRAMAQPSAPAASMLL PCPECPGPRFMTCCLSVSTFCS PSLRRPPGSIKSSGLGGG\SSRT SCRLSG\ALGAGSCRLGSAGGL GSTLGG\NSYSSCYSFGSGGGY GSSFGG\VDGLLA\GGEKA\TMH NLIDF\LASYLDK\PCPWKEAN TELEV\KIRD\WYQRQ\APGPAR DYSQYYRTIEELQNKILTATVD NANILLQIDNARLAC/ADDFT K\FETEQA\RLS\VEADINGL\R RVL\DELTLARADL\EMQIENLK EEAWPTLKERTTEGRRLNALR GQVGW*RSMLEMDAAPGVDL SRILNEMPSCVDHRVTRCINRP GAELKLGGSGGWTEELKREVA NSELVQSGKSKISEL\RTMQAL EIELQSQLSMKA\SLEGNLGGD RATAYCVQLS\QIQGL\IGSGED QL\AQLR\C\EMEQQ\NQDYKILL DVKTRLEQEIATYRRLLEG\ED AHLT\QCKKEPVTTTRQV\RTIVG KRSRD\GKVILLPRSRFHQTTR |
| 21027 | 51395 | C | 21153 | 58 | 252 | |
| 21028 | 51396 | A | 21154 | 2 | 190 | |
| 21029 | 51397 | A | 21155 | 2 | 432 | KMADGVVDHIDIYADVGEFNO EA EYGGHDQIDLYDDVISPSAN NGDAPEDRDYMDTPPPVPGYG PPPGPPPPQGGPPPPPGFPFPRPP GPLGPPLD/TLAPPPHLPGPVPPG \APPPA\PHVEPSFLFLPPINS GLHSDRPRFH |
| 21030 | 51398 | A | 21156 | 1 | 1070 | MGGIGARAAAAGKGRRRRARA PPGLPPPTSDGGGGAASSLR RLHAAPPPGPSAAGSASRVPTI GSEAAPAREDRRLHSGRVRAS GSPRLTRPRPVKRRGRTRGGGA PRQGSAAARPGGKGAHSAVAS ARAAAGPGSASRPHGAASAAG TWALTYLVLEFADIRVNVYVV HAVRHLPSACAAAAAASCRF ALVGVGSEASSKKLMDLLPKR ELHGQNPVVTPCNKQFLSQFE MQSRKTTQSGQMSGEGKAGPP GGSSRAAFPQGGRRGRFPGA VPGGDRFPGPAGPGGPPPPFQD PSVNSDPVCGTFG/EH*PPGYQT PSNLSVRPMAKPKPEGTDLSRS REGFFKSRFAPN |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21031 | 51399 | A | 21157 | 63 | 1750 | MKMAGGVNHIDIYADVGE*FN QEAEYGGHDQIDVHDDAISP ANNGDAPEDRDYMDTLPPTVG DDVGKGAAPNVVYTYTGKRIA LYIGNLTWWTTDEDLTEAVHS LGVNDILE\IKFFENRANGQSKG FALVGVGSEASSKKLMDLLPK RELHGQNPVVTPCNKQFLSQFE MQSRKTTQSGQMSGEGKAGPP GGSSRAAFPQGGRRGRFPGA VPGGDRFPGPAGPGGPPPPFA GQTPPRPLGSFQGPAPGPPPP PGQVLPPPLAGPPNRGDRPPPV LFPQQPFGQPPLGPLPPGPPPV PGYGGPPGPPPPQGGPPPPGPF P\PRPTGSNLGHPLTLAPPSAFP GP\PP\GAPPPSPHVNPAPFPPT NSGMPTSDSRGPPPTDPYGRPPP YDRGDYGPPGREMDTARTPLS EAEFEEIMNRNRAISSAISRAV SDASA/GVDYGSAIETLVTAISLI KTIPKYPADD/RCTKFLISSLQD CLHGIESKSYGSGSRRRERSRER DHSRSREKSRRHKSRSDRHDD YYRERSRERER\HRDRDRD\RD RERDREREYRHR |
| 21032 | 51400 | A | 21159 | 1 | 96 | TNFKSGLLGAAED*HCPIASE AP*TITDAEL |
| 21033 | 51401 | A | 21160 | 1 | 1056 | MWKGPKGLDMYGKSSVSPKTS DILGRDTLLLALKVQTVVLQTA CGEGHVAGNCGRPLETEGSLQ LTATKKLRDSVLQPKSPEFCQQ FTRAWNRTQVPDETEAPAGTY AAQSGDLPWEINPLSSCSLLHE KDPPTASGPQTDQPKHELTNFK SGFRGVVP/LQGRLPWSFTLSGK SRFSGEGASTPTPSLCVSTPSPPF WGARNTPQLLLHPEWQ/CPLF* RSKYPNLVSLCPSPLFPRPDLLS L/SAQSLISAPQLISLCPNPLFPC PDLLSLHPNPLFPRPNPFPAFLE GACYKCQKSGHQAKECLQPGI PPKLRPICAGPHWKSDCPHTLA ATPRAPGTLAQGSLTASQIFLA |
| 21034 | 51402 | C | 21161 | 283 | 408 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion; \=possible nucleotide insertion) |
|------------|--------------------------------------|------------|-------------------------------------|--|---|---|
| 21035 | 51403 | A | 21162 | 3 | 505 | ILNPVSGLFLFSSPLSLNLSSLSL NLFLLSILAPHFNLSILLISIPFIFP LEIELSNSPGSHSQSPWNSGPRL SDSFPDLLGLAAEE*HCPIASEA FSQTYRAYLSLSLSLSLSPEPPT AGDGVTH/HSSPVASTTITVLGQT /SKPAQCWLPKVCCHHSLTSD YVHPRP |
| 21036 | 51404 | A | 21163 | 164 | 420 | LANFCEESGAGEPGSHSQSPWN SGPRLSDSFPDLLGLAAEDRHC PIASEAPLLQRKSLYKSPCTSSTI S*CCIPRSGISELSVN |
| 21037 | 51405 | A | 21164 | 50 | 298 | |
| 21038 | 51406 | A | 21165 | 49 | 433 | SSSGIWPSHSQSPLRSSPAKLLS RFRCSSLSSLLLCLATLLLWQP LPEPLELWPKA/HLTDSFPDLLG LAAED/W/HCIPISEAP*TLTDAE LRVTLTVEGKSIPFGAGKEVTL ESYWVSLTLSFLICYMII |
| 21039 | 51407 | A | 21166 | 282 | 374 | CDLFLPHPN*SMYFVISPTPKKV LCNSPHT |
| 21040 | 51408 | A | 21167 | 71 | 333 | LRSGLPWEPINPLSSCSLFREED PPTTS GPQTNQPKHELTNFKSA AED*RCQFASEAP*TITDAKL RV SLTAEGLLATLFLNPKPEY |
| 21041 | 51409 | A | 21168 | 113 | 342 | AFGCFTTG VGRVTDSDGPLYTG PWAPGSHSQSPWNSGPRLSDSF PDLLGLAAED*HCPIASEAPFLT LIFLLCVIQ |
| 21042 | 51410 | A | 21169 | 301 | 608 | TFTPLKSYIKAPSSAGPVAEQE MTPEGKV GAGPE*LTWKNQFL FY |
| 21043 | 51411 | A | 21170 | 2 | 724 | FLVSLMLPPAVVMLNHCYSLIF TNALVKRLF AWMNLSELATCA GNLATGPRNARSPGFLLSCVPS VRDPTGNQTVQLTWQPLPEPLE LWPKA/HLTDSFPDLLGLATED *HSPIASEAPWAIMDAELRVTL TVEDRDSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSPCD LFLPHPN*SMYFVISPTLK KVL Y NVTHP*EVSL*FSPPLRM YFVRS IPCPQNIALNSTAYP |
| 21044 | 51412 | A | 21171 | 442 | 501 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21045 | 51413 | A | 21172 | 266 | 1003 | SCMCLALDPCNHGEGHQPDFS GVKFRRHGADNHEASAATATT AAATTVAIAAAAAAAAAAAR VTLTGSHFQSPWNSGPRLSDSF PDLLSLATED*RCPIASEVPWTI TEAELRVTLTVEGKSIPCLIDTG ATHSTLPSFQGPVSLAPITVVGMI DGQASKPLAKTPPLWCQLGQH SFMHSFLVIPHL/CPIFLIRGRNIL TKLSASLTIPGSTANISLVAFFP NPKPPLCPLTSPQYHPLQDLPS A |
| 21046 | 51414 | A | 21173 | 2 | 245 | LTALLRKSLDPRLISTGENTQTA ETMGPLSAPPCTQHITWAKGLLL TAETPKPSISSNLNPRGGHGRL CALILLILEDSG |
| 21047 | 51415 | A | 21174 | 3 | 324 | |
| 21048 | 51416 | A | 21175 | 3 | 552 | |
| 21049 | 51417 | A | 21176 | 3 | 435 | |
| 21050 | 51418 | A | 21177 | 3 | 1459 | GAVRTWGRGFQTEKCQASLLN FWNPPTTAQVTIEAEPTKVSKG KDVLLL VHNLPQNLAGYIWYK GQMKDLYHYITSYVVDGQIIHY GPAYSGRETVYSNASLLIQNVT REDAGSYTLHIVKRGDGRGET GHFTFTLYLIPWTL LYL* RSLA QVSHYETPGKTAPPCGSTA**L N*PPDLTLFSPVLFLLKYPVPGQ AFQYPKGLKTIGSSITHL*DVLG KGSCRENIPRAAK*D*N*EDSST ACSK*GPQVETPKPSISSNLYP REDMEAVSLTCDPETPDASYL WWMNGQSLPMTHSLQLSKNK RTLFLFGVTKYTAGPYECEIRN PVSASRSDPVTNLNLLPKLPKPYI TINNLPRENKDVLAFTCEPKS ENYTYIWWLNGQSLPVSPRVK RPIENRILILTQCSREMKQGPY QCEIQDRYGG\IRSYPTLECP/ HITTKHSGLYACSVRNSATGME SSKSMTVKVSAPSGTGHLPLGLN |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21051 | 51419 | A | 21178 | 3 | 1445 | IRADPAHELENCSCPGKRLSTE RGRTAQLTAVLREFLDPRLISTE ENTQAAETMGTLSPAPPCTQRIK WKGLLLTASLLNFWNLPTTAQ VTIEAQPPKVSEGKDVLLLVHN LPQNLTGYIWYKGQMRDLYHY ITSYVVDGEIIIYGPAYSGRETA YSNASLLIQNVTRDAGSYTLH IHKGGDDGTRGVTGRFTFTLHLET PKPSISSSNLNPRETMEAVSLTC DPETPDASYLWWMNGQSLPMT HSLKLSETNRTLFLLGVTKYTA GPYECEIRNPVSASRSDPVTNL LPKLPKPYITINNLNPRENKDVL NFTCEPKSENYTYIWWLNGQSL PVSPRVKRPIENRILILPSVTRNE TGPYQCEIRDYGGVRSRSDPVT NVLYGPDLPRIYPSFTYYRSGE VLYLSCSADSNPPAQYSWTINE KFQL\QGQKLFIP\HITTKHSGLY V\CSVRNSATGKESSKSMTEV SGKWIPASLAIGF |
| 21052 | 51420 | A | 21179 | 3 | 1380 | TAQLTAVLREFLDPRLISTEENT QAAETMGTLSPAPPCTQRIKWK GLLLTASLLNFWNLPTTAQVTI EAEPTKVSEGKDVLLLVHNLQP NLTGYIWYKGQMRDLYHYITS YVVDGEIIIYGPAYSGRETAYSN ASLLIQNVTRDAGSYTLHIIKG DDGTRGVTGRFTFTLHLETPKP SISSSNLNPRETMEAVSLTCDPE TPDASYLWWMNGQSLPMTHSL KLSETNRTLFLLGVTKYTAGPY ECEIRNPVSASRSDPVTNLNLLPK LPKPYITINNLNPRENKDVLNFT CEPKSENYTYIWWLNGQSLPVS PRVKRPIENRILILPSVTRNETGP YQCEIRDYGGIRSDPVTNLNL YGPDLPRIYPSFTYYRSGEVLL LVLF CGTLNPPAQYSWTINEKF QLPGQKLFIRHITTKHSGLYVC SVRNSATGKESSKSMTEVSAY SSSINYTSGNRN |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21053 | 51421 | A | 21180 | 2 | 1341 | TEGGRTAQLTAMLRQLLDPRLI STEENTQAAETMGPLPAPSCTQ RITWKGLLLTASLLNFWNPPTT AEVTIEAQPPKVSEKGDVLLLV HNLPQNLPGYFWYKGMTDLY HYIISYIVDGKIIYGPAYSGRET VYSNASLLIQNVTRKD\AGT\YT LHIIK\RGDETREEIRHFTFTLYL ETPKPYISSSNLNPREAMEAVR LICDPETLDASYLWWMNGQSL PVTHRLQLSKTNRTLYLFGVTK YIAGPYECEIRNPVSASRSDPVT LNLLPKLPIPYITINNLNPRENK DVLAFTEPKSENYTYIWWLN GQSLPVSPGVKRPIENRILILPSV TRNETGP\YQCEIRDYGGIRSY PVTNLNLYGPDLPRIYPSFTYYR SGENLDLSCFTESNPPAEYFWPI *GKFQQSGQKLFIPQITRNHSG LYACSVHNSAAGKEISVSLFRH |
| 21054 | 51422 | A | 21181 | 1 | 1532 | MTQFPMDKRQGRSRVAITNT AVTSLEWVPFHAFAPRSTLVS QQRLSTERGRTAQLTAVLREFL DPRLISTEENTQAAETMGTLA PPCTQRIKWKGLLLTASLLNFW NLPTTAQVTIEAEPKVSSEKGD VLLLVHNLPQNLTGYIWAYKGA MR\DLHYHYVTSYVVDGQIIKYG \PAYSGRETAYSNASLLIQNV\T RED\AGSYTLHIIKGDDGTRGV GRFTFTLHLETPKPSISSSNLNP ETMEAVSLTCDPETPDASYLW WMNGQSLPMTHSLKLSETNRT LFLLGVTKYTAGPYECEIRNPV SASRSDPVTNLNLLPKLPYITI NNLNPRENKDVLNFTCEPKSEN YTYIWWLNGQKPP/VSSPRVKR PH*KTGSLIPTPVFTRNETGP\YQ CEIRAR\YGG\IRSDPVTNLNLY GPDLPRIYPSFTYYRSGGKSSY LSCFCGTSNPP\AQYSWTIN*K VFSLPGTKALYSRHITTKHSGL YVCSVRNSATGKESSKSMTVE VSDWTVP |
| 21055 | 51423 | B | 21182 | 28 | 29751 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21056 | 51424 | A | 21183 | 158 | 1660 | EASLLEDDDDGMVYLRPLTSHQ YRTAQLRAMLRKFLDPRLSSTE ENTQAAETMGPLSAPPCTQRIT WKGLLLTASLLNFWNPPTTAQ VTIEAEPTKVSKGKDVLLLVHN LPQNLAGYIWYKGQMKDLYH YITSYVVDGQIIYGPAYSGRE VYSNASLLIQNVTRDAGSYTL HIVKRGDGTGETGHFTFTLYL ETPKPSISSSNLYPREDMEA VSL TCDPETPDASYLWWMNGQSLP MTHSLQLSKNKRTLFLFGVHK VHCRDPMECEIREPS*VASRS*P SSPWNL LPK\PKPYITINNLNP REKKDVLAF\CDPKSRNYTYI WWLNGQSLPVSPRVKRP\IENR DPSFL\SVTRNETGP\YQCEIRD \RYGG\IRSYPTLVNLYG\PDLP RIYPFISPIYHFREENLRTLSCFC GTFNPPGRVFLGTINGGSFQVIQ GQKALYSPRITTKHSGA/LYAW LCSVTSRPLAWESSQIPWT\KV SGSFQGTGTSSWGLNPL |
| 21057 | 51425 | A | 21184 | 927 | 1378 | QPPTLRSWDCWFAWGKRQLM SSP/STEPQVCFTIEGHEIDFLG TGMAFSVLISCPG*LSSRSVTIR GILG*PVTRYFSHLLSCNWETLL FSHNAKTQGGGTLTPKPSKSH RPWAVRGLAPGPAAAVLNFSP GLSCLPTGQGLGPAAHHA |
| 21058 | 51426 | A | 21185 | 1 | 221 | ILLAQLESQDGDILRQRDEFDLL VAGEICRFSALIEELE\EKNERPA RELLTVRPEPEPCPTCAVLRLLH LCLA |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21059 | 51427 | A | 21186 | 335 | 1963 | VCDPALPPWAKQREWALEGSH SSRTSMGLLVASVTSIGRWKF NCPI/CVQGTLEAGSLSNCG/H KNFCRACLT\RYCEIP/GPDLEE SP\TCPLCKEPFRP/GSFRPNWQ LANVVENIERLQLVSTLGLGEE DVCQEHGEKIYFFCEDDEMQL CVVCREAGEHATHMRFLDA A\APYREQIHKCLKCLKEREI QEIQSRENKRMQVLLTQVSTKR QQVISEFAHLRKFLQEQSILLA QLESQDGDILRQRDEFDILLVAG EICRFSALIEELEKNERPAREL LTDIRSTLIRCETRKCRKPVAVS PELGQRIRDFPQQALPLQREMK MFLEKLCFELDYEPAHISLDPQ T\SHPKLPLVPRTIQR\AQFS*QM GRTSPDNPQ\RF\DRATCVSRPT LGITGGRHTWVVSIDLAHGGSC TVGVVSEDVQRKGELRLRPEE GVWAVRLAWGFVSALGSFP\TR LTLKEQPRQVRVSLDYEVGWV TFTNAVTRPIYTFTASFTRKVI PFFGLWG\RGS\SFSLSSLRSSY LLSSKYRTHINPSTMWT |
| 21060 | 51428 | A | 21187 | 217 | 397 | |
| 21061 | 51429 | A | 21188 | 529 | 1526 | YCGRVGELAAGELVFLWSRVG PQNPRSSRLPPPTLAMFLTRSEY DRGVNTFS\PEGRLFQVEYDIEA IKLGSHSQLAPRHREGV\ALAV\ EKRIYLPHLMGAQAGI*GKLLG DLMLHIGLLPIEWGLICMLKT FNSIKSRVGRHR/YPWGSPYNG GH*QWESFEPKLCPNLGFSSFG EEDAESRVPM\SRLGSSHLFIW EELYEKGTPSLFP*GTPFWGPFV PVWMARSQFGSGFQRGAPRAP LPRKFPPTSPMTFERSPPSPSPHP SLKQVMGGRKLNANQTIEPRPT VPALAENFPHCSQRKKLEEVQ GHFKESWILRTSLGTISVLNNVP |
| 21062 | 51430 | A | 21189 | 211 | 382 | TSVSPSVPLPC*RHPGEPQTGN NASNGTSSSRDESPPVRVPPPP QTAVAITLSTA |
| 21063 | 51431 | A | 21190 | 3 | 96 | FFFPPQKYD*DR*EHPRFHKTLR NWRVGAQ |
| 21064 | 51432 | A | 21191 | 1 | 1320 | |
| 21065 | 51433 | A | 21192 | 1 | 339 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21066 | 51434 | A | 21193 | 289 | 3694 | MAFVPVIPESYSHVLAEFESLDP LLSALRLDSSRLKCTSIASVRK WLALGSSGGGLHLIQEGWKH RLFLSHREGAISQVACCLHDDD YVAVATSQGLVVVWELNQERR GKPEQMYVSSEHKGRRTALC WDTAILRVFVGDHAGKVSIAK LNTSKQAKAAAAFVMFPVQTIT TVDSCVVQLDYLDGRLLISSLT RSFLCDTEREKFWKIGNKERDG EYGACFFPGRCSGGQQPLIYCA RPGSRMWEVNFIDGEVI |
| 21067 | 51435 | A | 21194 | 2 | 128 | |
| 21068 | 51436 | A | 21195 | 1041 | 2238 | LLHPAQRSLSKDGTKESEDAA LMGEEGKPEINQQLSLESMELD ELALEKYPIAAPLPYPEKSSD GVGNPEAKILSGTPTYKRRVISL LVTIENHTPLVELSEYLGNTLS EILDSPWEGAKNVYKCPECDQ NFSHLSYLVHLHQIHSGEKKHK CGDCGKIFNHRANLRTHRRHT GEKPYKCAKCSASFRQSHLSR HMNSHVKEKPYTCSICGRGFM WLPGLAQHQKSHAENTYEST NCDKHFNEKPNLALPEETFVSG PQYQHTKCMKSFRQSLYPALSE KSHDEDSERCSG\CGDNFFFSK FKPLQCPDCDMTFPCFSELISHQ NIHTEERPH*\CKTCEESFALDSE LACHQKSHMLAEPFKCTVCGK TFKSNLHLITHKRTHIKKHHVK |
| 21069 | 51437 | C | 21196 | 156 | 389 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21070 | 51438 | A | 21197 | 1 | 2466 | MLSRLFRMHGLFVASHPWVVI VGTVTLTICMMSMNMF TGIAG LFTIFSSFVFSTVVIHFLDKELTG LNEALPFFLLLLIDLSRASTLAKF ALSSNSQDEVRENIARGMAILG PTFTLDALVECLVIGVGTMSGV RQLEIMCCFCGCM SVLAN YFVF MTFFPACVSLVLELSRESREGR PIWQLSHFARVLEEEENKPNPV TQRVKMIMSLGLVLVHAHSRW IADPSPQNSTADTSKVSLGLDE NVSKRIEPSVSLWQFYLSKMIS MDIEQVITLSLALLLAVKYIFFE QTETESTLSLKNPITSPVVTQKK VPDNCCRREPMLVRNNQKCDS VEEETGINRERKVEVIKPLVAET DTPNRATFVVGNSSLLDTSSVL VTQEPEIELPREPRNNEECLQIL GNAEKGAKFLSDAEIIQLVNAK HIPAYKLETLMETHERGVSIRR QLLSKKLSEPSSLQYLPYRGY NYSLW*WGACCENVIGYMPPI VGVAGPLCLDEKEFQVPMATT EGCLVASTNRGCRAIGLGGGAS SRVLADGMTRGPVVR LPRACD SAEVKAWLETSEGFAVIKEAFD STSRFARLQKLHTSIAGRNL YIR FQSRSGDAMGMNMISKGTEKA LSKLHEYFP*NCRF*AVSGNYC TDKKPAAINWIEGRGKSVVCET VIPAKVVREVLKTTTEAMIEVN INKNLVGSAMAGSIGGYNAHA |
| 21071 | 51439 | A | 21198 | 236 | 3022 | GEGSFRSATALTGARLSVGAGV RWPLVRSGGSKDSVATMLSRL FRMHGLFVASHPWVIVLTGT LTICMMSMNMF TGNKICGWN YECPKFEEDVLSSDIILITRCIA ILYIYFQFNLRQLGSKYILGIA GLFTIFSSFVFSTVVIHFLDKELT GLNEALPFFLLLLIDLSRASTLA KFALSSNSQDEVRENIARGMAI LGPTFTLDALVECLVIGVGTMS GVRQLEIMCCFCGCM SVLAN YF VFMTFFPAC |
| 21072 | 51440 | A | 21199 | 1 | 450 | CKSRGSNLRVHFKN TRETAQAI KGMHIRTATKY LKDVTLQKQC VPFRRYNGGVGRCAQAKQWG WTQGRWPKKSAEFLVIEHIQV NKAPKMRRRTYRAHGRJNPYM SSPCHIEMILTEKEQIVKPPEEEV AQKKKISQKKLKKQKLMARE |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21073 | 51441 | A | 21200 | 1 | 876 | |
| 21074 | 51442 | A | 21201 | 1 | 1725 | |
| 21075 | 51443 | A | 21202 | 278 | 889 | SVKMVRYSLDPGGTTPRKSC/S QRGSNLRVPFKDHS*KLPQAHQ RVCHIRKSPTKY\LKDVHLTRN QCVPIPDYNG*QLGQVCRRHK QMGP GTTKGR\WPQKGVLKFL PAHALKTAE\SNAEL\KGLDVDS LVIEHIQVNKAP\KMRRRTYR AHGRINPYMSSPCHNIEM\ILTEK EQIVPKPEEEVAQKKKISPEETE RNKNLLARE |
| 21076 | 51444 | A | 21203 | 1 | 1923 | |
| 21077 | 51445 | A | 21204 | 1 | 280 | |
| 21078 | 51446 | A | 21205 | 1 | 109 | |
| 21079 | 51447 | A | 21206 | 1 | 638 | |
| 21080 | 51448 | A | 21207 | 1 | 396 | |
| 21081 | 51449 | A | 21208 | 26 | 969 | HGVGCRDGLPMECRFLCQIFM AFMQMNSYCARHKKATRRTV* /CRNQDMTESSQKWTGKGS AV EHLVESGEWTMHPARPVSACR CPSDCHVPLSPGACWPKLECLS EGSSYISDGKEYLFYLNVCGET EIQFCNKKQAAVCQVKKSDTS QVKAAGRYHNQTLRPSESSWS LLFVVLVFFPGVHSPFSLDEALT LCPQNCLPPGTVSAPLNCVYPL ALSAAVALAAGSELMECHRLV NSLEVSTAAQGQSSKTQFYACL CRLSTHLWKYSEESGRRLVCSF YQPSELNPALNLSFLVGTRLQE GAALLFIQSGFTIV |
| 21082 | 51450 | A | 21209 | 1 | 465 | |
| 21083 | 51451 | A | 21210 | 217 | 453 | |
| 21084 | 51452 | A | 21211 | 1 | 840 | |
| 21085 | 51453 | A | 21212 | 1 | 663 | |
| 21086 | 51454 | A | 21213 | 176 | 957 | DEPIGVPLLSAPPAGTTKIKADQ LHLQGAAPKICPCLQDGS LGQH YCPFVSFSRYYINLCQKIYKGPL GCSERASICRRTTTGDVQVLG\L VHTQKLG VIGPRVVVTTSKRY PCGGNKTASSVIELTCTKPVGR PAFKRFEIDSCITYYFSWDSGAA CAVKPQEVQM VNGTITNPINGK SFSLGDIYFKLFRASGDMRTNG DNYLYEIQLSSITSSRN PACSGA NICQVKPNDQHFSRKVGTS DKT KYYLQGNPWLP TKFHI |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21087 | 51455 | A | 21214 | 3 | 7616 | SPVEPRSPRAPAPSPPPPLPWRR DPVPGAAPSSRAPLASRPPRSSG PGAMGAAAGRSPHLGPAPARR PQRLLLLLQLLLLVAAPGSTQA QAAPFPELCSYTWEAVDTKNN VLYKINICGSVDIVQCGPSSAVC MHDLKTRTYHSVGDVLSRSAT RSLLEFNTTVSCDQQGTNHRVQ SSIAFLCGKTLGTPEFVTATECV HYFEWRTTAACKKDIFKANKE VPCYVFDEELRKHDLNPLIKLS GAYLVDDSDPDTS |
| 21088 | 51456 | A | 21215 | 2 | 184 | VNCQPLGMISLMKR\PPGFSPFR SSRIGEIKEETTSHLRSCYKGR PPKAGAEPASEREVS |
| 21089 | 51457 | A | 21216 | 1 | 203 | |
| 21090 | 51458 | A | 21217 | 1 | 1107 | |
| 21091 | 51459 | A | 21218 | 1 | 915 | |
| 21092 | 51460 | A | 21219 | 1 | 1932 | |
| 21093 | 51461 | A | 21220 | 2 | 746 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21094 | 51462 | A | 21221 | 1 | 2157 | MGFPLRPSPAHLSSGRQQFPAK EERLLLSLTQESQSEEIDCNDKD LFKAVDAALKKYNSQNQSNQ FVLYRITEATKTVGSDTFYSFK YEIKEGDCPVQSGKTWQDCEY KDAAKAATGECTATVGKRSST KFSVATQTCQITPGGWFILWHC PGGKLTISDYPNSSRVLHCTQC VQGLNRRTRRHKTCPPLQAAS QIEERIGFEGRPGLESFRAPCLL ASPFPCLEKGAEGPVVTAQYDC LGCVHPISTQSPDLEPILRHGIQ YFNNNTQHSSLFMLNEVKRAQ RQAAP/GREFSSMDTFEGYEGA EDMEKLAGPFPVG*QSRNLFLQ IRFPGEEKHPGRKRRTR*GSN GDRQHQEGACWGVHAG*LLR GRRLVSRGRGARGPPPRRAAL PAVAPAPRLQSARIPERGDGDD GVRRWGHREAIGS*GQS/LS/CN GIIILIKEERLPCPFHCISLMKRPP GFSPFRSSRIGEIKEETTVSPPH SMAQAQDEERDSGKEQGHTRR HDWGHEKQRKHNLGHGHEQ RDQGHGHRGHLGHGHEQQ HGLGHGKFKLDDDLHQGGH VLDHGKHKHGHGHEGKHKNK GKKNKGKNGWKTEHLASSED STTPSAQTQEKTEGPTPIPSLAK PGVTVTFSDFQDSDLIATMMPP SPAPIQSDDDWPDIQIDPNGLSF NPISDFPDTTSPKCPGRPWKSVS |
| 21095 | 51463 | A | 21222 | 207 | 424 | HHINCVLLYLQSHLRS\CEYQG\ RPPKAGAEPASE\REVSLTNWA ESSTPRHIAPTTASNLEMEGQE ERWDRI |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21096 | 51464 | A | 21223 | 170 | 1487 | IMKLITILFLCSRLLLSLTQESQS EEIDCNDKDLFKAVDAALKKY NSQNQSNNQFVLYRITEATKTV GSDTFYSFKYEIKEGDCPVQSG KTWQDCEYKDAAKAATGECT ATVGKRSST\KFSVATQT\CQITP AEGPVV\TAQLRTCLG/CVWHPI IQRQSPDLEPILRHGIQYFNNNT QHSSLFTLNEVKRAQRQVVAG LNFRITYSIVQTNCSKENFLFLT PDCKSLWNGDTGECTDNAYIDI QLRIASF SQNWDIYPGKD VVQ PPTKICVGCPRDIPTNSPELEETL THTITKLNAENNAISYFKIDNVK KARVRVVAGKKYFIDFVAR\ET TCSK\ESNEELTESCETKKLG\Q RLG\CNAE\VVVVPWEEKIYPT/ VFNCSTTGEWIFT*WKRPPRVF SPFRS\SRIGEIKEET\TSHLRSCE YKGRPPK\AGAEPASEREVS |
| 21097 | 51465 | C | 21224 | 21 | 281 | |
| 21098 | 51466 | A | 21225 | 204 | 441 | QISQVLIICNQK*VILTGNFLDT YF*TTFINKKIDELRLCA/CAVA HSYNTTLCKKPRWKDCLRPV QDQPVQHSETLSL |
| 21099 | 51467 | A | 21226 | 333 | 604 | SSDRITKPPSAEFLPLQRTFLHSL QDTVIELLH*DLETPLTLVLQNH PSLPRPIAPPTLCPQTRWPHLR GHQGILAASHILETALAAIF |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21100 | 51468 | A | 21227 | 846 | 3269 | GFMEVLRDPIKKNSSSESKPAQS GFSRGN SPLSCPESVEASPAVNE KSVYSTHNYGTTQRHGCRGLP YADHNYGAPPPPTPPASPPVQTI IPRSDLNGLPSPVEERCSDSPNS EGETVPTWPCGLSQDGFLLNC DKCRGMSRGKVIRLHRRKQDN ISGGDSSATESWDEELSPSTVLY TATQHTPTSITLTVRRTPKRR KKSPEKGRAAPKTKKIKAFREG SRKSLRMKNPSEAQNLDENTT EGWENRIRLWTDQYEEAFTNQ YSADVQNALEQHLHSSKEFVG KPTILDTINKTELACNNTVIGSQ MQLQLGRVTRVQKHKILRAA RDLALDTLIEYRGKVMLRQQF EVNGHFFKK\PYPFVLFLLQNL NGVEMCVDARTFGNDARFIRR SCTPNAEVRHMIADGMIHLICIY AVSAITKDAEVTIAFDYEYSNC NYKVDCACHKGNRNCPIQKRN S*CYRTATPTTSSKPTHHSRD *T*KSRRKELEMEQQNEASEEN NDQQSQEVPEKVTVSSDHEEV DNPEEKPEEEKEEVIDDQENLA HSRRTREDRKVEAIMHAFENLE KRKKRRDQPLEQNSDVEITTT TSETPVGEETKTEAPESEVSNSV SNVTIPSTPQSVGVNTRRSSQA GDIAAEKLVKPPPAKPSRPRPK SRISRYRTSSAQRLKRQKQANA QQAELSQAAL EEGGSNSLV TPT |
| 21101 | 51469 | A | 21228 | 2 | 197 | CRPPSPRPVRAARPARPQASFSR EPPPRRMAP*SKRRRQSARGPV RPSRVWARIKAKPYSCCCQL |
| 21102 | 51470 | A | 21229 | 4 | 488 | GSYDINRQDTFQKDRQRVGPSG ASQKTEGFLRLLYSGLIIAHCS LEILGRNDPPASASKVAETTD GSLSLANT*PPTPR/VTSQTANA TSQAAPALPLGSVPGRRAADPR PLLA WAPAPPGPGTSRNTHPAP DGLDMLVPIGDGVLGGNCFRN QCKSVSTS |
| 21103 | 51471 | A | 21230 | 124 | 293 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21104 | 51472 | A | 21231 | 239 | 1393 | IYPQISFQKKFVMFFFSEALCTA RAEEDCDPIGLLNNPRTSRYSRL KPNSSLGGSESRTQMGPLPPP PKSPDGARVPVPGCIKEAGPARG RSRLAPNPGALRRG/VGLGR*S ARI*GLVSKAAAGQGGEARRGE AT*ARGALGRTTAGSFNAGWL TLDGARQQPGRQTPTRIPSCVA DNAAGPSRTTTPD/EALRPLRG GPACTAPASFDSRAPYSASSAPS EGRWPSRGFPPI/PLYSQLPETR SHEWQAASKIQPRKASTSQ*SA RMEAT*QQWAGPPAEP*SLWFP RLARRSVVHWRTPY/ISSITSPL PVAAGIPEDSGPGSTQSSSRPGN TSSSSRPPPPPPPP/QPLPPPPA GLASRPVRARRPARPQASFSR EPPPRRMAP |
| 21105 | 51473 | A | 21232 | 107 | 234 | |
| 21106 | 51474 | A | 21233 | 224 | 227 | LPQPGPGRRRACLRQASPRQYS RLPGRPPPSG*SW |
| 21107 | 51475 | A | 21234 | 67 | 607 | QRSWAGPGAGPEAGTRPPARG RRRQPGNVDPRRRAPQLRSQM QVAMARATTATGNRLWPGLLI MLGSVCHRGSPCGLSTHVEILL LEHQDAYQAGIVFPDCFYPSIC KGGKFHDVSESTHWTPFLNAS VHYIRENYPLWEKDTEKLVAF LFGITSHMAADVSWHSLGLEQ GFLRTMGAI |
| 21108 | 51476 | A | 21235 | 54 | 193 | |
| 21109 | 51477 | A | 21236 | 1275 | 1764 | STKCQYFSHLLLLFSASESKQLL LYSAFFRYVPVKDLLGIYEKLYI CFISLLQTGL*RYQE*YHIHFIFS FSLP*LYPTYSTKSPFLVEQFQE YFLGGLDDR*NSCL*RSR*MAN SFDCFLSDSVLQGVVFSVVTSL FLFLFNSSKMQKNDFHRNLTTTS |
| 21110 | 51478 | A | 21237 | 297 | 428 | QCQRGPGCSRGHGI*I*EHWTA FGLDLRLQWFARGSWASGHGP |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21111 | 51479 | A | 21238 | 3247 | 5958 | QRSWAGPGAGPEAGTRPPARG RRRQPGNVDPRRRAPQLRSQM QVAMARATTATGNRLWPGLL MIVMASLCHRGSSCGLSTHIEIG HRALEFLHLHNGHVNYKELL EHQDAYQAGTVFPDCFYPSLC KGGKFHDVSESTHWTPFLNAS VHYIRENYPLPWEKDTEKL VAF LFGITSHMVADVSWHSLGIEQG FLRTMGAIDFHGSYSEAH SAGD FGGDVLSQFEFNFNYLARRWY VPVKDLLGIYEKLYGREVITEN VIVDCSHIQFLEMYGEMLA VSK LYPSYSTKSPFLVEQFQEYFLG GLDDMAFWSTNIYHLTSFMLE NGTSDCSLPENPLFIACGGQQN HTQGSKMQKND FHRNLTSSLT ENIDRNINYTERGVFFSVNSWT PDSMSFIYKALERNVRTMFIGG SQLSQKHVSMP LRHHYFLSFPY ARLGWAMTSADL\NQDG\HGD LRGWGAPGLTAAPAHIPHSGR VYLIYGNDLGLPPVDL DLDKEA HRILEGFQPSGRFGSALAVLDF NLDGVAPDLAVGAPSVGSEQLT YKGAVYVYFGSKQGGMSSSPN ITISCQDIYCNLGWTLAADV N GDSEPD LVIGSPFAPGGGKQKG IVAAFYSGPSLSDKEKLNVEAA NWTVRGEEDFSWFGYSLHGVT VDNRTL LLVGSPTWKNASRLG HLLHIRDEKKS LGRVYGYFPPN |
| 21112 | 51480 | A | 21239 | 2 | 403 | VVAEEDTEL RDLLVQTL ENSGV LNRIKAELRAGVFLAEEQEKV ENKTP LVNESLKKFLNTKD LQ GLEGREN LARDLGII EAEGTVG GPLLLEVIRRCQ QKEKGPTTGE GALDLSDVHSPPKSPEGK TSAQ |
| 21113 | 51481 | A | 21240 | 3 | 1699 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21114 | 51482 | A | 21241 | 3 | 1812 | APRLKMGLHPNKPVSQSRVVN DGQCKLHAAVDSRDPDPGTR RVSSGGTGLPGPGRGPGLPAGA WLSAEGRGAGGSGDCGPSSGS AEPTQRPPRPSALPGAIPPLHLG LAPFRLASEAVAEQAPPPAPTLS FGAQWSGAPQGSVSSVNPEGA GPARCASGRGFGCVGRVARAR SVPCCGRWPLARLRRLSWRSK MAATAAAV\VAQEDTEL RDLL VQTLNSGVLNR\KAELRAAV FLALEEQEKVENKTPLVNESLK KFLNTKDGRLVASLVAEFLQFF NLDFTLA\VFQPETS/TIF*LLF*L QGLEGREN LARDLGIIIEAGTV GGPLL\LEVIRRCQKEKGPTTG EGALDLSDVHSPPKSPEGKTS QTTPSKIPRYKGQGGKKKTSQK AGDKKANDEANQSDTSVSLSE PKSKSSLHLLSHETKIGSFLSNR TLDGKDKAGLCPDEDDMEGDS FFDDPIPKPEKTYGLRKEPRKQ AGSLASLSDAPPLKSGLSLAG APSLKDSESKRGNTVLKDLKLI SDKIGSLGLGTGEDDDYVDDFN STSHRSEKSEISIGEEIEEDLSVEI DDINTSDKLDDLTQDLTVSQLS DVADYLEDVA |
| 21115 | 51483 | A | 21242 | 419 | 651 | TNIFSR LNPQTKNVFCARQLSS* SVTI*GVLGQAVTRYFSQALSC DWGTL LFSRAFLIMPESPTPLLG RDILAKAGA |
| 21116 | 51484 | A | 21243 | 555 | 888 | RTSSRRTPNPCSRIRKNYFKFH MEPKKSP/S*PRQC*AKRTKLEA SCYLTSNYTTRLQ*PKQHGWG TIRSFSSHEAIFQTITWGKTLDN TRLSRTEVPAAFHSA LCPWF IET |
| 21117 | 51485 | A | 21244 | 728 | 1428 | |
| 21118 | 51486 | A | 21245 | 238 | 505 | INVGRHHVILQGLSCPGQLSSRS VTI*G\VLGQAVTIYFSQPLSCD WRTLLFSHVFLIMPESPTPLLGR DILLYVCIGRFPIFRADCRT |
| 21119 | 51487 | A | 21246 | 940 | 1434 | QLAPCTLTEPRVCLTIEGQEVN CFLDTRAAF\VLLSCPRQLSSRS VAIRGVLGQAVT*YFSQPLSCD WGTLRFSHAFLIMPKSPTPLLG RDILAKAGAIHEKRKAFMRKR EIKKQARSSKVHTSAASSCART APLGESFAEHLIKIADFTPPSSSS PCTTLFFS |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21120 | 51488 | B | 21247 | 747 | 1138 | |
| 21121 | 51489 | A | 21248 | 1685 | 2051 | SSSRTEGARGKRQPMPS/STEP RVCLTIEGQEVNCLLDTGAAFS VLLSCPGQLSSRSVTI*GVLGQP VTRYFPQPLSCDWGTLLFSNAF LIMPESPTLLGRGILAKAGAIH HAVLVTAAL |
| 21122 | 51490 | A | 21249 | 2 | 1014 | GGAGPVVLRRAACSPGPAPR AARPPAMEPGPDGPAASGPAAI REGWFRETCSLWPGQALSLQV EQLLHRRSRYQDILVFRSKTY GNVLVLDGVIQCTERDEFSYQE MIANLPLCSHPNPRKVLIIIGGE GG\VL\REVVKHPSVESVVQCEI DEDVIQVSKKFLPG\MAIGYSSF EADTYMWGDGF*VSWKQKQ\D AFDVI\IDSSDPMGPA\ESLFKES YYQLMKTA\LLREDGVL\CCQG \ECQWLHLDLIKEMRQFC\QSL FPV\VLAYAYCTIPT/YTPSGQIG FMLCSKNPSTNF\QEPVQAVDN SSKVAKMQLK\Y\YNSEARATAA AFVLPE\FARQGLE |
| 21123 | 51491 | A | 21250 | 3 | 418 | FSYEKLLNWQEFVADLEHHSY RSFLGLTCLKQISTRTEDFIIDTL ELRRDMYILNESLTDPAIVKPL AEEMLSYARDDTHYLLYIDK MKLQMRERGNRQTVQLHVWV QRSRDICLKKFIKPIFTDESYLE LYRKLLK |
| 21124 | 51492 | A | 21251 | 1 | 1704 | |
| 21125 | 51493 | A | 21252 | 1 | 3104 | MFDTHQAARLLNLGRHSLDHL LKLYCNVDSNKQYQLADWRIR PLPEEMLSYARDDTHYLLYID KMRLEMWERNQGPVQLQVV WQRSRDICLKKFIKPIFTDESYL ELYRKQKKHLNTQQLTAFQLL FAWRDKTARREDESYYVLPN HMMLKIAEELPKPQGIIACCN PVPPLVRQQINEMHLLIQQARE MPLLKSEVAAGVKKSGPLPSAE \RENVKSQPVQVHL*QRPVLT GRKLLPACTFYMPACWGL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21126 | 51494 | A | 21253 | 2 | 2775 | QALARRAVQAEKMAPPSTREP RVLSATSATKSDGEMVLPGFDP ADSFVKFALGSVVAVTKASGG LPQFGDEYDFY\RSFPG\FQAF ETQGDR/LCFQCMSRVMQVPM GC\RSNIKDRSKVTELEDKF\D LL\VDAN\DVILERVGILLDEAS GVNKNQQPVLPAQLQVPKTVV \SSWNRKAAEYGKKAKSETFRL LHAKNIIRPQLKFREKIDNSNTP FLPKIFHSNPMVQ\KPLPQALSK ERRERPQDRPE |
| 21127 | 51495 | A | 21254 | 3 | 2668 | QALARRAVQAEKMAPPSTREP RVLSATSATKSDGEMVLPGFDP ADSFVKFALGSVVAVTKASGG LPQFGDEYDFYRSFPGFQAFCE TQGDRLQCMSRVMQYHGCRS NIKDRSKVTELEDKF\DLLVDAN DVILERVGILLDEASGVNKNQQ PVLPAQLQVPKTVVSSWNRKA AEYGKKAKSETFRLHAKNIIR PQLKFREKIDNSNTPFLPKIFIKP NAQKPLPQALSKERRERPQDRP EDLDVPPALADFIHQRTQQVE QDMFAHPYQYELNHFTPADAV LQKPQPQLYRPIEETPCHFISL DELVELNEKLLNCQEFVLDLEH HSYRSFLGLTCLMQISTRTEFII DTLELRSDMYILNESLTDPAIVK VFHGADSDIEWLQKDFGLYVV NMFDTHQARLLNLGRHSLDH LLKLYCNVDSNKQYQLADWRI RPLPEEMLS\YARDDTHYLLIY DKMRLEMWERGNGQPVLQV VWQSRDICLKKFIKPIFTDES LELYRKQKKHLNTQQLTAFQL LFAWRDKTARREDESYGYVLP NHMMLKIAEELPKEPQGIIACC NPVPPLVRQQINEMHLLIQQAR EMPLLKSEVAAGVKKSGPLPSA ERLENVLFPHDCSHAPPDGYP IIPTSGSVPVQKQASLFPDEKED NLLGTTCLIAATAVITLFNEPSAE DSKKGPLTVAQKKAQNIMESFE |
| 21128 | 51496 | A | 21255 | 98 | 286 | HARPRHGPRLRCEVGLRCAPG YAGASARPTCECGDTRYCPQDP NQT*SRPVPIIAHRYCLTG |
| 21129 | 51497 | A | 21256 | 1020 | 1280 | |
| 21130 | 51498 | B | 21257 | 153 | 3804 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21131 | 51499 | A | 21258 | 159 | 579 | PNVRWCPS\CYRNQDDHELQIT HGNKILCGIVWKKIAQVEQMR KFSRLEKQRTHVLSCSDLQAVR RFRGVVSEGSFEMGEKVYKRK DMFQLSLLTEQHGDSTLGSGSS YTQMPAENGSLVHTLVTAAPPF FAEKPHSITAG |
| 21132 | 51500 | A | 21259 | 1 | 1290 | MGASRSQKPGPSRDYSYTAGC DVDQRRRGAQKLSRSDTKRIV MSYGKKALKNDKFEIRAFSSSL EVRYRNQDDHELQIHTGTRFY VELCGFAVTRLRDPMLRHAA MALLPWRPPDYSASLLPDWLP VPSSKVVITYPGFTSIWAFSNT T/LCSEYKYYCEECSKQE/AHK RRKV*KLPMILAP/HLKRFBYK DQLHRFTKLFTRASLRGPRDER LKRVSRLFSLVVVTSRVFDVL LRILHRLGQYVSSEYYVALMCS EGHGPGAEDVTELLQSHEKTE WMRSCFFWMTKSGVFDGIYLW NAFNQEGEDLYKENCKTLMKE VEDAQINGKTSYAHGSEYCK MSILPRILLQISRDDCFKIVLKF CVDHQKTKKCCMITLKSSVVQ LAFTIKISVSEMCAREDFVVVIS FQHSEVPSRQLARCTFKEGYT |
| 21133 | 51501 | A | 21260 | 3 | 142 | |
| 21134 | 51502 | A | 21261 | 1 | 1368 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21135 | 51503 | A | 21262 | 1 | 2420 | MEEVAEAPQPIDPKPLATQPQSI IITTTITTTITTTTITTTTITTTIT IITTTITTTTITTTTITTTTITTTIT TITTTITTTITTTTITTTTITTTIT VITIITTTITTTITTTITPSSSSSPSS QADECWGEAEPLMSRQAHVW LRYRTGCREERPDQELTGSWG HGPRSTLVRAKAMAPPPPLAA STPLLHGEFGSYPARGPFRALT TSQALHIQRLRPKPEARPRGGL VPLAEVSGCCTLRSPSPSDSAA YFCIYTYPRGRRGARRKATRTF RADGAATYEENRAEAQRWAT ALTCLLRGLPLPGDGEITPDLPL RPPRLLLLVPFGGRGLAWQW CKNHVLPmiseaglsfnliqter QNHARELVQGLSLSEWDGIVT VSGDGLLHEVLNGLLDRPDWE EAVKMPVGILPCGSGNALAGA VNQHGGFEPALGLDLLNCSLL LCRGGGHPDLLSVTLASGSR FSFLSVAWGFVSDVDIQSERFR ALGSARFTLGTVLGLATLHTYR GRLSYLPATVEPASPTPAHSLPR AKSELTLTPDPAPPMASPLHR SVSDLPLPLQPALASPGSPEPL PILSLNCGGPELAGDWGGAGD APLSPDSTAGFTSWLSQGSSTLT RLRRGPRNSPILWAPTSHPCPG RGLHVRGPPDHLLPPLGTPLPPD WVTLEGDFVLMALISPSHLSAD LVAAPHARFDDGLVHLCCVRS |
| 21136 | 51504 | A | 21263 | 573 | 1025 | RKQSHEDWRSTNKTGVGHPSA RLYEPPWWAHTWTPPGGSKAP SDP/PLSHQLSPPAGQPHFASPEP TSKTPDPWPGNVFSSFLPQSLP ELRHTLYLPMGTTKPPGSSMIF YT*AQYPGTNSSATICRLLSYKS GQVYPNTGQAPPQQRGR |
| 21137 | 51505 | A | 21264 | 48 | 327 | EELEALRR\QRLAELQAKHGDP GDA\AQQEAKHREAEMRNSILA QVLDQSARAR\VSEQGLIEILKK VSQQTEKTTTVKFNRKVMDS DEDDDY |
| 21138 | 51506 | A | 21265 | 1 | 400 | |
| 21139 | 51507 | A | 21266 | 786 | 905 | VSEQGLIEILKK*CQLTEKTSTV KFNRKVMDSDEDDDY |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21140 | 51508 | A | 21267 | 907 | 1327 | PRLLQRSTPSPWRTEELEALRR\ QRLADAAGQNTGDPGDAA\QQ EAKAPGQAEMRNSILAQVPGSS PAPAPRLSNLSHLVKP*KNLKP V\ENYPYTRLARYWTT*VMTGI RNQGFN*KSLKKVKAQ\QTEKT TTVKFNQKKK |
| 21141 | 51509 | B | 21268 | 1 | 828 | |
| 21142 | 51510 | A | 21269 | 317 | 2390 | KWPKMNPQQORMAAIGTDKE LSDLLDFSAMFSPVNSGKTRP TTLGSSQFSGSGIDERG\GTTSW GTSGQSP\SYDSSRGFTDSPHY SDHLNDSRLGAHEGLSPTPFMN SNLMGKTSESGSFLYSRDTGL PGCQSSLLRQDLGLGSPAQLSS SGKPGTAYYSFSATSSRRRPLH DSAALDPLQAKKVRKVPPGLPS SVYAPSPNSDDFNRESPPSPK PPTSMFASTFFMQDGTNSSL WSSSNGMSQPGFGGILGTSTSH MSQ\SSSYGNLHSHDRLSYPPHS VSPTDINTSLPPMSSFHRGSTSS SPYVAASHTPPINGSDSILGTK GNAAG\SSQTGDALGKALASIY SPDHTSSSFSPNPSTPVGSPSPLT GTSQWPRPGGQAPSSPSYENSL HSLQSRMEDRLDRLDDAIHVLR NHAVGPSTSLPAGHSDIHSLLG PSHNAPIGSLNSNYGGSSLVASS RSASMVGTHR\EDSVSLNG\NH SVLSSTVTTSSDNLNKTQENY *RWPKKSQSGTVVPQEIKT\EN KEKDENLHEPPSSDDMKSDD* SSQKDIKVSSRGRTSSTNEDEDL NPEQKIEREKERRMANNARERL RVRDINEAFKELGRMCQLHLKS EKPQTKLLILHQAVAVIL\SLAQ QVRERNLNPKAACKLRREEEK VSAVSAEPPTTLPGTHPGLSETT |
| 21143 | 51511 | A | 21270 | 2 | 153 | QNASSPSKGSQLLTSKGTKLDG E*V**INRSRLQKVANNKLLWR KLKGQF |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21144 | 51512 | A | 21271 | 1 | 1230 | MRKTQCKNAESSKNQNASFPP KDHNSLTAREQNWIE NEFGELT EVGFRRLNQEEVEFLNRPITGSE IEAIINSLATKK\GPEGFIAEFY*R KTQCKNAESSKNQNASFPPKD HNSLTAREQNWIE NEFGELTEV GFRRLNQEEVEFLNRPITGSEIE AIINSLATKKRTRGIHSRILLEVI TSFYVERGGNAMSFMGKGVTK STILCLLHLSHEMMAQAGSLE WMSLWFLPLGSHSEHIPTQQG LAWLIPLWVDRDPEVRFTSLGL GSALTTLTETGCV ALANSCQNIS GGLWGTVVNILLDQSECSMR RESQHHVDVAKVYHLHPPEW WPKLYLGPLDHSREL RSSVLEC MEQRLEVT LGTTPYFSVPISKFI QAVTTKCLRLGASRFSVCLAGL SAAPEQKIHPPTQQFQQLPHD SVGFLQFSLHPKGNFGSGISSPD RSGDASHYSYPSLWQIRGT SRV KKQTWGSGNLKKWGIHKVQP QRLMMQNDTDEESI |
| 21145 | 51513 | A | 21272 | 1 | 987 | |
| 21146 | 51514 | A | 21273 | 180 | 466 | ARGSERAAASFASMYEGKKT KNMFLTRALEKILADKEVKKA HHSQLRKACR\VALEGNKAETE KQSPPHGEAKAGISTLPPVKSK TNFIEADKYF |
| 21147 | 51515 | A | 21274 | 1 | 1224 | |
| 21148 | 51516 | A | 21275 | 251 | 5986 | SCRCPRLQSPTSTSPFSLFLP LLLLPSSRWEPRVGRAAASFSA SMYEGKKTKNMFLTRALEKIL ADKEVKKAHHSQLRKS/CGRV ALEEIKAE TEKQSPPHG\ EAKAG SSTLPPVKSKTNFIEADKYFLPF EL\ACQSKCPRIV\STSLDCLQK L\IAYGAL*LG NAPDSTTPGKKL IDRIIETICGCFQGPQTDEGVQL QIIKALLTAVTSQHIEIHEGTVL QAVRTCYNILASKNLINQTTA KATLTQ |
| 21149 | 51517 | A | 21276 | 46 | 214 | KLRLTTTSVYAIPNRRRYDGFK LVQSCIFI*NFRS*DLRPPQYMPF LIEGGMTVSNSCRAAFSFTSLC RHRSEAWLQNTNTGGFGSTF |
| 21150 | 51518 | A | 21277 | 306 | 616 | |
| 21151 | 51519 | B | 21278 | 47 | 927 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21152 | 51520 | A | 21279 | 660 | 890 | GGKITASGSPVPRPSGA*ALPSG RCSTPRTSSCPRLPEPPGLAPSP PSAPANTTPDDSHAAP*GTRAH THRPPPH/PTAPSRPPTSPPVAT RTAPKAPQ/HHP/PTSCPTQRPT DPSVHEPSQPLATQHSTQPI*P VIVTQ |
| 21153 | 51521 | A | 21280 | 3 | 213 | |
| 21154 | 51522 | A | 21281 | 349 | 2616 | TTAMAHRKLESVSGMGLDHRV RPGVPVPHSQEPESDMELPLEG YVPEGLELAALRPESPAPEEQE CHNHSPDGDSSSDYVNNTSEEE DYDEGLPEEEEGITYYIRYCPED DSYLEGMDCNAGEEYLAHSAHP VDTDECQEAVEEWTDGAGPH HGHEAEGSQDYPDRQLPIPEDE PSVLEAHDQEEDGHYCASKEG YQDYYPPEANGNTGASPYRLR RGDGDLEDQEEDIDQIVAEIKM SLSMTSITSASEASPEHGPEPGP EDSVEACPPKASCSPSRHEARP KSLNLLPEAKHPGDPQGRGFKPK TRTPEERLKPHEQVCNGLEQP RKQQRSDLNGPVDNNNIPKTK KVASFPSLVAVPGPCEPKNLID GIIFAANYLGSTQLLSERNPSK NIRMMQAQEA VSRVKRMQKA AKIKKKANSEGDAQTLTEVDLF ISTQRIKVLNADTQETMMDHAL RTISYIADIGNIVVLMARRRMPR SASQDCIETTPGAQEGKKQYK MICHVFESEDAQLIAQSIGQAFS VAYQEFLRANGINPEDLSQKEY SDIINTQEMYNDLIHFSNSEN CKELQLEKHKGEILGVVVVESG WGSILPTVILANMMNGGPAAR SGKLSIGDQIMSINGTSLVGLPL ATCQGIIKGLK*PDHR*SFNIVS CPPV/TPRFLYSKRPLKYLQGF SVQNGHICSLMRGGIAERGGVR |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21155 | 51523 | A | 21282 | 20 | 771 | TTPNKQHMMQTRAGSAWYLR SRGCSQGAPQKASSGSGGSSW NRSVATVPGIVLGWRRPELLSE RGCAEARGAGVAGRQRLQLTG VQGKSVVRGRGLLGRREWCR GGGAAPRPTPAGTPVPRRPGTR AGPEEGEGAGAGARAAPEPRP HALSPPAAFGADGQLRPLLLTS LRAHHPGRGGLLLTSPTGHQPR RGRQGTPPPASPSPA/PEEGALP GVLPL*PPSPSP/SESPPHPG GGALAVTRRTAAA |
| 21156 | 51524 | A | 21283 | 1615 | 1985 | LGSTRQAAPGQLRGHQAPAPN SDATAGQGRCRSAD*GWGSR EQI*ALPLSGPAPLLPPLPPL PVPPSPPPSPSPSPPLPPGPP* PPLTFSVVTGGGLWCPPHRKSL NPTSKGVNEY |
| 21157 | 51525 | A | 21284 | 3 | 501 | |
| 21158 | 51526 | A | 21285 | 1 | 2646 | |
| 21159 | 51527 | A | 21286 | 31 | 319 | VIQDLHVPPREESAEQVDDPPE PVYRT*RGSPGPLHRAPLQPPF PARCGRRTTRAPGAPTTTTQT RELPPGSRPLRLPRVPPAQPPL PRWTAT |
| 21160 | 51528 | A | 21287 | 3 | 147 | |
| 21161 | 51529 | A | 21288 | 20 | 600 | PVTPRRTILPWALSVPALPLP* PHPPAGLVMSARTSRCSTPTTS LRSSG*GWRTPGSHSTIQRT LFDGSCPRSLSPLEASINPARM VTPQPRPALQRRRSQQSWML GAGRKSLLPQLL*GPRPWTRQG CSIAPRRQTRESGSGRSTGVPPG LCWRVAS*HSSRTQRPRLQAA* GSLPSFPPLSTQWS |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21162 | 51530 | A | 21289 | 383 | 1800 | TCSTQTSRLNPPRRPRAASLPQT CSRSRPSRAHSLTGRPPRFQSQ MPSRSPCC*IC*NIRIDLCGSVTH SDGRFELVFSGKKLALRASSQD EAEDWLDREVREALQKVRPQQE DEWVNVQYPDQPEEPPEAPQG CLSPDLLSEPAALQGTQFDWS SAQVPEPDAIKESLLYLYMDRT WMPYIFSLSLEALKCFRIKNNE KMLSDSHGVETIRDILPDTSLG GPSFFKIITAKAVLKLQAGNAE EAALWRDLVRKVLASYLETAE EAVTLGGSLDENCQEEKNNTK HTTARNAFEENDFMENTNMPE GTISENTNYNHPPEADSAGTAF NLRPTVKQTETKWEYNNVGTD LSPEPKSFNYPLLSSPGDQFEIQ LTQQQLQSLIPNNNVKRLIAHVIR TLKMDCSGTHVQVTCAKLISRT GHLMKLLSGQQEVKASKIEWD TDQWKIENYINESTEASEQKE KSLEAASGTQDGVHVQEP RPQ APSPDLQQPVESTSSQPSSTV SETAREVGQGNGLQKAQAHDG AGLKLVSSTSPQQVCKLWW SAGLHTPPPVTSLGTVGLQGPQ QRFPKFPDFFHPLEISCGKVA |
| 21163 | 51531 | A | 21290 | 2 | 667 | |
| 21164 | 51532 | A | 21291 | 84 | 377 | RMGKHCFENLLFRDGKAQRAC MGYTVCHSHIVGSGQKCWPA WPQVNLQPSRHQQVCCSLPRC AKCKTVFHQSCQAVVKKGCPR CAR* RKYQQQN VFA |
| 21165 | 51533 | A | 21292 | 2 | 1168 | FVLPVVS GRE TASSARRLRGCR SREPPSPRSSLRLVSCDSLREQL REWRCFQWWRMDWTPRLPSR HIISELEHLTFVNMDVGR CRAW LRLALNNGLMCEYLKLLLQEQ ARLREYYQPTALLRDAEEGEFL LSFLQGLMSLSFELSYKSAILNE WTLTPLALSGLCPLSELDP LSTS GAELQRKESLDSISHSSGSEDIE VHHSCHKIRRNQKPTASSLSLD TASSQLSCSLNSDSCLLQENG KSPDHCEEPMSYDSDLGTANA EDSDQSLQEVLLFEFSKAQAASG TQDGVHVQEPHPQAPSPLDLQ QPVESTSGQQPSSTVSETAREV GQGNGLQKAQAHDGAGLKL VSSPTSPNISSMIQSTRPVHFCIV STKHCTWEKVGMD E |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21166 | 51534 | A | 21293 | 263 | 813 | |
| 21167 | 51535 | A | 21294 | 130 | 1094 | NQPHRTKGCPNSSTECKNGSLT CDFMQVPILEMGKLRPEGERRV QDRDSNPSPSAGLFQARWS* PPRPSFLLPAGKRRGCDGGGRG GGRVVRAGGAPLRVHRQGRAPP QSTEHWVHVRKPGGRPFYLP AQYVRELPALGNPAADAPPGPP IGTRSP*AARLRLPVRERGC GSG PQRPPSGAPRRGQLPVRPCAAR RREP/RAAAWRPACPPACTCGP\ GARAARAVPGRPDARRRLASR RQPRKQRQLQGLQRSGLLGVP AAPVAQRLRERLRGHPGGTRP AAVGDREAGTTPGAEAGRLAE DSARREPGLEENHSAQRRA |
| 21168 | 51536 | A | 21295 | 2 | 3676 | |
| 21169 | 51537 | A | 21296 | 432 | 3453 | DLAGEVLLCGGAADYGTGLGFS SPA VQEANRGALCSSIERGHIIS ELEHLTFVNTDVGR CRAWLRL ALNDGLMECYLKLLLQEQARL HEYYQPTALLRDAEEGEFLLSF LQGLTSLSFELSYKSAILNEWTL TPLALSGLCPLSELDPLSTSGAE LQRKESLDSISHSSGSEDIEVHH SGHKIRRNQKLTASSLSLDTASS SQLSCSLNSDSCLLQENGSKSP DHCEEPMSCDSDLGTANAEDS DRSLQEVLLLEFS |
| 21170 | 51538 | A | 21297 | 64 | 2996 | LCPPAQAASQPQVELPAGWPQ PHALPLPHDHRAQHLLGCAHP GRAKPELQQHHDCACAAQIPHI PVRQPYQHPDPLCQPRRPACP ALPIHGRQLLLQEPLQAGTGGG PGCPPWPGQPHPPVTQVQQPHC GAPQPAFQPGVSAVVLGRIVK LAPEDLANLTALRVLDVGGNC RRCDHAPNPCMECPRHFPQLHP DTFSHLRLEGLVLKDSSLSWL NASWFRGLGNLRVLDLSENFL YKCITKTKAFQGLTQL |
| 21171 | 51539 | A | 21298 | 1 | 320 | PVRTPPIPAFSPLKTLRIMSLHQF LLEPNCGRPQLCRGTMARKPAP RKH*KHISRQCRVVLFEYKIGES VGFFKAVIFLVFLRFHSILDQS FSLSSLLWKIVTLT |
| 21172 | 51540 | A | 21299 | 1 | 443 | |
| 21173 | 51541 | A | 21300 | 1 | 1059 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21174 | 51542 | A | 21301 | 116 | 1559 | PRTARPSCAHARTVRAVATRRR RVHFRDLAAPSGLSVLRPRPT EPVRVDCPESANPPVRARPDSP DPRMFELLAASDARINGPFCAP RVLLAPLLGAFVTVSKIIVSKIAL SPK*SRRSHLLRRNGSQWVKV H\ELKEHNG\HITGID\WAPKSD RICH\CLGADRNCMLVWS\QK\D GVWKPMPG*FLRNLI GGGNFL* KWVPPRRTKFGCGGSGARLISV CYFESENDWWVSKHIKPIRST VLSLDWHPNNVLLAAGSCDFK CRVFSAYIKEVDEKPASTPWGS KMPFGQ\LMSEFGG\SGTG\GW VHGVSFS\ASG\DRLGWGSATD ST\VSVA*CLQKVVQVSTLKTIE FLAAP*VVSFVSREPASGLPAH DC\CPMLFNYG*PRAALTFRLP KLDIPK\QSIQRNMSAHGNAFG NMDKRATTED\RNTAL\ETLH\ QNSITQVLYLLRWKQD\CRKF CTTG\IDGEPWTIWDFQDPRSL PSQGLRIM |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21175 | 51543 | A | 21302 | 1 | 2223 | MKHYTRVQSSISPPAERQETHA WASPAVTSLESAACHELQEAD LSELSYPRIVSSSSSLQQYVAQG GSFPCFGMPWNFISGGAESTNA VISFANATTAVPMVLSRRESS LANNPGVVNYSALPENENVGP EMPERPANSSKNSTETANYPTL MGNYNGQNTASLSVFIPPYFAE KIILTEMPGTTETNVENNSQTV YYPALSGNTSAPYPASSYLPITS NFVLERVAEMPETAGTNVKNN TQTVNYPSSGRGRSQGNASLS LSIPPKFGIERHLGCFLVLAIRSK AAMNIIYHIGFV*TQAFISLRY/ MPKSAVAGSYGNALQNVLHIE MLFKTESGPQMSYGTMSYSYE MKNNCDQDDASASACLTPDFA LLPLNILVKVDNTENSVENTMN RSTLLDSDSGQDSSSSSVCIPP YGYLGDPKRNVRVLKIHLLAV QNMAKPKQAACYLVRILFSKEI LISSVDIHLKDSQSLDPNKMA ALREYLATTFPTCDLHEHGKD WQDCISGINSMIYCLCSEGKSTP KTVRKNNKRTNRVASASADR DQRGRDGGEGCSWMFQPMNN SKMREKRNLPNSNAIPEGMRE PSTDNPEEPGEAWSYFGRPWRN IRMPCSVLTLAKTKSCASLSAR YLIQKLFTKDLVQSNVYGNL KHGLCALDPNKISALREFLQEN YPICDLSENGRDWKSCVTSINS |
| 21176 | 51544 | A | 21303 | 1 | 297 | |
| 21177 | 51545 | A | 21304 | 1 | 162 | |
| 21178 | 51546 | A | 21305 | 11 | 212 | KGKNCVAIAADRRFGIQAQMV TTDFQKIFP/MGAQRLKFRNL YELKEGRQIKPYTLMSMVANL LYEK |
| 21179 | 51547 | A | 21306 | 37 | 554 | SSIKFGRSNPDYWIALPSRNLDP AIMSIMSYNGGAVMAMKGKN CVAIAADRRFGIQAQMVTRDF* KFFPMG*PACTPGMAGFAIDVQ TVAQRLKFRNLNLYELKEGRQIK PYTLMSMVANLLYEK/RDPDHL FETISQAMLNAVDRDAVSGMG VIVHIEKDKITRTLKARM |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21180 | 51548 | A | 21307 | 51 | 741 | YTAIMSIMS YNGGAVMAM\KG KNCVAIAADRRFGIQARLLTTN FQKIFPMGDRLYIGLGASPLD VQTS/VAQRLKFRAEPVMS*RE GRQ\KPYTLH*AMGGQPSLL*E KVFGPLTYTE\PVHLPGLGPERP FKALSICFSKTLIRVGPMDLN DFCGSSGNLAPNKMVG\MCESL WGGPTWDPDHLF*KPFSQGHG *MLWDRDGS/VSGMGSSLFHIE KDK\IPRTLKARMD |
| 21181 | 51549 | B | 21308 | 150 | 404 | |
| 21182 | 51550 | A | 21309 | 199 | 395 | |
| 21183 | 51551 | A | 21310 | 100 | 182 | SFLFWIKR*SFPDALYFSSKSGA CSCN |
| 21184 | 51552 | A | 21311 | 203 | 289 | KCLALDIALATRRSAI*FPSVKG PGRGV |
| 21185 | 51553 | B | 21312 | 166 | 411 | |
| 21186 | 51554 | A | 21313 | 232 | 317 | KCPALDIAVATRRSAI*FPAVKG PGRGV |
| 21187 | 51555 | A | 21314 | 129 | 278 | FYSSVSGVSSKDDRRFGCSGYS AAVISFRQC*SQLPGCSATYQR ESTFS |
| 21188 | 51556 | A | 21315 | 789 | 962 | |
| 21189 | 51557 | A | 21316 | 477 | 599 | |
| 21190 | 51558 | A | 21317 | 86 | 577 | ATEPLAPSERREVSIPLLVPAPL PPPPRPPVPSRTRTRPWRP*AC FPMTLAASCGPTRSPWPSQQPIP QPAPVG/PGNIKTLGDAYEFAV DVRDFSPEDIIVTTSNNHIEVRA EKLAADGTMNTFAHKCQLPE DVDPTAVTSALRKDGSLTIRAR RDPHTEHV |
| 21191 | 51559 | B | 21318 | 312 | 466 | |
| 21192 | 51560 | A | 21319 | 886 | 1338 | GFWQVIRALRGGEVHREGTSA PGRHRRRCGCRSAWNRCTAC SHVWPPRQMWPQG/PDVAMKT GNIKTLGDAYEFAVDVRDFSPE DIIVTTSNNHIEVRA/REA/ERPD GTMNTFAHKCQLPEDVDPTS VTSALREDGSLTIRAWRHPHTE HVQ |
| 21193 | 51561 | A | 21320 | 3 | 605 | KKLTPVRSRVERDPRVRRGLR PHPVLSSLRPPGQGPAPSVDEPQ NLFHLP SG EKIPFLFLLLFTPP PRPPVLSRPRTRPWRP*ACFP MTLAAICGPTSPWPSQPAPV/V AGNIKT*DAYEFVVDVRDFSP EDIIVTTSNNHIEVRPEKLAADG TVMNTFAQQCQLPEDVDPTSV TSALREDGSLTIRARGHPHTEH |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21194 | 51562 | A | 21321 | 3 | 450 | SSAAEVQEPRGAPGSPSIPSASR PGPAPRPASLPSPQMQLAAALPE EIRWLLEDAEEFLAEGLRNENL SAVARDHRDHILRGFQQIKA\G GDIGQDSSDDNHSGTLGLSLTY DAPFLSDYQDEGMEDIVKGAQ ELDNVIKQGYLEKKS*DH |
| 21195 | 51563 | A | 21322 | 1 | 399 | IGQDSSDDNHSGTLGLSLTSDA PFLSDYQD/EG*VHQISDHWEK LRTWC*VYCDKGMEDIVKGAQ ELDNVIKQGYLEKKS KDHSFFG SEWQKRWCVVSRGLFYFYANE KSKQPKGTFLIKGYSVRMAPHL RRDS |
| 21196 | 51564 | A | 21323 | 3 | 1189 | RLPARPPPDQGPRVPPLSRPAK CRLAVLPEEIRWLLEDAEEFLA EGLRNENLSAVARDHRDHILRG FQQIKARYYWDFQPQGGDIGQ DSSDDNHSGTLGLSLTSDAPFL SDYHDEGMEDIV*GAQELDNVI KQGYLEKKS KDHSFFGSEWQK RWCVVSRGLFYFYANEKSKQP KGTFLIKGYGVRMAPHLRRDS KKESCFELTSQDRRSYEFTATSP AEARDWVDQISFLLKDLSSLTIP YEEDEEEEEEKEETYDDIDGFDS PSCGSQCRPTILPGSVGIKEPTEE KEEEDIYEVLPDEEHDLEEDS GTRRKGV DYASYYQG\LWDC\ YGDQPDDL SL\QRGDLILFLSKE YNMYGWWVGELNSLVG\IVPK EYLHHLPLKWKERWKPREIYFF |
| 21197 | 51565 | A | 21324 | 47 | 225 | NSHHVRGRPRCADSSSPSGDRG QPEAQPA PDSSAPEHAQEPGRA AVKR PDL*SHMTRRP |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21198 | 51566 | A | 21325 | 66 | 725 | AILIIILLSSEGLWSSDQHRLVGV QDSPPQGSGLGCFYSAMATSEQS VCQARASVMVYDDTSSKKWVPI KPG\QQGFSRINIYHNTVSNTFR VVGVLQDQQ\VVINYSIVKGL KYNQATPTFHQWRDARQVYG\ LNFASKEEATTFSNAMLFALNI MNSQEGGPSSQRQVQNGPSPD EMDIQRQVMEQHQQQRQEF ERRTSATGPILPPGHPSSAASAP VSCSGPPPPPPPPVPPPTGA\TP PPPPPL\AAGGAQGSSESHFHV QDWPLAISWGPSLRRVPNGPED ASGGSSPSGTSKSDANRASSGG GGGGLMEEMNKLLAKRRKAA SQSDKPAEKKEDESQMEDPSTS PSPGTRAASQPPNSSK\AGRKP WERSNSRGYFCVLDVQNPAL WPKSPES*EPPSVSSL\ISRMKPA GS\SDMA\LDADFLL\RMKQEI LEEVVRELHKGERKEIID\AIRQ EA*SGISRKKNLGHRAPPTRTS FICSQRPLM |
| 21199 | 51567 | A | 21326 | 301 | 390 | |
| 21200 | 51568 | A | 21327 | 72 | 415 | |
| 21201 | 51569 | A | 21328 | 395 | 697 | RVMSPVHVNTICSPHPHSDGDV IVPIVLSNERYHWPVVLGWVGG VDCDEFFRVVLGEARLHLDGV AHQH*TKEGTISNLFQ\ATSVSH LVEVVPQKLSWVI |
| 21202 | 51570 | A | 21329 | 36 | 399 | VEILTSKRAGDWFKEELRLLGG LDHIVDKVKECVDHLSRDEDEE KLVASLWGAQRCLRVLQSVTV HNPENQSYLIAKDSQLIVSSA KALQHCEELI*QYNRAVDTLCL ADCKPLPHPTVL |
| 21203 | 51571 | A | 21330 | 1 | 177 | |
| 21204 | 51572 | C | 21331 | 198 | 350 | |
| 21205 | 51573 | A | 21332 | 113 | 228 | |
| 21206 | 51574 | A | 21333 | 1 | 466 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21207 | 51575 | A | 21334 | 1 | 4133 | ASGCWRKEVGAGSANGVEMV QGPVQTPALTIHRRKRRRRRRR RPSGGTQQALLPAPAVAASES* ARARPAALEAGREVAGPP\SCPP NRASYLPKAESLASLGSHLPAL LSRARVPRPPAGRKERE\RRKRP \VAKAPARLARGEYETG\VKMTS RFAKTYSRKGGNGSSKFDEVFS NKRTTLSTKWGETTFMAKLQ KRPNFKPDIQEIPKKPKVEEEST GDPFGFSDDES L P VSSKNLAQ VKCSSYSESSEA |
| 21208 | 51576 | A | 21335 | 3 | 221 | |
| 21209 | 51577 | A | 21336 | 1 | 580 | |
| 21210 | 51578 | A | 21337 | 2 | 1095 | ARGNRPPPPRTERGVLESRTS RHRAPRLPPAMPAPRAPRALAA AA\PASGKAKLTHPGKAILAGG LRGG\IQICMTFPTHEYVKTQLQL \DERSHPPRYRGIGDFVRQTVRS HGVLGLYRGLSSLLYGSIPKAA \RFGMFE\FLSNHMRDA\QGRL DSTRGLLC\SLGAGRGRP*VV VCPMETIKVKFIHDQTSNPKY RGFFHGVREIVREQGL\KGTYQ GLTAT\VLKQGSNQAI\RF\FVM TSLRQW\YPRGTTPNKAHEPF*1 TWGSFGA\IASASQVSFGNTPLD V\KTRMPGPWRPHK\YR\NTWD \CGL\QILKKGGSRAFYKGTV PPLGPGLAWDVA\VFV\YDEV G*SCFNKVWKNGIKA |
| 21211 | 51579 | A | 21338 | 3 | 375 | TAGDSGAEDGPASRVSQMPTLP PPMPWNLPAGVDCCTTSGVLAL TALFFKMEEANLASRAKAQELI QATNQILSHRKPPSSLGMTAP VPTSLGLPPGPSSYLLSGSPPLG GC\GSTPPTPPGLAA |
| 21212 | 51580 | A | 21339 | 51 | 3789 | GRGHPHGGGELLPASPRGSPEG DQPGQGDPEEKEGRVVPARGGA PDVPSAHALVPEPQTVLGLHQR VTAQPGRHGAH*LHGDR LHSG RPQRPTHGTWAPCLPYPTLGSG *RRHHGNPAGTPRSLLFPF\PEK ELEAPPAPRFDIYDPFHPTDEA YSPPPAPEQKYDPFEPTGSNPSS SAGTPSPEEEEEEEEEEEEEEED EEEEEGLSQSISRISETLAGIYDD NSLSQDFPGDES PRPDAQPTQP TPAPGTPPQ |
| 21213 | 51581 | A | 21340 | 286 | 393 | |
| 21214 | 51582 | A | 21341 | 64 | 610 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21215 | 51583 | A | 21342 | 1 | 4433 | MWAQLLLGLMLALSPAIAEELP NYLVTLPARLNFPVSVQKVCLDL SPGYSDVKFTVTLETQDKTQKL LEYSGLKKRHLHCISFLVPPPAG GTEEVATIRVSGVGNISFEEK KKVLIQRQGNQTFVQTDKPLYT PGQQVYFRIVTMDSNFVPVND KYSMVELQDPNSNRIAQWLEV VPEQGIVDLSFQLAPEAMLGTY TVAVAEGKTFGTFSVEEYVLSP FLLLLSSVLPKFKVEVVEPKELS TVQESFLVKGGL*) |
| 21216 | 51584 | A | 21343 | 3 | 522 | ELRTWIEGLTGLSVGPDFQKGL KDGITLCTLMNKLQPGSVPKIN RSMQNVHLENLSNFIKAMVS YGMNPVDLFEANDLFESGNMT QVQVSLLAGKMGTKNCASQ SGMTAYGTRRHLYDPKNHILPP MDHSTI\SLQMGTKNCASQVG MTAPGTRRHLYDTKLGTDKCD |
| 21217 | 51585 | A | 21344 | 1 | 1230 | MHQEDLRAWYLDLGLPSHQNE TTDVSVVYERFSLTDATYPKQA KQWDFPFLRVSTAQPTAWKCQ RAPSPYTHQDTALIPSPTARWL SPEKEPKQGEVGEKSLLPDPTLP LTDPRLTGSTEQKKDLAAGPVG SALRRRPPAVSSTQFNKGPSYR LLADVQNRLLPKYDSQKEAEL RSWIKGFTGLSIRPDFQKGLKD GIILCTLVNKLQPGSVPKINASV *NWH*LENLSNFLKAMVSYGM /NPVDLFEANDLFESGNMQVR VSLLAGKAKTKGLRSGVDIR DKYSKKQNFDDTTMKASQCVI RLQITNKCASQSGMTAYGTRR HLYDPKNRILPPMDNSTISLQM GTNKYASQVGMTAPGTQRHIY DTNLGIDKCENSSMSLKMGYT QVANHSGQVFGLRQIYEPKY |
| 21218 | 51586 | A | 21345 | 2 | 389 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21219 | 51587 | A | 21346 | 1 | 1113 | MHQEDLRAWYLDLGLPSHQN AQPTAWKCQRAPSPYTHQDMA LIPSPTARWLSPEKEPKQGEVG EKSLLPDPTLPLTDPRLTGSTEQ AHAEGLAALMSALRVSHLQGR GGVVTLVDSQLGVIAVSSTQFN KGPSYRLLADVQNRLLPKYDS QKEAELRSWIKGFTGLSIRPDFQ KGLKDGIIILCTLVNKLQPGSVP KIN\ASV*NWH*LENLSNFLKA MVSYGM/NPVDLFEANNLFESG NNMQVRVSLALAGKAKTKGL RSGVDIRDKYSEKQNFDDTTM KASQCVIRLQITNKCASQSGMT AYGTRRHLYDPKNRILPPMDNS TISLQMGTNKCASQVGMTAPG TQRHIYDTKLGDKCENSSMSL |
| 21220 | 51588 | A | 21347 | 353 | 1260 | SCWCLKLALAVSST/QFNKGPS YRLLADVQNRLLFKYDSQKEA ELRSWIKGFTGLSIRPDFQKGLK DGIILCTLVNKLQPGSVPKINAS V*NWHQLENLSNLIKAMVSYG M/NPVDLFEANDLFESGNNMQ VRVSLALAGKAKTKGLQSGV DIRDKYSEKQNFDDTTMKARL CVIRLQITNKCASQSGMTAYVT RRHLYDPKNRILPPMDNSTISLR MGTNKCASQVGMTAPGNQWH IYDTKLGDKCENSSMSLKMGY TQVANHSRQVFGLGRQIYEPKY QPGGPVAHGAPSAGNCPGPGE |
| 21221 | 51589 | A | 21348 | 3 | 530 | |
| 21222 | 51590 | A | 21349 | 1 | 853 | MPESWLAAFPYGDIIKVVGL QLKEGLHQNLTMQDSIQIFDFQ LPGLLRPSSVLWTLKPYHTAGL ASDRDSYKGILACMPMFGSRR SPLRDIKSHQADLELEVKNSLD TIHRLESELKKQSKIQSQMKVE KAHLEEEIAELKKSQAQDKAKL LEMQESIKDLSAIRADLANKLA EEERAKKTSAGAFGP/LIAQAN SRDEGTATITQLELERDVHQRE LKDLTSSLQSVKTKHEQNIQEL MKHFKKEKSEAENHIRTCLKVPL LNYPPDDTEGIFLVAHEVNKA |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21223 | 51591 | A | 21350 | 1 | 652 | NTSLINTKKKLETDISQIQGEME DIIQEARNAEKAKKAITDAAM MAEELKKEQDTS AHLERMKKN LEQTVKDLQHRLDEAEQLALK GGKKQIQKLEARVRELEGEVES EQKRNVEAVKGLRKHERKVKE LTYQTEEDRKNILRL\QDLV DK LQAKVKS YKRQAE EAEQSNV NLSKFRRIQHELEEADFRADIA ESQVNKL RVKSREVHTKIIEE |
| 21224 | 51592 | A | 21351 | 21 | 5868 | PAAMSSDSEMAIFGEAAPFLRK SERERIEAQNKPFDAKTSVFVV DPKESFVKATVQSREGGKVTA KTEAGATVTVKDDQVPMNPP KYDKIEDMAMMTHLHEPAVLY NLKERYAAWMIYTYSGLFCVT VNPYKWL PVYNAEVVTA YRG KKRQEAPPHIFSISDNAYQFML TDRENQSILITGESGAGKTVNT KRVIQYFATIAVTGEKKKEEPA SGKMQGTLEDQIISANPLLEAF GNAKTVRNDNSSRFGKFIR |
| 21225 | 51593 | A | 21352 | 54 | 399 | |
| 21226 | 51594 | A | 21353 | 441 | 1585 | VPPMGGGPPFVGPVGFPGDRS HLDSPEAREAMFLRRAAVAPQ RAPILRPAFVPHVLQRADSALSS AAAGPRPMALRPPHQALVGPP LPGPPGPPMMLPPMARAPGPPL GSMAALRPPLEEPAAPRELGLG LGLGLKEKEEAVVAAAAGLEE ASAAVAVGAGGAPAGLAVIGP\ SLPLALAMPLPEPEPLPLEVV RGLLP\LRITELLSLRPRPRPPR\ PEPPPGLMALEVPEPLGEDKKK GKPGEIEHRCIATA/AQGASWE DPPTCWKWDAE*LSRVFCGDL G\NEVND*HLGHAASARFPIPSL KAKVIR*QSAQARPKGYG\FVS FKDP\SDYVRP\MREMNGKYVV LAPPIKLRKSMWKDRNLDVFR KKQKEKKLGLR |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21227 | 51595 | A | 21354 | 1 | 1122 | MPGGKIGFLIEKGATEQSSTGN DFDELREEGGRRSNYSELQEDI QTKGKEVENFEKNLEECVTTIS NTEKCVKELMELKTKARELRE ECRSFRSQCNQLEERVAMPKDE MNEMKREGKFREKRIKRNEQS LQEIWDYVKRPNLPLIGVPESD RENGTKLENTLRDIIQENFPSLT RRGQPFRIEMENTENAPKDNLLE KEQLPRHNNCLELTQEEPAWD LQFDLLDLNDISSALKHHEEKN LISLLPQRGADYLSFRSHFQKNF VCVENC SLQERTVTGTGVKVN VSFEKKVQIRITFDSWKNYTDV DCVYMKNVYGGTDSDTFSFAI GLPPVIPTEQKIEFCISYHANGQ IF\WDNK*WGRKYKNCVIVQW |
| 21228 | 51596 | A | 21355 | 71 | 1124 | GPPPLCLMSCTRMIVLDPRL TSSVMPVDVAMRLCLAHSPV KSFLGPYDEFQRRHFVNKLKPL KSCLNKHKAKSQNDWKC SHN QAKKR VV\FADSKGLSLTAIHV FSDLPEQPAWDLQFDLLDLNDI SS\ALKHH\EEKNLIDFP\QPST DYL\SFRSHFQK\NFVCL\ENCSL QERTVTGTV\KVKNVEF*GRKF QIRYHFSDSWEKLTLDVDCVY MENVY/GVGTGSDTFSFAIDLPP VIPTEQKIEFCISYHANGQVFW DNNDGQ\NYWIVHVQWKPDG VQTQMAPQ\DCAFHQTS PKTEL ESTIFGSPRLASGLFPEWQSWG RMENLRLLCDELSNNVTGLDLS YSPMQS |
| 21229 | 51597 | C | 21356 | 204 | 273 | |
| 21230 | 51598 | B | 21357 | 1 | 1062 | |
| 21231 | 51599 | A | 21358 | 1 | 397 | QRPI*PTKPIGQRVSKGHQPTR H\DFQTQFLAAHETISRLVG FSA GQV\QYLDLIKK\DP SKLFNEER LIDKTKVTY LKWLPES ESLFLA SHASGHL YLYNVSHPCASAPPQ YSLKQGE GFSVYAAKYNDLF |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21232 | 51600 | A | 21359 | 71 | 1736 | FRTSLKD V W H T P L T P F L P P L K S I D L N K P I D K R I Y K G T Q P T C H D F N Q F T A A T E T I S L L F G S F S P R R T W A W C G P A V * A G P C P T A F L G T L R L I D K T K V T Y L K W L P E S E S L F L A S H A S G H L Y L Y N V S H P C A S A P P Q Y S L L K Q \ A W G F S F Y A A K S K A P R N P L A K W A V G E G P L N E F A F S P D G R H L A C V S Q D G C L R V F H F D S M L L R G L M K S Y F G G L L C V C W S P D G R Y V V T G G E D D L V T V W S F T E G R V V A R G H G H K S W V N A V A F D S L Y T T R A E E A A T A A G A D G E R S G E E E E E E P E A A G T G S A G G A P L S P L P K A G S I T Y R F G S A G Q D T Q F C L W D L T E D V L Y P H P P L A R T R T L P G T P G T T P P A A S S R G G E P G P G P L P R S L S R S N S L P H P A G G G K A G G P G V A A E P G T P F S I G R F A T L T L Q E R R D R G A E K E H K R Y H S L G N I S R G G S G G S G S G G E K P S G P V P R S R L D P A K V L G T A L C P R I H E V P L L E P L V C K K I A Q E R L T V L L F L E D C I T A C Q E G L I C T W P R P G K A F T D E E T E A Q T G E G S W P R S P S K S V V E G I S S Q P G |
| 21233 | 51601 | A | 21360 | 2 | 467 | L M Q \ N W D A A M E D L T R L K E T I D N N S V S S P L Q S L Q Q R T W L I H W S L F V F F N H P K G R D N I D L F L Y Q P H M L A D K L N M T P E E A E R W I V N L I R N A R L D A K I D S K L G H V V M G N N A V S P Y Q Q V I E K T K S L S F R S Q M L A M N I E K K L N Q N S R S E A P N W A T Q D S G F Y |
| 21234 | 51602 | B | 21361 | 1 | 909 | |
| 21235 | 51603 | A | 21362 | 3 | 3617 | Y W K E R P T Q K V I P R A T E N H G L K S Y L Q K T K L S I D E A A F L L P D T N L K S E L L E L L T H W L Q V G V P M T P S L G S I N L L G W L T E L R E T H T Y I C W F I V K E T T R D T D E E M C R T E P A L A C S I S H Y C D D G C I Q M L N T P E T L Q C S A K D S K H F I P K E C S I P G E N R P P S D T G K T V K F L S L N I F N L Q L A E S T D A E Q R A N C I L R C F L T E T T L N Y Q K I L S V R P G T K L A T A S H V S G L G L Q T P P F G L A Q H L I R P H A F L A P K D P L T S F T E R N S R S G |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21236 | 51604 | A | 21363 | 75 | 2141 | GPRLGLTTMWHEARKLGRRRLR GLLFDSRKRAERRREYEEKIKK DPAQLQVHGRACKVHLD VALAAESPVNMMMPWQGD TNNMIDRFDVRAHL\DHIPDYTPPLA HHHFSQNQESDER\KCNERYR GLVQNDFAGISEEQCLYQIYIDE LYGGLQRPSEDEKKKLAEKKA SIGYTYEDSTVAEVEKAAEKPE EEESAAEEESNSDEDEVIPDIDV EVDVDELNQEQQVADLNKQATT YGMADGDFVRMLRKDKKEAE AIKHAKALEEEKAMYSGRRSR RQRREFREKRLRGRKISPPSYAR RDSPTYDPYKRSPSESSSESRSR SRSPTPGREEKITFITSFGGSDEE AAAAAAAAAASGVTTGKPPAP PQPGGPAPGRNASARRRSSSSSS SSSASRTSSSRSSSRSSSRSGG GYRSGRHARSRSRSWSRSRSR SRRYSRSRSRGRRHSGGSRDG HRYSRSPARRGGYGPRRSRSR SHSGDRYRRGGRGLRHSSRS RSSWSLSPSRSLTRSRSHSPSP SQSRSRSRSPSPSPAREKL TRPAASPAVGEKLLKTEPA\AG KETGAAKVPKLTPEKLLKLRM QKPL\NRQFKADKAAQRKR*S QAEHERQERKDEA\RAMARKIG MKERER\REKEREWERQYSRQ SRSP/LP/RDYSREYSSRRRSRSR SRSPHYRH |
| 21237 | 51605 | A | 21364 | 1 | 609 | |
| 21238 | 51606 | A | 21365 | 1 | 1227 | |
| 21239 | 51607 | A | 21366 | 1 | 1626 | |
| 21240 | 51608 | A | 21367 | 370 | 4388 | GFIWNRITPTEDGQTRELQNLH GLSAPVPRGRKGKKVKTQTSSF DIQKAEWLKYNPEQLQDEG YKKHIKHHCNKVLLRVRLYY LKQEVIGNECQKVFDDGVDASDI DVWVPEPDHSEVPAEWDFD ADKSLIGVFKHGYEYNTIRA DPALCFLERVGKPDEKAVAAE QRANDYMDGDVEDPEYKPAPA IFKDDIEDDVSSPGDLVIADGDG QLMEGDKVYWPTQSALTTRLR RLITAYQRTNKNRQIQIQ |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21241 | 51609 | A | 21368 | 1 | 530 | AEADAI IQMVREGQRARRQQQ AATSESSQSEASVRREESPM DV DQPSPSAQDTQSIASDGT PQGVE KEKEERPPELPLLSEQLALDEL WDM LG ECLKELEESH DQH AVL ETHRTVLNQILRQSTTHLADGP FAVLVDYIRVLDFDVKRKYFR QELERLDEGLRKEDMAVHVRR DHVF |
| 21242 | 51610 | A | 21369 | 1 | 217 | |
| 21243 | 51611 | A | 21370 | 274 | 599 | PVSKESRVAPLCDFCLPFIQSES SQSEASVRREESPM DV DQPSPS AQDTQSIASDGT PQG EKEKEER PPELP/LLSEQLSLDELWDM LG E CLKELEESH DQH AVLVLQPA |
| 21244 | 51612 | A | 21371 | 2 | 731 | TPTPPTAPTPTVSAPALVAATAI STIVVAASTTVTTPTTATTTVSI SPTTKGSKSPAKVSDGGSSSTD FKMVSSGLTENQLQLSVEVLTS HSCSEEGLEDAANVLLQLSRGD SGTRDTV LKLLNGARHLGYT LCKQIGTLLAELREYNLEQQR AQ CETLSPDGLPEEQPQTTLK GKMQSRF\SGLG SASSIQA AVR QLEAEADAI IQMSESSQSEASVR REESPM DV DQPSPAQDTQSI A |
| 21245 | 51613 | A | 21372 | 208 | 423 | LYVKPTAPPK*AL*SEGLE*MSP QCLWQGLQQGKAQKKLLEVP NKLTQTIN*PANVLILA*GGSS YRPPHK |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21246 | 51614 | A | 21373 | 1 | 2002 | MPQLPGISLPEGVDPSFLAALPD DIRREVLQNQLGIRPPTRTAPST NSSAPAVVGNPGVTEVSPEFLA ALPPAIQEEVLAQQTAEEQQRPE LAQNASSDTLMDPVTLIQTLPS DLRRSVLEDMEDSVLAVMPPDI AAEAQALRREQEARQRQLMHE RLFGHSSTSALSAILRSPAFTSR LSGNRGVQYTRLAVQRGGTFQ MGGSSSH\NRPSGS\NVDTLRL RGRLLLDHEALSCLLVLLFVDE PKLNTSRLHRVLRNL CYHAQT RHWVIRSLLSILQRSSESEL CIET PKLTTSEEGKKKSSKSCGSSSHE NRPLDLLHKMESKSSNQLSW/L SSVSMDAALGFR\TNIFQIQRS GRKHTEKHASGGSTVHIHPQA APVVC RHVLDTLIQLAKVFPSH FTQQR TKETNCESDRERGNKA CSPCSSQSSSSGICTDFWDLVK LDNMNVS RKGKNSVKSVPSA GENKVSE AQANS GSGASSTTTA TSTTSTTTTAASTTPTPTAPT VTSAPALVAATAISTIVVAASTT VTTPTTATTTVSISPTTKGSKSP AKVSDGGSSSTDFKMVSSGLTE NQLQLSVEVLTSHSCSEEGLED AANVLLQLSRRPARMLAMHW PSLYNVETEKTLALPNLIALQTS PFASGVIAKSSTDRLINQCAPV WRWR |
| 21247 | 51615 | A | 21374 | 1 | 6384 | MVSPEPKTGHSIRNWLDELKDL PILHAYSNLPSSPAVDLAIHSSK EGRMDWTEGQVTGPVVRSAAT SGAGSTTSGVVSGSLGSREINYI LRVLGPAAACRNP DIFTEVANCC IRIALPAPRGSGTGNGSSRIPRES APEMATAESLVEELSEDAAGG ASPGVELPALGCSELPAAEVSP TASSKNLETICEYAYCMAMLPE TGLDPYPKRGFLDLTQERIWTD IPSPGNIPTTHPLMVRHADHSS LTLGSGSSTT |
| 21248 | 51616 | A | 21375 | 1 | 1356 | |
| 21249 | 51617 | A | 21376 | 80 | 608 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21250 | 51618 | A | 21377 | 298 | 1374 | GRGDWPDILNLTQATASWTPR WCCLRKPV EAPSGGATEERTLS LTSLGLSMPADPCEGGARSCLV TESARGGLQNGQSVDVEETLPS EPENGALLRSERYQGPRRRACS ETLAESRTAVLQQRRAAQLPG GPAAAGEQRASPSKARLKEFLQ QCDREDLVELALPQLAQVVTV YEFLLMKVAESLGITEFLRKKEI HPDNLGPKHLSRDMDGEQLEG ASSVEKREREEAEEGLASVKRP RREALSND\TTESLAANSRGRE KPRPLHALAAGTIVSQEEDIVT VTD/GRGACLRMGPLEGVPLEA VESVVTVEPEPSQ*NGVRY*NS SDFIQRSMASNVYFSNVNIAQ MNLLFIKNNVFL |
| 21251 | 51619 | C | 21378 | 354 | 530 | |
| 21252 | 51620 | A | 21379 | 1 | 1272 | MVLSEKASGSTLRGCTEERTLS LTSLGLSMPADPCEGGARSCLV TESARGGLQFLQQCDREDLVEL ALPQLAQVVTVYEFLLMKVAE SLGITEFLRKKEIHPDNLGPKHL SRDMDGEQLEGASSEKREREA AEEGLASVKRPRREALSNDTTE SLAANSRGREKPRPLHALAAES HTTTVSGGNGSVFQAGPQLQA LANLEARRGSIGAALSSRDVSG LPVYAQSGEPRLTQAQVAAFP GENALEHSSAQDTWDSLRS PGF CSPLSSGGGAESLPPGGPGHAE AGHLGKVCDFHLNHQQPSPTS VLPTEVAAPPLEKILSVDSVAV DCAYRTVPKPGPQPGPHGSLLT EGCLRSLSGDLNRFPCGMEVHS GQRELESVVCLSAETMAF*NFP\ MGA\MSYCL\RD\RSRFLFRLPM GLSCPLQVQ |
| 21253 | 51621 | A | 21380 | 90 | 204 | |
| 21254 | 51622 | B | 21381 | 13 | 423 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21255 | 51623 | A | 21382 | 1513 | 2405 | RRAQYRRWRRWRRRRHREPE KEKRRHSRSHSRRTLIF*TQS RSRRE*LHCQSRSR**FKSPRQ RRSRERGRSTARHYRST\KER QQRSSRSGTRSPKKSRCPKRKL SLSPSPGKHKKKKKDKERNRY ERERSTSKKKSKDREKDQERKS ESDTDVKVTRVYDEEEQGYDT SQEIEMHADNPAAIQTTVVLQRD DLQNGLLSTCRELSRATAELER AWREYDKLEYDVTVTRNQMQ EQLDHLGEVQCWCYRTEKYV MERGPEQDPKRAFLDFVQERIQ GESAVQSESKFIKTVKK |
| 21256 | 51624 | A | 21384 | 1 | 180 | |
| 21257 | 51625 | A | 21385 | 3 | 115 | |
| 21258 | 51626 | A | 21386 | 3 | 312 | LPTALLRSTSMALLHSGRVLPGL AAAPHPL/AA/AASARASSWW THVEMGPPDPILGVTEAFKRDT NSKKMNLGVGAYRDDNGKPY VLPSVRKFVTVTQISGTGAL |
| 21259 | 51627 | A | 21387 | 3 | 395 | SMALLHSGRVLPGLAAAFHPCV LAAAASARASSWWTHVEMGPP DPILGVTEAFKRDTNSKKMNLG VGAYRDDNGKPYVLPSVRKAE AQIAAKNLDLLPLLNVCVSLSS HTVSPAAQGGTRKEDILGFACC |
| 21260 | 51628 | A | 21388 | 1 | 303 | |
| 21261 | 51629 | A | 21389 | 2 | 425 | RPE*WKEIATVVKKRNLFALFD MAYQGFASGDGDKDAWALHH FIEQGINVCLCQSYAKNMGLYG EHVGAFTVVCKDADEAKRVES QLKILISPMYSNSPLNGAQIASTI PNTPVGLKVWVMGGLHDHPQ VMSDEKETTLRA |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21262 | 51630 | A | 21390 | 3 | 1508 | HEAGAGSLCVC PARPLLRPAAA HCPSYRSTMAHACTSGRVLP GIAAA\FHPGLAAAASARASSWW THVEMGPPDPILGVTEAFKRDT NSKKMNLGVGAYRDDNGKAL PCCPSVRKAEGPRLPQKIWDKE YL\PIGGVLAEFCKASAELALGE NNRSLERVGRFVTQTHFWEL GALRI\GASFL\QRFFKFSRDVFL PKPTWGETTHPSFRDAG\MQL\ QGYRIYYDPKTCGFDFGTGAVED ISKIPEQSVLLALHACG/HNNPTG VDPRPEQWKEIATVVKKRNLF AFFDMAYQGFASGDGDKDAW AVRHFIEQGINVCLCQSYAKNM GLYGERVGAFTMVCKDA\DES KRVESQLKILIRPMYSNPPLNG ARIAAAILNTPDLRKQWLQEVK GMADRI\IGHAGLQLVSNLQGR EG\STHNWATHSPTKLGMFCF HRG*KLEQVERLIKEFSIYMTK DGRISVAGVTSSNVGYLAHAIH QVTKYVSLVRGNGDNLSVLSL |
| 21263 | 51631 | A | 21391 | 1 | 184 | |
| 21264 | 51632 | A | 21392 | 70 | 253 | |
| 21265 | 51633 | A | 21393 | 1 | 351 | VMEFYCQSCETAMCRECTEGE HAEHPTVPLKDVVEQHKASLQ VQLDAVNKRWGTLPKPPTGCL YLRPGLMASC\QLTNQKASI/VD DIHSTFDELQKTLNVRKSVLLM ELEVNYGLKHK |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21266 | 51634 | A | 21394 | 208 | 2546 | WLHCMQQQRAGSKTAGPP\CQ WSRMAS\EGTNIP\SLVVGGQ\NDK QFLICSICLERYKNPKVLPCLHT FCERCLQNYIP\AHS\TLSCPVC RQTSILPEKGVAALQNNFFITNL MDVLQRTPGSNAEESILETVT AVAAGKPLSCP\NH\DG\NVMEF YCQSCETAMCRECTEGEHAEH PTVPLKDVVEQHKASLQVQLD AVNKRWGTLPKPPTGCLYLRLP GLMASC\QLTNQKASIVDDIHST FDELQKTLNVRKSVLLMELEV NYGLKHKVLQSQLDTLLQGQE SIKSCSNFTAQTLNHGTETEVLL VKKQMSEKLNELADQDFPLHP RENDQLDFIVETEGLKKS\IHNL GTILTTNAVASETVATGEGLRQ TIIGQPM\SVTITTKDKDGELCKT GNAYLTAELSTPDGSVADGEIL DNKNGTYEFLYTVQKEGDFTL SLSLYDQHIRGSPFKLKVIRSAD VSPPTEGVKRRVKSPGSGHV\KQ KAVKRPASMYSTGKRKENPIED DLIFRVG\TKGRNKGEFTNLQGV AASTNGKILIADSNNQCVQIFSN DGQFKSRFGIRGRSPGQLQRPT GVAVHPSGDIIIADYDNKWVSI FSSDGKFKTKIGSGKLMGPKGV SVDRNGHIIIVVDNKACCVFIFQ PNGKIVTRFGSRGNGDRQFAGP HFAAVNSNNEIITDFHNH\SVKV FNQEGEFMLKFGSNGEGNGQF |
| 21267 | 51635 | A | 21395 | 1 | 591 | |
| 21268 | 51636 | A | 21396 | 3 | 608 | LEGDQRWINTVSQALHLLSTLY GPFPCYIGIRCAKMAYELWR NLEEEEDGETKGRRPEIGHIFLL DRGKLCPAFLSSFSPRRHGNME GVVAKLKS*S*GCESQL*GAWV LGPMESIKAALGHAV*KAGSGR TFMVRDLCF\DVDFVTALCSQV VYEGLVDDTFRIKCGKCYGPLH LGKMDGSSALAPATWGRVCGR DPHPE |
| 21269 | 51637 | A | 21397 | 268 | 402 | |
| 21270 | 51638 | A | 21398 | 139 | 452 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21271 | 51639 | A | 21399 | 1 | 2497 | MGPVAAPLGLSLPATDGAHSV RGNSVLVPSGLIPKDYRSLKTQ YLQSYGPEHLLTFSNLRRAGLL TEQAPGDTLTAVESKVSKLVT KAAGKITDAFSSLAKRSNFRAIS KKLNLIPRVDGEYDLKVPRDM AYVFGGAYVPLSCRIIEQVLER RSWQGLDEVVRLNCSDF DMTKEDKASSESLRLILVVFLG GCTFSEISALRFLGREKGYRFIF LTTAVTNSARLMEAMSELP KDLFIETDLMSPDLRIANVSL QHEVDKLYKVENKPALSSNEQ LCFLVRPRIKNMRYIASLVNAD KLAGRTRKYKVIFSPQKFYACE MVLEEEGIYGDVSCDEWAFSL PLDVDLLSMELPEFFRDYFLEG DQRWINTVAQALHLLSTLYGPL SQT CYGIGRCAK\MA YEFVEGT WEEEDGRNPRARREGFG\HIF LLADR\DVDFVDSTLLPKLVYEG LVDDTFRIKCGSVDFGPEVTSS DKSLKVLLNAEDKVFNIRNEH FSNVFGFLSQKARNLQAQYDR RRGMDIKQMKNFVSQELKGLK QEHY\LLSLHIG\ACESIMKKKT KQDFQE\LIKTEHALLEGFNIRE STSYIEEHIDRQVS\PIESLRMC LLSITENGLIPKDYRSLKTQYLQ SYGPEHLLTFSNLRRAGLLTEQ APGDNLTAVESKVSKL\VTDKA AGKITDALSLAKRSQFRAISK |
| 21272 | 51640 | A | 21400 | 1 | 216 | |
| 21273 | 51641 | A | 21401 | 2 | 270 | |
| 21274 | 51642 | A | 21402 | 1 | 600 | SGRALHASWAAGGVGAYSGRL RSDALEGESFA\LSF\SSASDAEF DAVVGYLEDIIMDDEFQLLQRN FMDKYYL\EFEDTEENKLIYTP\I FNEYISLVEKYIEEQ\LLQR\IPEF NMAAFHHNITPSVPVCRHHKD EVAW*QYSAMLAPPFTFRFSWA F*RNVFGTYRGRKKEGRGL\DL SSGLV\VTSLCKSSSLPASQNNL RH |
| 21275 | 51643 | A | 21403 | 1 | 297 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21276 | 51644 | A | 21404 | 1 | 1419 | MGAPLLSPGWGAGAAGRWW MLLAPLLPALLLVRPAGALVEG LYCGTRDCYEVLGVSRSAKGA EIARAYRQLARRYHPDRYRPP GDEGPGRTPQSAEEAFLLVATA YETLKIVFPELKIVKELTLLMP SRAVWIIWSHKMSGGGAGPEL DIGYVPVLLHMPKRIGSGMDTS RSTTVIPVEIRNKELIALLVKAQ DRQEEETNYKLRFNGLSYEVG YLVILQDEETRKDYDYMLDHP EEYYSHYYHYYSRRLAPKVDV RVVILVSVCAISVFQFFSWWNS YNKAISYLATVPKYRIQATEIA KQQGLLKKAKAKSKNNKVQR RNS*EEENIIKNIKSKIDIKGGY QKPQICDLLLFQIILAPFHLCSYI VWHCRWIYNFNIKKEYGEEE RLYIIRKSMKMSKSQFDSLEDH QKETFLKRELWIKENYEVYKQ EQEEELKKKLANDPRWKRYRR WMKNEGPGRLTFVDD |
| 21277 | 51645 | A | 21405 | 1 | 1266 | |
| 21278 | 51646 | A | 21406 | 1 | 739 | |
| 21279 | 51647 | A | 21407 | 1 | 428 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21280 | 51648 | A | 21408 | 99 | 2338 | MPEEVHHGEEEVETFAFQAEIA QLMSLIINTFYSNKEIFLRELISN AS\DALDKIRYESLTDPSKLD SG KELKIDHNPQEPYPGLWVD TG IG\MTKADLINNLGTIAKSGTKA FMEALQAGADISMIGQFGDGFY S\ANLVAKKVVVITKHP\DDEQ YAWESSAGGSFTVRADHGEPIA RGT\QVILHLKEDQTEYLEERR V\QEVVKKH\SQFIGYPITLYLE KEREKEISDDEAEEEEKGEKEEE DKDDEEKP KIEDVGSDEEDDSG KDKKKKTKKIKEKYIDQEELNK TKPIWTRNPDDIT\QEEYGEFYK SLTNDWEDHLAVKHFSVEGQL EFRALLFIPRRAPFDLFENKKKK NNIKLYVRRVFIMDSCDEL VPE\ YLNFI PGVV DSEDLPLNIFRKML QQNK/ILWKVIRKNIVKKCLELF SELAEDKENYKKFYEA FSKNLK LGIHEDSTNRRRLSELLRYHTS QSG\DEMTSLSEYVS\RMKETQ MSIYYITGESK\EQVANSAFVER VRKRGFEVVYMT\EP\DEYCVQ QLKEFDGKKLVSVTKEGLELP EDEEEKKKMEESKAKFENLCK LMKEILDKKVEK\VTIS\NRL\VS SPC\CIGHKHLGAGQALIERDHE KPRALRDHPPQGGIMMGKKAP *ESPPDHPHFVETRAGRKADAR QVMIRAVKD/LWWVLLV*NPP LLSSGF\SLEDPQT/HTPNRIYRI |
| 21281 | 51649 | A | 21409 | 1 | 426 | |
| 21282 | 51650 | A | 21410 | 1 | 1305 | |
| 21283 | 51651 | A | 21411 | 446 | 3180 | VAVRLGSASQFPSGARPQLPRP PSWSSSIHSPISTTGLSESTDS DS KSGLRGFSAYNPSSRI PKSTTSS NSSDGAVTASNQDTGIPWVLV TGPTPPVNSPVESLQGS AFSSGF STPRGLVKGPTLPPDSNLTSVSD YTWIFVRGPPIPNDLSQVSIQAP PTPSNTPECQYKGLPHPQCPASP GVWYQDHLYPITFPQCRHKHL LHPITSPQCQGRRLPPPQCLTLR GVQYKNLLHPVILSSCRHKDIL NLITLAE |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21284 | 51652 | A | 21412 | 24 | 667 | MLPWLNCITTGVPWPTPSKRW LRNSKVCDCCKTPSNAFSLLS VPPTTTSPASLAWWSGCARLLD LGSSSLMMSPTMASPACRPWL GQRWRLISGSWAWAIVPVT*VP VPEPSWKNRAG*PGCSSYESPH MRRPTRPSASCLEWAPRASLA MHLMATSFVLLSSARITSEKA PLSGEGIHKVKWNWNPSPFPASPP FPMGSVTTAGPRTWMTLP |
| 21285 | 51653 | A | 21413 | 1 | 304 | RAQVLPARCYPGSTVSPLGFRG LPLPRGGSEIPRCATAATRPHR MPFLFYLFLLQQHRPHHWHGG AAVPGFWTSAHPA\CDVTYHGF PSLQALAGPPWQCI |
| 21286 | 51654 | A | 21414 | 1 | 7629 | |
| 21287 | 51655 | A | 21415 | 180 | 423 | |
| 21288 | 51656 | A | 21416 | 17 | 753 | QAHTRRAGGRAQVLPARCYPG STVSPLGFRGLPLPRGGSEIPRC ATAATRPHRMPFLFYLFLLQQH RPHHWHGGAAVPGFWTSAHPA \CDVTYHGFPSLQALAGPEVEA HLRKLGLGYRARYVSASARAIL EEQGGL/RLAAAATRVLI*GGP QGPLHPAWSGHQGG*LHLPDG PRQAPGCARGCPYVAHCPT*LQ LAPYHVPGEGETEPPDQQTGKL FPEPVGTLCWLGPSALSGHHHF YDLSRTP |
| 21289 | 51657 | A | 21417 | 17 | 1087 | QAHTRRAGGRAQVLPARCYPG STVSPLGFRGLPLPRGGSEIPRC ATAATRPHRMPFLFYLFLLQQH RPHHWHGGAAVPGFWTSAHPA \CDVTYHGFPSLQALAGPEVEA HLRKLGLGYRARYVSASARAIL EEQGGL/RLAAAATRVLI*GGP QGPLHPAWSGHQGG*LHLPDG PRQAPGCARGCPYVAHCPT*LQ LAPYHVPGEGETEPPDQQTGKL FPEPVGTLCWLGPSGWIRCLLK NYRLLPLDLEGLLGNAFDGHQ LLRPLIFCQDHLREGPPIGRGDS QGEELEPQLPSSLSSIPYGFCDH CWTKDVDDPPLVTHPSPGSRD GHMTQAWPVKVVSPLATVIGH VMQASLLAL |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21290 | 51658 | A | 21418 | 3 | 1584 | TQKNTAVRAHRLWGREKISRK EGAGPTPQESRRIGARSGALMT RKGRGMQEVEELSETGKVVKQ HRVGEALRVVVLVWAGSLG/D RRGLVLGRRGYYGAVPAVEMP ARALLPRRMGHRTLASTPALW ASIPCPRSELRLDLVLP SGQSFR WREQSPAHWSGVLADQVWTL TQTEQLHCTVYRGDKSQASRP TPDELEAVRKYFQLDVTLAQL YHHWGSVDSHFQEVAQKFQG VRLLRQDPIECLFSFICSSNNNIA RITGMVERLCQAFGPRLIQLDD VTYHGFPSLQALAGPEVEAHLR KLGLGYRARYVSASARAILEEQ GGLAWLQQLRESSYEEAHKAL CILPGVGTKVADCICLMALDKP QAVPVDVHMWHIAQRDYSWH PTTSQAKGSPQTNKELGNFFR SLWGPYAGWAQAGLLGNAFD GHQLLRPLIFCQDHLREGPPIGR GDSQGEELPQLPSSLSSIPYGF CDHCWTKDVEDPPLVTHPSPG SRDGHMTQAWPVKVVSPLATV IGHVMQASLLAL |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21291 | 51659 | A | 21419 | 837 | 2785 | WTRMLFAVSCNDGECQNSNVI LFCDMCNLAVHQECYGVPIPE GQWLCRRCLQSPSRAVDCALC PNKGGAFKQTDGGRWAHVVC ALWIPEVCFANTVFLEPIDSIEHI PPARWKLTCYICKQRGSGACIQ CHKANCYTAFHVTCAQQAGLY MKMEPVRETGANGTSFSVRKT AYCDIHTPPGSARRLPALSHSE GEEDEDEEEDGKGWSSEKVK KAKAKSRIKMKKARKILAEKR AAPVVSVPICPPHRLSKI'TNRL TIQRKSQFMQRLHSYWT LKRQ SRNGVPLLRLQLTHLQSQRNCD QVGRDSEDKNWALKEQLKSW QRLRHDLERARLLVELIRKREK LKRETIKVQQIAMEMQLTPFLIL LRKTLEQLQEKDTGNIFSEPVPL SEVPDYLDHIKKPMDFFTMKQ NLEAYRYLNFDDFEEDFNLIVS NCLKYNAKDTIFYRAAVRLRE QGGAVVRQARRQAEKMGIDFE TGMHIPHSLAGDEATHHTEDA AEEERLVLLLENQKHLPVEEQLK LLLERLDEVNASKQSVGRSRA KMIKKEMTALRRKLAHQRETG RDGPERHGPSSRGS LTPHPAAC DKDGQTD SAAE SSSQETSKGL GPNMSSTPAHEVG\GEPQFCSP KRTRRQ/HGPPKRPGRPPKNRES QMTPSHGGSPVGPP/RAPHHEFP ASAQAG*EPQFCSPKRTRRQLD |
| 21292 | 51660 | A | 21420 | 1 | 2625 | MENKITGYTTVDISQWHRKEHF EAFQSVAQCTYNQTVQLDITAF LKT V K K N K H K F Y P A F I H I L A R L MNAHPEFRMAMKDGELVIWD SVHPCYTVFHEQTETFSSLWSE YHDDFRQFLHIYSQDVACYGE NLAYFPKGF IENMFFVSANPWV SFTSFDLNVANMDNFFAPVFTM GKYTTQGDVKVLMPLAIQRDSE DKNWALKEQLKSWQRLRHD ERARLLVELIRKREKLKRETIKV QQIAMEMQLTPFLILLRK |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21293 | 51661 | A | 21421 | 164 | 1401 | PPKGRGMQEVEELSETGKVVK QHRVGEALRVVVLVWAGSLG/ DRRGLVLGRRGYYGAVPAVE MPARALLPRRMGHRTLASTPA LWASIPCPRSELRLDLVLP SGQS FRWWREQSPAHWSGV LADQV WTLTQTEEQ LHCTVYRGDKSQ ASRPTPDELEAVRK YFQLDVTL AQLYHHWGSVD SHFQEVAQKF QGVRLLRQDPIECLFSFICSSNN NIARITGMVERLCQAFGPRLIQL DDVTYHGFP SLQALAGPEVEA HLRKLGLGYRARYVSASARAIL EEQGGLAWLQQLRESSYEEAH KALCILPGVGTKVAD CICLMAL DKPQAVPVDVHMWHIAQRDY SWHPTTSQAKGSPQT NKELGN FFRSLWEPYAGWAQATPPSLQ VLFSADLRQSRHAQEPPAKRRK |
| 21294 | 51662 | A | 21422 | 751 | 2107 | SSEHPRELHRIPISWAMSELKDC PLQFHD\FKSV DHLKVCPRYTA VLARS\EDDGIGIEELDTLQLEL ETLLSSASRR\LRVLEAETQILT D\WQDK\KGDRRFLKLG\RDH\E FGAPPKHGKPKK\QKLE\GKAG HGPGP\CPGRPKSKNLQPK\IQE YEFTDDPIDVPRIPKNDAPNRF WASVEPYCADITSEEVRTL EEL LKPPEDAEHYKIPPLGKHYSQ RWAQEDLLEE QKD GARAAAV ADKKKG LMGPLTELDTKDVDA LLKKSEA QHEQPEDGCPFGALT QRL LQALVEENIISP MEDSPIPD MSGKESGADGASTSPRNQNKP FSVPHTKSLESRIKEELIA\QALL *AGDLLAKDSEDEVLAELRKR QG\EL\KALSAHNRTKKA\DLLR LAKEEVS RQELRQR\VRRAERE GMDAFRKIHGLPGRRKRN SPPK K\EKDQAWKNS*KEREEHP |
| 21295 | 51663 | A | 21423 | 107 | 331 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21296 | 51664 | A | 21424 | 387 | 1071 | NNPEWRTLIIYVDKENGEPGTR VVAKDGLKLG\SGPSIKALDGR SQVSVTPRFGKTFDAPTQPYLKL PRKALG\TVNR\TTEKSVKDPGD PSNKKQPKLFRPKKDGPEEGLL KAKKPLFPGLQD*CPIPEIRKIPF PFNPS*TLRSF*PCPEEHPDCGTF PL*VG\PLMIPLTREREL*KSW FQLGPPFHLWKDGPLPPWGPIC LQFSFQGISVRTWGV\DLPPVCC DIDI |
| 21297 | 51665 | A | 21425 | 480 | 1270 | RSVKKVGAQRPGSGGGWGGN EGWVPQATAPGWAYTHVLFY LFVTPISAALRADGFGDNPFY HCLVAEILPAPGKLLGKSTWPL EVHLSSRPQRSPhRLPEALLPFS LSQG/HCVVGYGIYYFIYSTWK GRTIYLEDIYVMPEY/RGYWAE AEAGVGAKHPTDPTVIPCPQSP AGVIF*SPSAQTIAIFCLFLSTTG QGIGSKIHKVAEVALDKGCSQ FRLAVLDWNQRAMDLYKALG AQDLTEAEGWHFFCFQGEATR KLAGK |
| 21298 | 51666 | A | 21426 | 182 | 797 | LPFARPWDFGPRQRGSGWLPC GSREAKEGDCGDILRLIRVKTA GPelaEFekLFGSGERSVEEAL ESRLAFGDNPFYHLFW*AEILP APGESYWG/HCVVGYGIYYFIY STWKGRTIYLEDIYVIAGNIGV QGIGSQK*SKKV\AEVALGIRGC SPNFRLARPLD\WNPEGPWDLY KAPRSPKI*RKLEGWHFFCFQG EATRKLAKG |
| 21299 | 51667 | A | 21427 | 224 | 490 | QAGFISARNITWR*ANRRSTWR SYRRKSGRTANCPPISPACSRC SAPIFIPKNGWWRAMVAPLKW PSTGAFNRLFVPLLTWWRSPDR |
| 21300 | 51668 | A | 21428 | 301 | 773 | HGPGTQQRPRSIWRMPQ*ARPG GRSLAVGGGPRPRAAGGFP*VA SRARRCQR\AHGCHCAFSPSP ALLSQDAGLCQSRPLLLGQRR LSQEVWSGLGNVHFCQPPEDA ATTPSCPEALTAQGQQASVCDR VSHRFSTWSMVRCSDRTEGQR LQTLGD |
| 21301 | 51669 | B | 21429 | I | 1380 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21302 | 51670 | A | 21430 | 1 | 1660 | AGVLASHPNSTDVHIINLSLTFH GQELLSDTKLELNSGRRYGLIG LNGIGKSMLLSAIGKREVPPEH IDIYHLTREMPSPDKTPLHCVM EVDTERAMLEKEAERLAHEDA ECEKLMELYERLEELDADKAE MRASRILHGLGFTPAMQRKKL KDFSGGWRMRVALARALFIRPF MLLLDEPTNHLDLDACVWLEE ELKTFKRILVLVSHSQDFLNGV CTNIIHMHNKKLKYYTGNYDQ YVKTRLELEENQMKRFHWEQD QIAHMKNYIARFGHGSALKAR QAQSKEKTLQKMMA SGLTERV VSDKTLSFYFPPCGKIPPPVIMV QNVSFKYTKDGPCIYNNLEFGI DLDTRVALVGPNGAGKSTLLK LLTGELLPTDGMIRKHSVKIG RYHQHLQEQLDLDSPLEYMM KCYPEIKEKEEMRKINGRYGLT GAKQQVSPIRNLSDGQKCRVCL AWLAWQNPHMLFLDEPTNHL DIETIDALADAINFEFGMMLV SHDFRLIQQVAQEIVVCEKQTI TKWPGDIL\AYKEHLKSKLVD\ |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21303 | 51671 | A | 21431 | 78 | 2022 | NNSNLPLWVIIMPSTDLAKKAA KKKEAAKARQRPKNGHEENG VVTEPQVAEKNEANGRE/TTRE VDLLTKELEDFEMKKAAARAV TGV LASHPNSTDVHIINLSLTFH GQELLSDTKLELNSGRRYGLIG LNGIGIGKSMMLFAIGKREVP EHIDIYHLTREMPSPDKTPLHCV MEVDTERAMLENEAERLAHED AECEKLMELYERLEELDAD*AE MRASRILHGLGFTPMQRKKL KDFSGGWRMRVALARALFIRPF MLLLDEPTNHLDLDACVWLEE ELKTFKRILVLVSHSQDFLNGV CTNIIHMHNNKKLYYTGNVDQ YVKTRLELEENQMKRFHWEQD QIAHMKNYIARFGHGS AKLAR QAQSKEKTLQKMMASGLTERV VSDKTL SFYFPPCGKIPPPVIMV QNV SFKYTKDGPCIYNNLEFGI DLDTRVALVGPNGAGKSTLLK LLTGELLPTDGMIRKHSVKIG RYHQHLQEQLDLDSPLYMM KCYPEIKEKEEMRKIIIGRYGLT GKQQVSPIRNLSDGQKCRVCLA WLA WQNPHMLFLDEPTNHLDI ETIDALADAIN EFEGGMMLVSH DFRLIQQVAQEIWVCEKQTITK WPGDILAYKEHLKSKLVDEEPQ LTKRTHNVCTLT LASLPRP |
| 21304 | 51672 | A | 21432 | 313 | 599 | |
| 21305 | 51673 | A | 21433 | 737 | 1006 | DNPVVVFVFGSVYMLDYVY*FS YVEPPLHPWDEAHLIMVDKLF DVLLDSVCQYFIEDFCINVNQG YWSKILFFCCISARLWYQDDAG |
| 21306 | 51674 | A | 21434 | 1108 | 1260 | GVNFNLSCFLLWAFSAIHFP LH TALNVSQRFWYVVSLSLFSK NIFISAF |
| 21307 | 51675 | A | 21435 | 804 | 917 | |
| 21308 | 51676 | A | 21436 | 158 | 298 | |
| 21309 | 51677 | A | 21437 | 1 | 1068 | |
| 21310 | 51678 | A | 21438 | 1 | 1188 | |
| 21311 | 51679 | A | 21439 | 122 | 352 | |
| 21312 | 51680 | A | 21440 | 647 | 662 | ICGVISEGSLVLFH*SISLFWYQY HAVLVT/DSL VV*FEVT*HDASS FVLLA*DRRPEGSSPKSP |
| 21313 | 51681 | B | 21441 | 53 | 692 | |
| 21314 | 51682 | B | 21442 | 1 | 925 | |
| 21315 | 51683 | A | 21443 | 606 | 900 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21316 | 51684 | A | 21444 | 33 | 852 | CWKFWARAN*AGGITLPDFKL YYKATVTKTAWKFHFTMFGV DLKETCTAPSLWKDLALNTVE LVCKLCVRQVEGARQIFQLNCT VSE |
| 21317 | 51685 | A | 21445 | 3 | 795 | |
| 21318 | 51686 | A | 21446 | 475 | 1023 | CWFSAGDGGPLPGPDYGQDFAA HPAGAGALYKCRDLINDNILRT VSCQSHDDGDIRGMAFARQ*Q RPVQIDHNMARRG**AATFQPI NKTFSGIHWPHGMRTGGTNP FENIECTNHIHTLGLPFSEVERN DCDGFNFQLHIFRQTRDLHTAP GRIGRLMLIEELLIDFVDGGKII QIGDKHGH |
| 21319 | 51687 | A | 21447 | 1637 | 2020 | PSSEFTGGPARGFPERARAQL TGRTPGQRTQLDNDLLTKSTP WRGVMGPTLLPGLLAGPFQPL GHTGPFYPQGFRWQKTHWVRL AQAHWQF*LGQFRGPKTADGG GSKGPGLSASHGAKHHVITYV |
| 21320 | 51688 | A | 21448 | 1051 | 1185 | |
| 21321 | 51689 | A | 21449 | 1290 | 2025 | |
| 21322 | 51690 | B | 21450 | 1 | 1410 | |
| 21323 | 51691 | A | 21451 | 3269 | 3678 | SLSIRLATAPCWLRYPASSRRFQ PTRSAGSVTDSSVTASASSPG*R *NASP\CRERSHRSSRGQARRSL HLWDRSDR*TLPCDHGRCCCHA NDQQVGFAGNYSTAGQT*RWT GFTAGHAGRDINKSADKLPAT AGKR |
| 21324 | 51692 | B | 21452 | 2655 | 2825 | |
| 21325 | 51693 | A | 21453 | 1 | 896 | MGDFNTPLSTLDRSMRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQNHSTTWKLN NLLLSDYVWHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLELEKQEQTTHSKASRRQE ITKIRAELEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDKGDITTDPT\YK LPSENTTNTSTQIN*KI*KKWIN SSTHTLSQD |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21326 | 51694 | A | 21454 | 23 | 559 | TPGLRQSSLSPSAFASQNAGVS GIGGFLVSLTSRMKPWTLAMFR CVWSFFLLVGSWSCWLQE*SC RPSQ*VSQFL/NSSASGVVCCSC LELFVPPGGFVVS LASRVKLQT FTVSVTAHKGGVDPKSEQQQD LVQKAKEHSFCSVEADLSGLPL LAGAACFYSLMEPHPHPADWSI LQRAD |
| 21327 | 51695 | A | 21455 | 26 | 323 | |
| 21328 | 51696 | A | 21456 | 221 | 734 | |
| 21329 | 51697 | A | 21457 | 293 | 2103 | PCHSALSSPLPHRDCIALCFLNS GTSFVAGFAIFSILGFMFQEQG VPISEVAESGPGLAFIAYPRAVV MLPFSPLWACCCFFMVVLLGL DSQFVCVESLVTALVDMYPHV FRKKNRREVLILGVSVISFLVGL IMLTEGGMYVFQLFDYYAASG MCLLFVAIFESLCVAWVYGAK RFYDNIEDMIGYRPWPLIKYCW LFLTPAVCTATFLFSLIKYTPLT YNKKYTYPWWGDALGWLLAL SSMVCIPAWSLYRLGTLKGPF EVIIPVSIRMTKVAGTAGLSGN VGPRCDLSRIEELPDGGTRCGM DSRVSGTTSNGETKPVYPVME KKEEDGTLERGHWNKMEFVL SVAGEIIGLGNVWRFPYLCYKN GGVVGFYNSIKNIPILQRVILFV RIHNMLNKGQGVLA KCDAAK KIEEKEADAGSASVPGDVMRT KKLSFEGAWHPCLLVGLKLS ALELRGGFISARIAGPRAAESDS VGLERELRVCIANKLPGEADAA GPGTTFWKHCSPITDGADAV EGRNTQEAFFRQLNPEAAFLHF MEMVDTNALHVHGIHTRKNHP GQKEAAHSQHGTFFIRWTLNLL KRTFQKGNRAEPNSPAM |
| 21330 | 51698 | A | 21458 | 1 | 419 | MKLRTLAVSATALKVARLEFV PFDVRMCSEFLSSGVKLQTFV SVTALNALRLELFVPPGGLMVS LASGVKLQIFTVSVTAHKSSVD PKTLG/CVDGTGRRGAGGGAH RGGLGRTGAHGGGGRLRHGGL QVSSPAPRKGS |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 21331 | 51699 | A | 21459 | 24 | 1639 | GGMDSRVSGTTSNGETKPVYP VMEKKEEDGTLERGHWNKMK EFVLSVAGEIIGLGNVWRFYPL CYKNGGGGAFFIPYLVFLFTCGIP VFLLETALGQYTSQGGVTAWR KICPIFEGIGYASQMIVILLNVY YIIVLAWALFYLFSSFTIDLPGW GCTHEWNTGNWVDVVE/HGG* GEWCGNGSNTPHVCR/VTGWT W*SRWLKGMVWEWQHTPCV QGTGWTW*STWLKG/PGNRVD VVEHVAEGNGVGMPTHTPCA GNRVDVVEQVAEGNEHCMEF QKTNGSLNGTSENATSPVIEFW DSPPGPQFVCVECLVTASIDMF PRQLRKSGRRELLITIAVMCY LIGLFLVTEGGMYIFQLFDYYA SSGICLLFLSLFEVVCISWVYGA DRFYDNIEDMIGYRPWPLVKIS WLFLTPGLCLATFLFSLSKYTPL KYNNVYVYPPWGYSIGWFLA LSSMVCVPLFVVITLLKTRGPFR KVGGVGESDLLKEGTERGWT WGRTHNWQGADTNSECGAA LQSHRILTRRTLKTSPVAFQKCS |
| 21332 | 51700 | A | 21460 | 1358 | 4787 | RRCYCGIWSRYLLKRLWKWIS GEGWAEKDSARRRGICTFWLE FE/VTCLSWNSLF/YAHINVDISG MKVPWLYVGMCFSSFCWHIED HWSYSINYLHWGEPKTWYGVP SHAAEQLEEVRELAPELFESQ PDLLHQLVTIMNPNVLMHEGV PVYRTNQCAGEFVVTFPAYHS GFNQGYNFAEAVNFCTADWLP IGRQCVNHYRRLRRHCVFSHEE LIFKMAADPECLDVGLAAMVC KELTLMTEEETRLRESVV |
| 21333 | 51701 | A | 21461 | 1 | 5773 | MEEKPLKVKGKDSSEKKRKRK LEKVEQLFGEGKQKSKELKKM DKPRKKKLKLGADKSKELNKL AKKLAKEEERKKKKEKAAAK VELVKESTEKKREKKVLDIPSK YDWSGAEESSDENAVCAAQN CQRPCDKVDWVQCDGGCDE WFHQVCVGVSPEMAENEDYICI NCAKKQGPVSPGSHKAVITVV VKAVSYLKFEESTSELMWLL AAFSSFWVGICALDFVWPLA REEKEIGDNKDLERNKIGVNM |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21334 | 51702 | A | 21462 | 85 | 1333 | STSRALSGAQRFGRLIDHGARV PALLLLLLPL\VHVSATTPEPR\E LDDEDFRCVCNFSQPQDWSEA FQCVSA\VEVEIHAG\GLNL\EPF LK\RVDAADADPRQYA\DTVKGF PR\VRASQVGAAQVPA\QLLV GALR\VLA\YSRFKELTLEDLKI TG\TMPPLPLEATGLALS\SLRLR NVSW\ATGRSWL\AEL\QQWLK PG\LVLSIAQAHSPAFCSEQVR CFPGPSPA*DLSDNPGTGANAE LMAALCPHKFPA\IQNL\ALRNT GNRRPQGVCAALAAAGVQPH SLDVSHNSLRANRNP\AP\RCM \WSNA\LNSPQICRFAGAGTGVP KGPAPAKL\RVLRSSACNRL\NR A\QPWTSLE\VDNLGQLDGNP FPGSPGTGPSPTGSMN\SGVVP SLCNVRTCRVGVSGTLVLLQG ARGFA |
| 21335 | 51703 | A | 21463 | 1640 | 5804 | TITGSSPLAGGHHSTCRGRMDM VENADSLQAQERKDILMKYDK GHRAGLPEDKGPEPVGINSSIDR FGILHETELPPVTAREAKKIRRE MTRTSKWMEMLGWETYKHS SKLIDRVYKGIPMNIRGPVWSV LLNIQEIKLKNPGRYQIMKERG KRSSEHIIHIDLDVRTTLRNHV FFRDRYGAKQRELFYILLAYSE YNPEVGYCRDLSHITALFLLYL PEEDAFWALVQLLASERHSLPG FHSPNGGTVQGLQD |
| 21336 | 51704 | A | 21464 | 1 | 960 | |
| 21337 | 51705 | A | 21465 | 1 | 1317 | |
| 21338 | 51706 | A | 21466 | 1 | 3393 | |
| 21339 | 51707 | A | 21467 | 2745 | 6141 | QGSKGTCHPQAQQPWDEGVW QEAPSQSEPWGQSQEPPTMPQR LPHARQHTPLPLGSADYRRVVS VRPQGPHRDPKDSRDAAKREQ GSLAPRPVPASRGGKTLCKGYR QAPPGPPAQFQRPICASPPWAS RFSTPCPGGAVREDTYPVGTQG VPSLALAQQGGPQGSWRFLWK SMPRLPTDLDIGGPWFPHYDFE RSCWVRAISQEDQLATCWQAE HCGEVHNKDMSWPEEMSFTAN SSKIDRQKVPTTEKGATGL |
| 21340 | 51708 | A | 21468 | 65 | 320 | |
| 21341 | 51709 | A | 21469 | 3 | 505 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21342 | 51710 | A | 21470 | 2 | 1756 | CRCHSELSSGSSL*/CCTRGIGGAI GAVGFRSQAASLAGQPDGNG VCVHAGNSRIFVPLPVGLEVKG FSHSAFTFGIESHISQSNINGTLV PPSALISILQKGLQYVEAEISINK DGTVFDSRPIESLSLIVAVIPDV VQMRQQAfGEKLTQQQASAA ATEASAMAKAATMTPAAISQQ NPPKNREATVNGEENGAHEINN HSKPMEIDGDVEIPPNKATVLR GHESEVFICAWNpVSDLLASGS GDSTARIWNLNENSNGGSTQL VLRHCIREGGHDVPSNKDVTSL DWNSDGTLLAMGSYDGFARIW TENAPALDVDWQNNMTFASCS TDMCIHVCR LGCDHPVKTFQG HTFCTCIESICFWGGLRKLTTM TEGKRLRPKTFCS DGGALLPPA GRRPHLLTGPDIFFKRLSALFQN EVNAIKWDPSGMLLASCSDDM TLKIWSMKQDACVHDLQAHSK EIYTIKWSPTGPATSNPNSSIML ASASFDSTVRLWDVEQGVCTH TLMKHQEPVYSVAFSPDGKYL ASGSFDKYVHIWNTQSGSLVHS YQGTGGIFEVCWNARGDKVGA SASDGS\VCILWQLSGKQ |
| 21343 | 51711 | A | 21471 | 1 | 1647 | |
| 21344 | 51712 | B | 21472 | 4 | 267 | |
| 21345 | 51713 | A | 21473 | 1 | 1824 | |
| 21346 | 51714 | A | 21474 | 33 | 543 | TFEGANNFVGDPIVLPCNPPKG LPPLHIYWMNIELEHIEQDERV YMSQKGDLYFANVGRKRDSRN DYCCFA\AFPRIKGLLYRKMPM /RNLTVNSSNSIKAKENPKLLLA SPLRSGSESSITLKGEILLLECF AEGLP TPQVDWNKIGGDL PKG REAKENYGKTLKIENVY |
| 21347 | 51715 | A | 21475 | 197 | 516 | TYLAAGRTPTLDPWNQERCTM PSGSIWILETHSSFGWVTVAH LSSDPKGCQF*VGSRIGEGSATD PAFCASCSATWTIRPSRNGA*G VNG**VCWLEPLAGPHR |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21348 | 51716 | A | 21476 | 1 | 1766 | MNVALTHIDTHHAEFEMALQA ALVWNTLRTAGGKKSIVHLASA LLVHEIHDGANLTISNVTLEDQ GIYCCSAHTALDSAADITQVTV LDVPDPENLHLSEQRNRSVRL TWEAGADHNSNISEYIVEFEGN KEEPGRWEELTRVQGGKTTVIL PLAPFVRYQFRVIAVNEVGRSQ PSQPSDHHETPPAAPDRNPQNIR VQASQPKEMIIEWEPLKSMEQN GPGLEYRVTWKPQGAPVEWE EETVTNHTLRVMTPAVYAPYD VKVQAINQLGSGDPQSVTLYS GEDLPEQPTFLKVIKVDKDTAT LSWGLPKKLNGNLTYLLQYQ IINDTYEIGELNDINITPSKPSW HLSNLNATTKYKFYLRACTSQ GCGKPITEESSTLGEGSVSLEKC ENKLIRNIGTKKQGTAIRIPENV EAALELRKQKLEECGGFRRRE NANEQQGVTEEFKQQNEKLRF LLLKIVILAVAREMTWNGEGR DLSEPSLTVVFADLSSPAYSLHT TMAQEPGPGFLSLSTIPWPISII PMIHASVQVSWIPLLRNSLMVH IHSSLEQRNLKVHISKEQKKLNS VDSDLTDNPPTHTVN |
| 21349 | 51717 | A | 21477 | 1 | 1440 | |
| 21350 | 51718 | A | 21478 | 266 | 3974 | RAMEPLLLGRGLIVYLMFLLLK FSKAIEIPSSVQQVPTIIKQSKVQ VAFPFDEYFQIECEAKGNPEPTF SWTKDGNPFYFTDHRIIPSNNS GTFRIPNEGHISHFQGKYRCFAS NKLGIAMSEEIEFIVPSVPKFPK EKIDPLEVEEGDPIVLPCNPPKG LPPLHIYWMNIELEHIEQDERV YMSQKGDLYFANVEEKDSRND YCCFAAFPRLTIVQKMPMKLT VNSLKHANDSSSTEIGSKANSI KQRKPKL |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21351 | 51719 | A | 21479 | 1 | 2421 | QAGAMASGSVAECLQQUETTCP VCLQYFAEPMMLDCGHNICCA CLARCWGTAETNVSCPQCRETF PQRHMRPNRHLANVTQLVKQL RTERPSGPGGEMGVCEKHREPL KLYCEEDQMPICVVCDRSREHR GHSVLPLEEAVEGFKEQIQNQL DHLKRVTRLKFTDFLAQGEQA RAELLSLTHMEREKIVWEFEQL YHSLKEHEYRLRLARLEELDLAI YNSINGAITQFSCNISHLSSLIAQ LEEKHQQPTRELLQDIGDTLSK AERIIRIPEPWITPPDLQEKIHIFA PKCLFLTESLKQFTEKMQSDME KIQELREAQLYSGGSIVGGHEP GEPGRGIKAGYGTNCNCFPEEEKC FCEPEDIQDPLCDEL CRTVIAAA VLFSFVSVLLSAFCIHCHYHKF AHKPPISSAEMTFRRPAQAFPVS YSSSGARRPSLDSMENQVSVDA FKILEDPKWEFPRKNLVLGKTL GEGEFGKVVKATAFHLKGRAG YTTVAVKMLKENASPSEL RDL LSEFNVLKQVNHVPHVIKLYGAC SQDGPLLLIVEYAKYGSRLRGFL RESRKVGPGYLGSGGSRNSSL DHPDERALTMGDLISFAWQISQ GMQYLAEMKLVHRDLAARNIL VAEGRKMKISDFGLSRDVYEE DPYVKRSQGRIPVKWMAIESLF DHIYTTQSDVWSFGVLLWEIVT LGGNPYPGIPPERLFNLLKTGH |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21352 | 51720 | A | 21480 | 79 | 2253 | PSATLSCPTSVAAASLGEPAVFPL SLRGHRRRHRPGHSPSVRGRV WDTGPGGAALRPPGASQEQR GESAGELGSVQSSAPGMPVVRP RRPGAMASGSVAECLQQUETC PVCLQYFAEPMMLDCGHNICC ACLARC\WGTEET\NVS\CPQCR E\TFPQRHMRPNRHLANVTQLV KQLRTERP\SGPGGEMG\VCE\K HREPLKLYCEEDQMPICVVCDR SREHRGHSVLPLEEAVEGFKEQ IQNQDLHLKRVDLKKRRRAQ GEQARAELLSLTQ\MEREKIVW E\FEQLYHSLKEHEYRLARLEE LDLAIYNSINGAITQFSCNISHLS SLIAQLEEKQQQPT\RELLQDIG DTLSRAERIRIPEPWITPPDLQE KIHIFAQK\CLFLTESLKQFTEK MQSDMEKIQELREAQLYSVDV TLDPDATYPSLILSDNLRQVRY SYLQQDLPDNPERFNL\FPCVLG SP\CFIAGETIIWEGRGWGDKAK WTIG\VC*RLSCQEKGGVTSAP QNGFW\AVSLWYGK\EYW\ALT SPMTALPLRTPFQ\RVGIFL\DYD A\GEVSFYN\VTERC/HTPFTFSS CLPFGGLVRPLLSSLSYSGREK VQLPLINLPP*SGIDGGFLAHVG \NHGSFPWKTFPFEGRVNSGPK GLLA VILRPGTRHLVCLANVLS KLGILNHVPRPCSGRHGCPCSLP SFFLPMQIVKCNEMYQDILEIKT |
| 21353 | 51721 | A | 21481 | 1 | 1068 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21354 | 51722 | A | 21482 | 955 | 2548 | MSLCGARANAKMMAAYNGGT SAAAAGHHHHHHHHLPHLPPP HLHHHHHPQHHLHPGSAAAVH PVQQHTSSAAAAAAAAAAAAA MLNPGQQQPYFSPAPGQAPGP AAAAPAQVQAAAAATVKAHH HQHSHHPQQQLDIEPDRPIGYG AFGVVWSVTDPRDGKRVALKK MPNVFQNLVSCKRVFRELKML CFFKHDNVLSALDIL*PPHIDYF EEIYVVTELMQSDLHKIIVSPQP LSSDHVKVFLYQILRGLKYLHF RLGILH\RDIKPGNLLVNSNCVL KICDFGLARVEELDESRHMTQE VVTQYYRAPEILMGSRHYSNAI DIWSVGCIFAELLGRRILFQAQS PIQQLDLITDLLGTPSLEAMRTA CEGAKAHILRGPHKQPSLPVLY TLSSQAT\H*TGHLLFAECGFDP SKRISAKDALSHPYLDEGRRLRY HTCMCKCCLSPS\TGRVNT\SDL EPVT\NPKFDDTFEKNLSPVRQV KEIIHQFILEQ\QKGNRV\PLWIN PQSAVFKSFISSTVAQPSEMP\SLVWE |
| 21355 | 51723 | A | 21483 | 119 | 692 | SYKSRLARKS\TGGKAP\RKQLA YKKPASQECGPLTGGVKKPHR YR\PGTVAAP*NLDGYQKSTE\L MIRK\LRFQR\LVREIAQ\DFKT DLRFQSAVIRWLCRMAS\EAYL VWPFLKDTNLVCLSMPCRVTIY AKKTFQLSTPASRGERALRIHS WMGKHFILKKKKKKFLFFLL VVLNVRYFFFHGVKRYLSI |
| 21356 | 51724 | A | 21484 | 2 | 363 | RFTKVEMKEK\MLSAAREKGR VTHKGKPISLKADLSAETLQAR REWGPIFNILKEKNFQPRISYPA KLSFISEQEIKYFTDKQMLRDFV ITRPALKELLKEALNMERNNW YQPLQKHAKL |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21357 | 51725 | A | 21485 | 1 | 1468 | MRNLRNIQKAKATINLGISFDE GLKGFMSWSRIEAAPLPNTRWC LPHGYSGPANSGGCYYITTGMS CWLSLDLYPRHDGVHVGGLQKK DLEHDIPVDLGSRPVSVDVPSRS APGPQGPAPVDSGSRTTPANP GAGPSPVDPSSRPAPVASGFRLI MIDQNTKLIPVPGWPLRLRLKI YLSSRSASLDGSRFAPVDTNFI PVPTDRGHSHAPEDPVDRLTSV DPTKEKNWMENEFDKLTEVGF RRSVITNFSELKEHVLTHRKEA KNLEKRLDEWLSRITCAEKSLN DLMELKTTVRELREAYTSFMS QFDQAEERISVIEDQINEIKLKS QAQEDARHRNTDQRSSNNRRS EPWSLEERKREQWNSLKQNAD QQDTEAMSDYK/RYSSET*RRR *LFCLLRKVHSKEGP*KKDQRE TRNQKGLGFLDRPQWVSGKM KQECLQLGTPWP*IIIGWQYFP RDGMGVRTDFCRIFQRLARMR LCEGCLMNS |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21358 | 51726 | A | 21486 | 1 | 2589 | MSPVTLWVRTSSRGEDRCGMC TPGRDTGFAPISGMCSKYRSCTI NEDTGLGLAFTMPMSLDTKHIP NFGKVHGYIMRHHKNEDTIPW RRNTKKEEARGTQPLEADDQN PGWEDGKPGSLENEGRSHRG NPAPDMPQPPKEDFILPDEYK SCLRHKRSLLRSHRNEELNVET LVVVDKMMQNHGHENITTY VLTILNMERILKKTSTIIHPSA MERCPLNLQIRDSLWNHCFSL ATTVHRFHPVGRHALKKMYKL PSAYINVSITKYTORFALTYISC VFHRNAAFVAVPGEGRCCAGV DVPAPMSLRSPGPHWPQEHGA LWISCTVRGMASCLGQLCRVS MRVRANIGKVQKPRLRISNGK GLHTQSELSGSAYLEKGWRGA APGLDSRNEKGTEGARDSGTPG RQSQTLQRGPPGPVPGSSKIAPQ TLTRQGSMTASRKLVLLEPFC ERTGEQSGQLYPPSPLLVEWV MPAGTSSTVDPLLPELCRRWER QALSLCRLYRQRTSVSIKALCD HTETRSVALSTCQGLECNSSPA RKQNWMEFEELTEVGFRKS VITKFSKLKEHILTHRKEAKNLE KRLDEWLTRITSVEKSLNDLME LKTTVRKILHEAYTSFNSRFDQ VEERILVIEHQINEIKQEDKVRE KRVKRNEQSLQEIWDCVKRPN LCLIGVPESDGENGTKLENTLQ |
| 21359 | 51727 | A | 21487 | 260 | 1292 | RLCAFNKRMTFQFNFTIEDHLE NELTPIRDGALTLDSSKELSVSE SQKGEERDRKCSAEQFDLPQD HLWEHKSMENAAPSQDSDSPL SAASSSRNLEPHGKQPSLRAAK EHAMPKDLKKMLNENKVIETLP GFQHVKLSVVKTILLKENFPGE NIVSKSFSSHDLITGVYEGGLK IWECTFDLLAYFTKAKVKFAG KKVLDLGCSSGLLGITAFKGG KEIHFQDYNMVIDEVTLPNV VANSTLEDEENDVNEPDVKRC RKPKVTQLYKCRFFSGEWSEFC KLVLSEKLFVKYDLNLTSETIY NPDYYSNLHQTFRLRLSKNGRV LLASKAHVQRNSLSRL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21360 | 51728 | A | 21488 | 263 | 1466 | RLCAFNRMTFQFNFTIEDHLAE NELTPIRDG\ALTLDSSKELASVS ESQKGRKE\RDRCSCAEQF\DL P QDHLWGNISSMGKWQAPS\QG HRTSSTSVAASSRNLEPHGKT ALLAGAGQSRMAMPKRF*RRC LEN*SPLETLPGFQHVKLSVVK TILLKENFPGENIVSKSFSSHSDL ITGVYEGGLKIWECTFDLLAYF TKAKVKFAGKKVLDLGCGSGL LGITAFKGASKEIHF\QDYN SMV IDEVTLPNVVA\NS\TLEDGGKM DVKWSPDVEKMPGNPKVTQ\ L YKC\RFFS\GEWS*VL*ALYLSSE K\LFVKYDPHSSPSET\IYNPDY YSNLHQTFRLRLSKNGRVLLA SKAHYFGVGGGVHLFQKFVEE RDVFKTRILKIIDEGLKRFIIEITF |
| 21361 | 51729 | A | 21489 | 2 | 367 | |
| 21362 | 51730 | A | 21490 | 2 | 376 | QTYSLRRATPRHIIVGFTK VEM KEKVLRAA/NKPIRLTVDL SAET LQARKEGGPIFNILKEKNFQPRI SYPAKLSFISEGEIKSF TDKQML KDFVTTTRPALQELLKEALNME RNNQYQPLQKHAKW |
| 21363 | 51731 | A | 21491 | 1 | 690 | |
| 21364 | 51732 | A | 21492 | 1 | 714 | |
| 21365 | 51733 | A | 21493 | 1 | 1536 | |
| 21366 | 51734 | A | 21494 | 1 | 765 | |
| 21367 | 51735 | A | 21495 | 1 | 972 | |
| 21368 | 51736 | A | 21496 | 1 | 2670 | |
| 21369 | 51737 | A | 21497 | 2 | 1178 | |
| 21370 | 51738 | A | 21498 | 2 | 827 | |
| 21371 | 51739 | A | 21499 | 1 | 777 | |
| 21372 | 51740 | A | 21500 | 168 | 1057 | IRLKNHDH GELRNKTICINRNL AEIKKFS ENYENKETMYLNLW DVAKAVLRGQFIALNARIKKLE KSQVYNLISQLKELENQEQTNP KASRRQEITKIRAE LKEVETWK TLKKINESGRGVDCSS/DASNGT KPDGE*L**VDKSR/PSEARQAN IHIQEIHGTPQR*SLRRATPRH/II VRFTKVEMKEKMLRAARKKG WVTHKGKPIRLTADLLAETLQ ARREWGPIFNILKEKNFQLRISY PAKLSFIREGEIKAFTEKQILRDF VTTRPALQELLKEALNMERND RYQPLQKHAKL |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21373 | 51741 | A | 21501 | 3 | 1263 | GRTIQTKGKEV\ENFEKNLEECI TRITNTEKCLKELMELKTKARE VREECRSLRSQCDQLEERVVSAM EDEMNMKQEGKFREKRIKRN EQSLQEIWVYVVRPNLRLIGVP ESDVENGTKLENTLQDIIQENFP NLARQANVQIQERQRTTPQRYSS RRATPRHIIVRFTKVEMKEKMG LLVPNWTNHSPLFRILFDYKG FCRFGTTHQTGFSPAGANQRGP LAATLSGPGGEGQSAVARLTGL IGVPESDVEKETKLETTLQDIIQ ENFPILARQANVQIQEIQRTTPQR YSSRRATPRHIIVRFTKVEMKE KMLRAAREKGRVTLKGKPIRL TADLSAETLQARREWGPIFNIL KEKNFQPRISYPAKLSFISEGEIK SFTDKQMLRDFVTRPALKELL KEALNMERNNRYQPLQNHAK |
| 21374 | 51742 | B | 21502 | 1 | 2356 | |
| 21375 | 51743 | A | 21503 | 2 | 484 | |
| 21376 | 51744 | A | 21504 | 2 | 902 | ASFFSKKTSFGGGWGAGGPGD PGMGNHGGFRGGFSRGIRGWG HSRGQGPQGGRGAHRGKTKDK EWT SIPKLGH LVKDMKIKFLEEI YLFFLAIKEFEIIDFFLGASLKDE VLKIMPVQKQTHASQRTLRKG FIVIGDYNG/HVGLGVKCSKEV A/TAIRGAILG*LSIVPMCRGY WGSKIGKPHTVPCKVTGHCGS VLVHFIPAPRG TGIVSVPM P/KK LLL MAGIYDCY/ARSCTATLGN FTKATFDAISK TYSYPTPNLWK ETVFTKSP/YEFRNSGQEFTDYL VKT/HIRVSVQRTQAPAVATT |
| 21377 | 51745 | A | 21505 | 2 | 407 | STISCGGNFPIPRGGSGVASLER AESSSTEPAKAIKPIDRKS VHQI CSGPVVP SLSTAVKELVENS LD AGATNIDLK LKDYGVDLIEVSG NGCGVEEENFEGLTLKHHTSKI QEFADL\LS DVTISTCHVSAKVG |
| 21378 | 51746 | A | 21506 | 362 | 490 | |
| 21379 | 51747 | A | 21507 | 3009 | 3889 | |
| 21380 | 51748 | A | 21508 | 1 | 504 | LDDLHKWFLSSFLLT AISIGIKF LLKIHISRGSGVLLQLLPGNPSP AAHGTEELEPKFLEQGYLRAVL PGPRVHATA*LEPTVTDQGYAR AGLPIQEVEDVLFGVLVLLHV IGQVAEDRNQVAAQGH HQES/C PAQCWGDCTHLEIAGWRGIRRS DANPRSQRKGFG |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21381 | 51749 | A | 21509 | 2 | 1101 | WTERRLGSVRGDRLRERSRPA VNRTPRMSRVPSGAPRGTPSRR WWMKCDWHQPLG*IPAPHV GPLAG/IRKKEWSDESEEEPEKE LAPEPEETWVVEMLCGLKMKL KQQRVSPILPEHHKDFNSQLAP GVDPSPPHRSFCWKRKREWW ESESLEEEPRKVLAPPEEIWV AEMLCGLKMKLKRRLVSLVLP EHHEAFNRLLDPVIKRFLAWD KDLRVSDKYLLAMVIAYFSRA GLPSWQYQRIHFFLALYLAND MEEDDEDPKQNIIFYFLYGKTRS RIPLVRNRRFQLCRCLNPRARK NRSQIALFQKLRFQFFCSMSG AWVSREELEENTGPRGDVDFQ QELYSNANGRQQERGEPEFVQI |
| 21382 | 51750 | A | 21510 | 3 | 918 | |
| 21383 | 51751 | A | 21511 | 1 | 792 | |
| 21384 | 51752 | A | 21512 | 3007 | 3885 | |
| 21385 | 51753 | A | 21513 | 615 | 845 | GHTASPPPRSPQAQGRAPSVAP PPTTPQICPTTPSSFSSKRTYAG GWDLPQQQADC*SPCGAQGG WVTLAVASASS |
| 21386 | 51754 | A | 21514 | 357 | 562 | GSSTCGRETERVVLKKRKRSP HFQYRNSPTAEARPQLE\PTQW GRRSHSPRPSAPLPCSCPQKSRK SV |
| 21387 | 51755 | A | 21515 | 1 | 1335 | |
| 21388 | 51756 | A | 21516 | 537 | 1164 | SSTEPAKAIKPIDRKSVHQICSG PVVLSLSTAVKELVENS LDAGA TNIDLKLDYGVDLIEVSDNGC GVEEENFEG LISFTLKHHTCKI QEFADLTEVETFGFQGEALSSL CALSDVTISTCHASVKVGTRLV FDHDGKIIQETPYP\HPRGTTVS VKQLFSTLPVRHKEFQRNIKKR ACFPFAFCRDCQFPEASPAMLP VQPAELMAV |
| 21389 | 51757 | A | 21517 | 224 | 903 | GFTWYIGMAQPKQERVARARH QRSETARHQRSETAKTPTLGNR QTPTLGNRQT PRLGIHARPRRR ATTSLLTLLRAFGKKTQS/STEP AKAIKPIDRKSVHQICSGPVVLS LSTAVKKIVGNSLDAGATNIDL KLKDYGM DLIEVSGNGCGVEE ENFEGLSWDSTGVFDHDGKIIQ KTPYPHPRGTTVS VKQLFSTLP VRHKEFQRNIKKPVGEKYMRS VDTQACSCI |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21390 | 51758 | A | 21518 | 2 | 1321 | VKSRAALLGPGA/LSPLEVSRRR PWTERRLGSRGDRRLRERSRPA VNRTPRMSRVPSGAPRGTPSRR WWMKWCWDHQPLG*IPAPHV GPLAG/IRKREWSDESEEEPEKE LAPEPEETWVEMLCGLKMKL KQQRVSSILPEHHKDFNSQLAP GVNPSPPHRSFCWKRKMEWW DQSEESLEEEPRKVLAPPEEIW VAEMLCGLKMKLKRRRVSLVL PEHHEAFNRLLDPVIKRFLAW DKDLRVSDKYLLAMVIA YFSR AGFPSWQYQRIHFFLALYLAND MEEDDEDSKQNIHFFLYRKNRS RIPLLKRWFQLGHS MNPRARK NRSRIPLLKR RFQLYRSTNPRA RKNRSRIPLLCKRRFQLYRSMN SRARKNRSQIVLFQKRRFHFFCS MSCRAWVSPEELEENTGPRGD VDFQQELYSNANGRHQAGGEE |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21391 | 51759 | A | 21519 | 1 | 2654 | RSACGSPA WNFPSPRGGSGVAS ME\RAESSSTEPAKAIKPIDQKS VHQICSGQVVLSTAVKELVE NSLDAGATNIDLKLKDYGVDLI EVSDNGCGVEEENFEGLTLKH HTSKIHEFADLTQVETFGFRGE ALSSLCALSDVTIFTCHASAKV GTRLMFDHNGKIIQKTPYPRPR GTTVSVQQLFSTLPVRHKEFQR NIKKEYAKMVQVLHAYC\SFQ QASV*VAPISLDK/RKRQPVVCT GGSPSIKENIGSVFGQKQLQSLI PFVQLPPSDSVCEEYGLSCSDA LHNLFYISGFISQCTHGVGRSST DRQFFFINRRPCDPAKVCRNVN EVYHMYNRHQYPFVVLNISVD SECVDINVTDPDKRQILLQEEKLL LAVLKTSLIGMFDSNVNKLNVN QQPLLDVEGNLIKMHAADEK PMVEKQDQSPSLRTGEEKKDV SISRLREAFSLRHTTENKPHSPK TPEPRRSPLGQKRGMLSSSTSG AISDKGVLRPQKEA VSSSHGPS DPTDRAEVEKDSGHGSTSV DSE GFSIPDTGSHCSSEYAASSPGDR GSQEHVDSQEKAPETDDSFSDV DCHSNQEDTGCKFRVLPQPTNL ATPNTKRFKKEILSSSDICQKL VNTQDMSASQVDVAVKINKKV VPLDFSMSSSLAKRIQLHHEAQ QSEGEQNYRKFRAKICPGENQA AEDEL RKEISKTMFAEMEIIIGQF |
| 21392 | 51760 | A | 21520 | 238 | 413 | |
| 21393 | 51761 | A | 21521 | 288 | 467 | |
| 21394 | 51762 | A | 21522 | 1 | 3038 | MDVGWDLGEDCWQEHLHTAF SFDCWPCSQNGDRVPSVNPVG GGAPRSYLQVASAECWAAAPA VHVGEVHAGGLHTEGADPV IGLYLVHRRGGACQPTVGNRQ TPTLGIHARPRRRATTSLTLLL AFGKNAVRTEPAKAIKPIDRKS VHQICSGPVVPSLSTAVKELVE NSLDAGATNIDLKLKDKESGLI KVQANEWGVEETSKGLLLKH HTSKIQEFADLPQVETFGFRGE ALSSLCALSDVTISTCHV |
| 21395 | 51763 | A | 21523 | 34 | 256 | ETGPPGSAPGRLEFTNIKR VVVP QERVELETLLVSYFSRTPRRTP PPFPHPCS*EDNVITVFSSIKNGP GSSR |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21396 | 51764 | A | 21524 | 727 | 2953 | HVSGYDDVPLGTLSDIWPPAL FSVVSFAAFFFTPIEAVLKSFSC LLVWYIGMAQPKQERVARARH QRSETARHQRSETA/KTPTLGN RQTPTLGNRQTPLGIHARPRR RATTSLLTLLRAFGKKTQS/STE PAKAIKPIDRKSVMHQICSGQVVL SLSTAVKKIVENSLDAGATNID LKLKDYGMDLIEVSGNGCGVE EENFKGLTLKHHTSKIQEFADL TRVETFGFRGEALSSLCALSDV TISTCHVSAKVGTRLVFDHDGK IIQKTPYPHPRGTTVSVKQLFST LPVRHKEFQRNIKKAQR/PQAR/ CYRCS*PNVSPGPGMAAASTLS A*PRSQSSYFISCKA/EDNAICPI AEQKAEGKFSSRYRNHDSAEN RRDGSMTRPRTDWTLKRACTE KRRPQHASSFEWRGHSWCWDR EQRDAETLKMLLDSGLSVQKK TKDRTEFRFGEMGQILGKIMMS HQPQPQEEQSPQRSTSGYPLQE VVDDEVSGPSAPGVDPSPRRS LGWKRKRECLDESDDPEKEL APEPEETWVAETLCGLKMKAK RRRVSLVLPEYYEAFNRLLDP VIKRLLAWDKDLRVSDKIPSEP TILGASPKTLPPASRICIRPSNTP PPRNFHMSTVTPMLSYLANDM EEDDEAPKQNIIFYFLYEETRSHI PLLRELWFQLCRYMNPARKN CSQIALFRKYRFHFFCSMRCRA |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21397 | 51765 | A | 21525 | 1054 | 2349 | SCPQIIFLSSCLQVASAECWAAA PAVHVGEVPVHAGGLHTERGAD PVIGLYLVHRGGACQTPVIGSR QTPTLGIHARPRRRATTSLTLL LAFGKNAVRCALIGPGSLTSRT RPLTEPLGEKERREVFPPRPER VEHNVESSRWEPRRRGACGSR GGNFPSPRGGSGVASLERAES SSTEPAKAIKPIDRKSVHQICSG PVVPSLRPNAVKELVENS LDAG A\TNVDLKLKDYGVDLIEVSG\ NGCGVEEENFEGL/TLSALKH HTSKIREFADLTRVETFGFRGE/ AL*ASLCALSDVTISTCHVSA\ VGTLTGVFDHDGKIIPENPPNPH PRGTTVSVKQLFSTLPV\RHKEF QRNIKKKRA\CFPFAFCRDCQFP EASPAMLVQPAELTPR\STP\PH PCSLEDNVITVFSS\VKNGPGSS KMICTNGSSPSS |
| 21398 | 51766 | A | 21526 | 2 | 393 | |
| 21399 | 51767 | A | 21527 | 2 | 165 | |
| 21400 | 51768 | A | 21528 | 3 | 196 | |
| 21401 | 51769 | A | 21529 | 1 | 411 | |
| 21402 | 51770 | A | 21530 | 1 | 1727 | GPQGVGRMAEGKAGGAAGLF AKQVQKKFSRAQEKVLQKLGK AVETKDERFEQSASNFYQQQA EGHKLYKDLKNFLSAVKVMHE SSKRVSSETLQFIYY\SEWYGHEE LKAIVWNNDLLWEDYEELIA DQAVRTMEIYVAQFSEIKE\RIA KRGRKLVLDYDSARHHLEAVQN AKKKDEAKTAKAEFEFNKAQT VFEDLNQELLELPILYNSRIGC YVTIFQNISNLRDVFYREMSKL NHNLYEVMSKLEKQHSNKVFV VKGLSSSSRRSLVISPGVRTATV SSPLTSPTSPSTLSLKSESESVSA TEDLAPDAAQGEDNSEIKELLE EEEIEKEGSEAGSSEEDDPLPAC NGPAQAQSPPTTERAK\SQEEV LPSSTTPSPGGALSPSGQLSSSA TEVVLRTRTASEGSE\RPKKTAS IQRTSAPRRPPPPRATASPRPCS GNIPSSPTASGGGSA\TSPRASL GTGTASPTSLEI*PNPE\PEKP VRTPEAKENENIHNQNPEELCT SPTLMTSQVASEPGEAKKMED KEKDNKLISADSSEGQDQLQVS MVPENNNLTAPEPQEEVSTSEN |
| 21403 | 51771 | A | 21531 | 1 | 1530 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21404 | 51772 | A | 21532 | 499 | 1587 | HPRDPEAPSGPLWSASLPALYS QGHANEFDGSNSTSHAVLVLV QKHIKAVLSNKLCLSTSSLVQG VNAHLGTLIWPQPRGYLSRSA IPWFSVPTVTSGLHFPWEVQ*LF LLSCWGKAHQSLPQRMPLLC CQGMWVPEGSMATVGLSQQLF DSALLLLQKAGALNLDITGQLR SDDNLLNTSALGRLIPEVARQF PEPMPVVLKVRLGATPVAHGS TQTTATLRPASPFVGGSWATGP PNSAFPSPSSP/CLVVVNL RTPAS L/SSKGEALREHVC AWWMSQL TVASSNVGFIDTDQVRTLMGTV FEKPLLDHLNGLSLGHGELPSLV WVN LH YVAPEIFVYEGYVVISS GTLLPEPEAKTTGRP |
| 21405 | 51773 | A | 21533 | 1385 | 3111 | IAPSEVKEHKMVLEMLNPIHYN ITSIVPEAMPAATMPVLLLTGLF LLVWNYEGTSSIPGPGYCMGIG PLISHGRFLWMGIG\SACNYYN RYVGEFMRVWISGEETLIISKSS SMFHIMKHNHYSSRFGSKLGLQ CIGMHEKGIIF\NNNP ELWKTR PFLYERLCHAPASVRMVTVCA ESLKTHLDR LAEEVTT\ESGLCG TCLTLLRRVHGWDTSN TVFL\G IPL\AESAI VVKIQG\YFDAWQAL LIKPDIFFKISWLYKKYE\KSVK DLAKDA\EVLIAEKRRRISTEEK LEECMDFATELILA EKRGDLTR ENVNQ CILEMLIAAPDTMSVSL FFMLFLIAKHP\NVEEAIKEI\QT VIGERDIKIDDIQKLKVMENFIY ESMRYQP VVDLVMAQSL*EG* C*SMGYPV\KKGTNIYSWNIG\R VHRL*FFPKPNEFTLENFAKNV PYRYFQPF GFGPRGCAGKY/LS AMVMMKAIL\VTLLRTDST*RT LPGTSVFESIQEGYTTCPWHPD\ ETKNMLAEMDLYPKETSDRCLG TLRRKAGQYLT LGAFSPSVCSP TNHPILCPLVFILHSGT LSGPMA |
| 21406 | 51774 | A | 21534 | 129 | 378 | IVCKFSVSTHKNIRAKKPDRLP ECGTQIRKDTLKRVRRTVLHYL C\PPPSVPEIPAWR\GDCSP/VGK EGKCTPDLNPNIELRPV |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21407 | 51775 | A | 21535 | 1 | 474 | MQKQIISVTEVEWYPKYNSNM KEYWSTQNHQFEQLSTHKNIR AKKPDERLPECGTQIRKDTLKR PCPLDRPLWPHITAEQGSKPST WPAPCDP/IF*ANIHLPSLHTGPC RSKVQAHSSRPGCQASSTCVPR LQDLPC*PRFRLTLVDQDARPA APVYQGSRTYPADPDSRPAPVD SGCIISGQADW |
| 21408 | 51776 | A | 21536 | 2 | 325 | |
| 21409 | 51777 | A | 21537 | 2 | 1011 | WAFSITERREFQVYYNSCPSSS WIGDARAFSPDPDTGLYPIYSQ DTQTFRLWLNYNITDFPGSPAC KWQAMELLSPQSPFRVDRGEH LPFLVKGARYTLVPAGQEGAL AAWLEALRGQLGRRGAVVSM MDAEGLERSSPDCAMGLSDGE WQLVLNVWGKVEADIPGHG\Q EVLIRLFKGHPETL\EKFDK/FTR HLKSED\EMKASED\LKKHMCH TVLTPLVGHILREKGGH*RQR FKPLGTSSHCHPSTKIPPLKVTL EFHLPGIAFIQVLAEQAI PGDFG\ AECPGAQLKQRPWELFRKNNG LPTYKEAGAFQGARALAGFPTP THLGPPGFKKRAGV |
| 21410 | 51778 | A | 21538 | 157 | 322 | |
| 21411 | 51779 | B | 21539 | 1 | 975 | |
| 21412 | 51780 | A | 21540 | 218 | 388 | RKLPLAGLPCINRQHS*SNVNIC FLTPV*KIQN*LQSEQFLPYPTIV IITLCFFAV |
| 21413 | 51781 | A | 21541 | 663 | 933 | GCAGPCLVNQMFGKQYYLGKS HHP\SLVSLNRGAHCTVGKPQG PSGP*KLGYYFKVFPPCG*FWK YGPSWGMEERA WTGSPLGPGP PLKKV |
| 21414 | 51782 | A | 21542 | 389 | 1033 | NQGLRNLGLCRTCLVNKMFTS SILGKSHRHSLVSINQGNALW KAAG\PLPLKAGYC\QGFSPCHS LKYG\SWDEKDLTVPPDTLKG SVLRWISKRGKPLAVEIEEGHC L\CLPLGTECLGIK/PIVHLFNSE IGE\NRPYGG*DMFCSNGCLG* FL*LPLRCLG\GEKHKSGL/HVHI PVIVPPLELNYDIDSFAHMFV DLS\LIITLLSCYIPFC |
| 21415 | 51783 | A | 21543 | 82 | 163 | |
| 21416 | 51784 | B | 21544 | 1 | 211 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21417 | 51785 | A | 21545 | 71 | 1086 | NMNLSLVLA AFCLGIASAVPKF DQNLDTK WYQWKATHRRLYG ANE EGWRR AVWEKNMKMIEL HNG/EKYSQ GKH\GFTMAMNA FGDMTNEEF RQMMGC FRNQKF RKGKV FREPLFLDLPKSV DWR KKG YVTPVKNQKQCGSCWAFS ATGALEGQMFRKTGKLVSLSE QNLVDCSRPQGNQGCNGGFMA RAFQYVKENGGLDSEESYPYV AVDEICKYRPENSVANDTGFTV VAPGKEKALMKAVATVGPISV AMDAGHSSFQFYKSGI\YF*PDC ISKNL DQGV LVVGYVFEGANS NNSKYWL VKNSWGP\EWGS\N GYVKIAKD\KNNHCGIATAASY |
| 21418 | 51786 | A | 21546 | 170 | 412 | LWLSFLLMHW H*IPLA AVSVFT VSN/PILDFS* IQLKTPKHFGNLG NTGFLGKQLRLLLRSLVSVSRL HCLLG YRRTQMPPL |
| 21419 | 51787 | A | 21547 | 1 | 753 | |
| 21420 | 51788 | A | 21548 | 125 | 464 | TAVFLTQSLFGGLFTRTRMKFG TMTRI/RGDL PWEINPLSSCSLL HEKDPPTTSGPQT NQPKHLTN FKSRKVERTKGLLKTHLTKLSH QLKKA WTILLPLSLLRIQACPR NAT |
| 21421 | 51789 | A | 21549 | 1 | 753 | |
| 21422 | 51790 | A | 21550 | 291 | 671 | |
| 21423 | 51791 | A | 21551 | 10 | 453 | TALLLTQSLFGGLFTRTRMKFG AMTRIG\DL PWEINPLSSCSLLC EKHPPTTSGPQTDQPKHLTNF KSETKETCFIHEPKTLAPVTDW EGSLPLVFNHCRDGLSDHSATF QGCQTMQGC LPWSFTLSGKSR FPGAGASTPQPLLLHP |
| 21424 | 51792 | A | 21552 | 740 | 1010 | TAMLLKQSLFGCLFTRTRMKF GAVTRIG\DL P*ETNPLSSCSLLR DKDPPTTSSPQTHQPKHLTNF KSGCSPGRARSQSFLSLCSSTL |
| 21425 | 51793 | A | 21553 | 134 | 358 | TAMLLTQSLFGGLFTRTRMKFG AVIRIG\DLLWEINPLSSCSLLHE KDPPTTSGPQTDQPKHLTNFK SSCSSPG |
| 21426 | 51794 | A | 21554 | 392 | 645 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|---|
| 21427 | 51795 | A | 21555 | 1 | 1900 | MQNALESLSNRIEQVEERNSEL EDKFFELTQSNKDKEKRIRKYK QSLKEVWDYVKGPNLRIISVPE EEENSKSLENIFGEIIEENLPSLA RHLDNQIQEAQRTLWKLIAKRS LPRHIVIRLSKVKTKERILRAVR QKHQVTHLTCKESYKLVKVG WKRHFQMMDTKNEQGIKNEN HLIISIDVEKASDKIQQRFMIKTL SKIGIQGKYLVNIKAIYDKPTAN ITLNREK/LESIPSEKLKAFPLRT GTRQGCPLSPLFFNTVLEVLAR AIRQEKEIKGIQIGKEEVKLSLF ADDMIMYLENPKDSSRKLLLEWI KESNKVSGYKTHVHKSVALLY TKQ*\QAENQIKNRNPFAIAAKK KKKKKKKKKRNSRIYLTKESK DLYKENYKTLTKEIIDNMNKW KHIPCSWMGRISIVKKL*LQKA IYKLNAILIKIPLLFTELEKTILK FIWKS\NKS\RIAKVILSKKNKSG GITLPDFKLYYTIRKINSKWIKD LNLRPETIQILEDNIGKTLLEIGL GKDFMTKNPKANAKKTKINR WDLIKLKSFACTAGTVSRVKRT HRVGENLPHYTSIHPTIYTIYTS DKGLISRIYNEFKQIVTRTTCVF LHPHPKAKTTSYGDQLLGGN |
| 21428 | 51796 | C | 21556 | 10 | 339 | |
| 21429 | 51797 | B | 21557 | 97 | 1458 | |
| 21430 | 51798 | A | 21558 | 1 | 387 | |
| 21431 | 51799 | A | 21559 | 3 | 604 | GSVIAYYWSEFSIPQHLVEEAE RVMAEERVFMPPRARSLKSFV VTSVVAFRESEGQGWAWDWPP FHGVGLGPGPLQGTGTPRAQCP REKTTCPGTSL*IIRKQE*GNG LYQEMLYSPSYSSATDSKTVQR TQDNCSFGLHARGVELMRFTT PGFPDSPYPAHARCQWALRGD ADSVLSLTFRSFDLASCDEARS DLV |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21432 | 51800 | A | 21560 | 1000 | 2084 | FRGTPVQRGGGWADLPGRGCE LGRRLRSEEQARRVHKAPS/DF GTG/LKENTGKVNGLLEEGVEFL PVNNVKKVEKHGPGRWVLA AVLIGLLLVLGIGFLVWHLQY RDVRVQKVFNQYMRITNENFV DAYENSNSTEFVSLASKVKDAL LYSGVPFLGPYHKESAVTAFM WWREGSVGCTPDWLGVGSG YSVWGTREMVLVLDWRAK EGPRCVLLEGSVIAYYWSEFSIP QHLVEEAERVMAEERVVMLPP RARSLKSFVVTSVVAFPTDSKT VQRTQDNSCSFGLHARGVELM RFTTPGFPDSPYPAHARCQWAL RGDADSVLSLTFRSFDLASCDE RGSDLVTVYNTLSPMEPHALV |
| 21433 | 51801 | A | 21561 | 3 | 2820 | TGALILQKGEIRVINQTTCE PQQITPRMMCVGFLSGGVDSC QVPPGQEGGRQFPLKETNNRK GRLPKRLRPHTWCCYSLECSSY SLRCTEDTWTEQKVNGLLEEG VEFLPVNNVKKVEKHGPGRWV VLA AVLIGLLLVLGIGFLVWH LQYRDVRVQKVFNQYMRITNE NFVDAYENSNSTEFVSLASKVK DALKLLYSGVPFLGPYHKESAV TAFSEGSVIAYYWSEFSIPQHLV EEAERVMAEERVVMLP |
| 21434 | 51802 | A | 21562 | 111 | 465 | |
| 21435 | 51803 | A | 21563 | 2 | 197 | |
| 21436 | 51804 | A | 21564 | 359 | 405 | EMQSRED*RK*YL*RIVNCVPL RERLGYVCGGLGERSKEGTLWI YQGLQKSQDTGRV |
| 21437 | 51805 | A | 21565 | 208 | 287 | IVSRSEKGVWVMYVEGWEREAR REHYGYIKGYKNHRIHMMQSS KALV*LEDLRKHI*IFRCVFSNP QVILML |
| 21438 | 51806 | C | 21566 | 141 | 305 | |
| 21439 | 51807 | A | 21567 | 170 | 973 | RMAACRALKAVLVDLSTGLHI EDAAVPGAQEAALKRLRGASVII RFVTNTTKESKQDLF\KRLRKL GFDISEDEIFTSL\TAARSL*R KQVTPMLLVD*SGHYLIFKGIQ TSDPNAVVMGIGTRTFSLSKF WNQAFRLLLGWSTSDSNSQSQ GFQEFKMGLALGPWTIL*LL*K YATDTKATVVGKPEKTFFLGS AGHWLLNLEAVMIG\DDCRG\ DVGGAQDVGMGLGILVKTKYR ASDEEKINPPPYLTCESPHADV |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21440 | 51808 | A | 21568 | 42 | 211 | |
| 21441 | 51809 | A | 21569 | 92 | 366 | AGSEMRPGLTWACSLARLLLSP SFIKHWFLSCLLSCSRSGGYA QWCPPHQSASAAGHCQTPAHA QAYLSSPPQMDHSSVRSLEAC QTY*SASAAGHCQTPAHAQAY LSSPPQMDHSSVRSLEACQTY |
| 21442 | 51810 | A | 21570 | 1 | 834 | |
| 21443 | 51811 | A | 21571 | 3 | 835 | |
| 21444 | 51812 | A | 21572 | 1 | 1649 | MPIVLVDWSDIREQKRLMVLR ASVALHGRSVTLYEKAFPLSEQ CSKKAHDQFLADLASILPSNTT PLIVSDAGFKVPWYKSVEKLG WYWLSRVRGKVQYADLGAEN WKPISNLHDMSSSHSKTLGYKR LTKSNPISCQILLYKSRSKGRKN QRSTRTHCHHPSPKIYSASAKEP WVLATNLPVEIRTPKQLVNIYS KRMQIEETFRDLKSPAYGLGLR HSRTSSSERFDIMLLIALMLQLT CWLAGVHAQKQGWDKHFQAN TVRNRNGSLLTNWPSVPPTIKE EENSEEELAAATTSKEQEPIGTD LDAVRTPEPLEEFPKREDQEGS PPETSLPYKWVVEAANLLIPAV GSSLSEALDIESDPDAWCDLS KFDLPEEPSAEDSINNSLVQLQA SHQQQVLPQRQPSA\LVPSVTEY RLDGHTISDLSSSRG\ELIPISPS TEVGGSGIGTPPSVLKRQRKRR VALSPVTENSTLSFLDSCNSLT PKSTPVKTLRFS\PSQFLNFWN KQDTLELESPLTSTPVC SQKV VVTTP LHRDKT PLHQKHAA |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21445 | 51813 | A | 21573 | 59 | 2384 | PRPGSRSGLCRRAGERGAVRAG GMSRRTRCEDLDELHYQDTDS DVPEQRDSKCKVKWTHEEDEQ LRALVRQFGQQDWKFLASHFP NRTDQQCQYRWLRVLNPDLVK GPWTKEEDQKVIELVKKYGTK QWTLIAKHLKGRLGKQCRERW HNHLNPEVNKSCWTEEDRIIC EAHKVLGNRWAEIAKMLPGRT DNAGKNHWNFTIQK/RKGDGTG GFLREYKD*KPPVYLPL\ELEDK DGLQSAQPTGQRSLLTNWPSV PPTIKEEEN\SEEELAAATTSKE QEPIGTDLD\AVR\TP\EPLEEFPK REDQEGSPPETD/SLPYKWVVE AVNLLIPAVVS\SLYEALDLIGS\ DPDAWCDLSRFDLPEEPSIEDSI NNSLVQLQAS\HQQQILPPRQP SA\LVPSVTEYRLDGHTISDLSR SSRGELIPISPSTEVGG\SGIGTPP SVLKRQRKRRVALSPVTENSTS LSFLDSCNSLTPKSTPVKTL PFS PSQFLNFWNK\QDTLELESPLA DYPPQVCSQKVVTTP LHR\DK TPLHQKHA\AFVTPDQKYSMD NTPHT\TPFKNALEKYGPLKPL PQTPHL\EEDLKEVLRSEAGIELI IEDDIRPEKQKRKPGLRRSPIKK VRKSLALDIVDEDVKLMMSTL PKSLSCRTTAPSN\SSTLTLSGIK EDNSL\LNQGLLAGPSPRKAAC VPEGPESHFHGQLAPYVPVPGK |
| 21446 | 51814 | A | 21574 | 190 | 889 | SLPRRLESPGRLAMAARGVIAP VGES/LCRYAEVPCSPSAKR PDA DVDQQRLVRSLIAVGQGVAAAL AFAG\RYAL\RIWKPLE\QVITET AKGRFQTPRFSSY**GG/FLNII* LRREA\GLILGVSPSAGKAKIRT \AHR\RV MILESPQIKGGSPYVA AKINEAKD\LLETTTKRLMLKD HTEGKKNEGTSKKKKSPAKYS KTWSFLIFYMGFDHSLIFRPLSC ITNKMLIVLLFIIF |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21447 | 51815 | A | 21575 | 2 | 652 | EGYIC/RHFTGSSALLTRTHITY GVIANVAVVRINSPNS\RMLAA CKTLQEVTLQSQEAQRIVEKLE KSTKPIVAAINGSCLEGGLEVAI SCQYRIATKDRKTVLGTPEVLL GALPGAGGTQRLPKMVGVPAAL DMMLTGRSIRADRAKKMGLV DQLVEPLPGPLKPPEERTIEYLE EVAITFAKGLADKKISPKRDKG LVEKLTAYAMTIPFVRQQVY |
| 21448 | 51816 | C | 21576 | 98 | 316 | |
| 21449 | 51817 | A | 21577 | 35 | 247 | |
| 21450 | 51818 | A | 21578 | 1 | 2391 | LQLKMVACRAIGILSRFSAFRIL RSRGYICRNFTGSSALLTRTHIN YGVKGDVAADRINSPNSK\VNT LSKELHSEFSEVMNEIWASDQI RSAVLISKPG\CFIAG\ADITML AACK\TLQ\EVTQLSQEAQR\IV EKP*KSPQSLIVGCPSNGSCLGR RTLRLPISSPQYRIATK\DSKTVI *VPPEVFLGGPLPGRQGGHTK GCPKMGGVCLPAFGHECLTGR SIR\ADRAK\KMGLVD\QLVGTP GTQGLKPPEERTIEYLEEVA\ITF AKGLADKKISPKRDKG\LVEKL TA\YAMTIPFVRQQVYKKVEEK VRKQTKGLYPAPLKIIDVVKTG IEQGS DAGYLCESQKFGELVMT KESKALMGLYHGQVLCCKKNKF GAPQKDVKHLAILGAGLMGAG IAQVSVDKGLKTILKDATLTAL DRGQQQVFKGLNDKVKKKAL TSF\ERDSIFSNTLGQLDYQGF* KRPDMGELKAVFEDP*SLSHR VLKGVGSR*FPDHWYSLPSNT SALPISEIAAVQQKT*EG*LGMH YF\SPVDKMQLL\EITTEKTSKD TSASAVA\VLKQKG\VIIV\VK DG\PGLLVTYQGVFAPMMS\EVI RILQEGS\VDPKKLGFPTTSFG FPVGAATL\DEVGCGMLAK HVAEDLGKVFG\ERFGGNGPE L\LTQMVS KGFLG\RKSGEGLLT SSGRVVKRKILNSTMD\SI*ASL |
| 21451 | 51819 | A | 21579 | 119 | 387 | VEDSKEIFSSA*DYLSTHSHKHP ASHESYHVNPNCNPVAPTSGA HSIV*KWPSWLGTVAHSCNPSN FGRPRRADCLSSRSSRPAWPTR |
| 21452 | 51820 | B | 21580 | 73 | 3177 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21453 | 51821 | A | 21581 | 1399 | 5140 | SGEPERALRGAAMRPSGTAGA ALLALLAALCPASRALEKKVC QGTSNKLTQLGTFEADHFPQPS QRMF\NNCEVV\LGNLEITLCER NYDLSFLKTI\QEVAGYVLIALN TVERIPLLENLQIIRGNMYEYNSY ALAV\LFNYDANKTGLKELPMR NLQEILHGAVRFSNNPALCNVE SIQWRDIVSSDFLSNMSMDFQN HLGSCQKCDPSCPNGS\CWGAG EENCQKLTKIICAQQCSGRRCRG KSPSDCCHNQ |
| 21454 | 51822 | B | 21582 | 82 | 305 | |
| 21455 | 51823 | A | 21583 | 122 | 219 | YAKRIYDVYYVHTAYTCTFHA *KIRGMTQ*NW |
| 21456 | 51824 | A | 21584 | 404 | 1228 | GLAAFLARARGRRRKELPGSPR PLPQLPAGGPSRWRAMRPSQR RPPTLPMAASPAHWPRESLVLY HWTQSFSSQKVRLVIAEKGLVC EERDVSLPQSEHN/EMPWFMR NLGEEVPV\IIHRDNIIQ/CTMDQ IHLTMWERTFHRERHVGALMP EVGSRAA\PRVLQYRELLDALP MDAYTHGCILHPELTTDSMIPK YATAEIRRHLANATTDLMKLD HEEEPQLSEPYLSKQKKLMAKI L\EHDDVSYLKKILGELAMVLD QIEGGAGRKRKLENE |
| 21457 | 51825 | A | 21585 | 3 | 1194 | KNLSVKLSENGTLKNCVVADS ETDIDVYMYTRVYVYIPRIENS WNDTIKLVGTATISAVGGDIDA QGEWAFPLLGIPSLSPGPEWKV RVVIPDKGLVCEERDVSLPQSE PKEPWFMRINLGEEVPV\IIHRD NIISDYDQIIDYVERTFTGEHV ALMPEVGSQHARVLQYRELL DALPMDAYTHGCILHPELTTDS MIPKYATAEIR/SDI*PNATTDL MKLDHEEEPQLSEPYLSKQKKL MAKILEHDDVSYLKKILGELA MVLDQIEAELEKRKLENEGQK CELWLCGCAFTLADV\SLGATL HRLKFLGLSKKYWEDGSRP\NL QSFFERVQRRFAFRKVLGDIHT TLLSAVIPNAFRLV\KRKPPSFFR ASFLMGSLG\GMGYFALHGTSR |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21458 | 51826 | A | 21586 | 1 | 929 | MDPSIYFLPSKREGHLQAYIRDS VPEDPLILIFFSASSDQRPWLKA PHLPALRGFRGGGAGGGAQSR TTEDYVAWAKGNSPTSPSPRSR GGCSAKLSGPRRPPRRPGRLFN MAASANSVSRAWRTESPEGLE SLHSTLSAISVSRPEGGAELSD TADTMGFGDLKSPAGLQV\PTI TWRTRATSRGMCHHKQMWQY LKPCPAHRLPTCVMPIV/GYNH IKSYEKEKASLPGVKKALGKYG PADVEDTTGSGATDSKDDDDID LFGSDDEEESEEA KRLRE/DTSC TI*IKESQKTCTCCQVFHLTRCE |
| 21459 | 51827 | A | 21587 | 1 | 2405 | MALRVVRSVRAVLCSLHVACE KVGMPQIPRCYHERLSVAGNC RMCLVEIEKAPKDQSMFMFGND RSRFLEGKRAVEDKNIGPLVKT IMTRCIQCTRCIRFASEIAGVDD LGTTRGRNDMQVGTIEKMF SELSGNIIDICPVGALTSKPYAFT ARPWETRKTESIDVMDAVGSNI VVSTRTGEVMRILPRMHEDINE EWISDKTRFAYDGLKRQLTEP MVRNEKGLLTYTSWEDALSRV AGMPPALALQSAEIAASARPPP RLGSEEPCLAAHRLGCEEPLC LAASLESEERLCPAAIPGNLRY VFISAKTDKYSKLAPVEWVTV EKVPENVEVTLELGNRQSRDR VSRI PGNAIWIWFTGFKWKKTV TTLWFLNLAIADFI LLFLPLYIS YVAMNFHWPFGIWLCKANSFT AQLNMFASVFFLT/GDQPGPLY PLDPSCLISSASNPQELSDCHYI HLAFGFSNWRSCPVLPGHCGV Q*SYSL*QFSEA*S*PHFDQAP CSDLGEIYHWLSLPFANNEYLL LVSHLQGEAAKHPDLQ*AFLDN SGCGCGLCGLLDLSLPV*HLGA HHSPQ*LFPPCDAGWNPPLHWF GIPQ*LLEPHPLCPN**EVPSSLP VLSC*DTQVHTVGSQFLWQVL KEAKKPMVVLGSSALQRNDGA AIIAAVSSIAQKIRMTSGVTGD WKVMNILHRIASQVAALDLGY |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21460 | 51828 | A | 21588 | 1 | 2065 | MLRIPVRKALVGLSKSPKGCVR TTATAASNLI\RVFVDGQSLM\V EPGTTVLQACE\RIGMQIPRFCY HERLSVAGNCRMCLVEIEKAPK DQSMFMFGNDRSRFLEGKRAVE DKNIGPLVKTIMTRCIQCTRCIR FASEIAGVDDLGTTRGRNDMQ VGTYIEKMFMSSELSGNIIDICPV GALTSKPYAFTARPWETRKTES IDVMDAVGSNIVVSTRTGEVM RILPRMHEDINEEWISDKTRFA YDGLKRQRLTEPMVRNEKGLL TYTSWEDALSRVAGMLQSFQG KDVAIAAGGLVDAEALVALKD LLNRVDSDTLCTEEVFP\TAGA GTDLRSNYLLNTTIAGV\EEAD VVLLVGTNPRF\EAPLF*C*EFR KSWLHND\LKVALIRAVPVDL\ TYTYDHLG\DSPKILQ\DIASGK/ SHPFSQVLKEAKKPMVV\LGSS ALQRNDGAAILAAVSSIAQKI\R MTSGVTGDWKVMNILHRIASQ VAVLADLGYKPGVEAIRKNPPK VLFLLGADGGCITRQDLPKDCF IIY\QGHGHDVGAPIADVILPGA AYTEKSATYVNTEGRAQQTKV AVTPPGLAREDWKIIRALSEIAG MTLPYDTLDQVRNRLEEVSPL VRYDDIEGANYFQQANELSKL VNQQLLADPLVPPQLTIKDFYM TGEVTEINEALAENPGLVNKSR YEDGWLIKMTLSNPS |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21461 | 51829 | A | 21589 | 56 | 2352 | ATRPPRGSSWCRQFSRTASAAP GRSNMLRIPVRRALVGLSKSPK GCVRTTATAASNLIIEVFVDGQS VMVEPGTTVLQACEKVGMQIP RFCYHERLSVAGNCRMCLVEIE KAPKVVAACAMPVMMKGWNIL TNSEKSKKAREGVMEFLLANH PLDCPICDQGGCEDLQDQSM FGNDRSRFLEGKRAVEDKNIGP LVKTIMTRCIQCTRCIRFASEIA GVDDLGTGRGNDMQVGTYIE KMFMSSELSGNIIDICPVGALTS KPYAFTARPWETRKTESIDVMD AVGSNIVVSTRTGEVMRILPRM HEDINEEWISDKTRFAYDGLKR QRLTEPMVRNEKGLLTYTSWE DALSRVAGMLQSFQGKDVAI AGGLVDAEALVALKDLLNRVD SDTLCTEEVFPTAGAGTDLRSN YLLNTTIAGVEEADVLLVGTN PRFEAPLFNAWIRKSWLHNDLK VALIGSPVDLTYTYDHLGDSPK ILQDIASGSHPFQVLKEAKKP MVVLGSSALQRNDGAAILAAV SSIAQKIRMTSGVTGDWKVMNI LHRIASQVAALDLGYKPGVEAI RKNPPKVLFLLGADGGCITRQ DLPKDCFIYQGHGHDVGAPIA DVILPGAAYTNK SATYVNTEG *ASASIMLA VTT PGLSREDW KI IRALSEIAGMT/LFPYDTL/DIQV RNQIGKKSSPNLVIRYDDIEGVA |
| 21462 | 51830 | A | 21590 | 246 | 761 | MRLQGAIFVLLPHLGPIVWLF TRDHMSGWCEGPRMLSWCPF LQSLICLLQTAINYSVVG*VLVS HTWPWYPMGWEQVLYI*ITYA VQLTISWTVLVFFTVHNPGLV RHTVLSSRSNVGEGETTWLQK HILAAALLLPYLAWLTVTSALT YHLWRDSLCPVHQPPTEKSD |
| 21463 | 51831 | A | 21591 | 1 | 1497 | |
| 21464 | 51832 | A | 21592 | 1 | 1731 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21465 | 51833 | A | 21593 | 1 | 6626 | PRSLCFSLWAEAAVLADGGLR RRRRLLRGTMSASFVPNGASLE DCHCNLFCLADLTGIKW*KYV WGGPTSAPILFPVTEHPILSSSS RCLTAHVLGVRRRDQRPERR\A L*IFWWGEDP\VLLTLFTMTYQ KKKMECGRMDPFMNAVLCFS KAVHNLLERCLMNRNFVRIGK WFKPYEKDEKPINKSEHLSCS FTFFLHGDSNVCTSVEINQHQP VYLLSEEHITLAQQSNSPFQVIL CPFGLNGTLTGQAFK |
| 21466 | 51834 | A | 21594 | 1263 | 1906 | AVRGMVRNARAVLKTGGTFLS PALEPLVAGGSGG/EFSQLGAEE RKAIAARF/AIDHVDRRVPVLIGT GG/TNARETIELSQAHAQQAGRT ASTIDSVAHLRSMIHTVK/GAHP HFTVLCGYDDHLF/NTLLLGDD GAISASGNFAPQVSVNLLKAW RDGDVAKAAGYHQTASIPDQLI HPYESRLFKCQHVLTRGITSF*L LCPPGSLRRQGISTYHSLLN |
| 21467 | 51835 | B | 21595 | 113 | 484 | |
| 21468 | 51836 | A | 21596 | 300 | 780 | KSGTNETIRRKARGGKIK\MDD LRG\PRCQ*EPWKRLMTIMPS CLHLWAQNTTVSILSFVDKDLL EPGCSVLLNHKVHAVIGVLM DTDPLVTVMKVEKAPQETYAD IGGLDNQIQEIKESVELPLTHPE YYEEMGIKPPKGVHPFGPTWPR VKPFCPRQ |
| 21469 | 51837 | A | 21597 | 2 | 840 | AIEHCQSGDNPESTRRGFLLQQW LGRNPALVPHPGRTGHSQPPVT FHRHPSDCQRSPAGRFKGGPSH RGQPPPFHKSPMTTASHLARC ARTYHQ\DSEAAINR\QINLELY ASYVYLSMSYYFDRD\DVALK NFAKYFLHQSHEER\EHC*ENL MKACRTNEGWPNLFSQDIKET KTCDDWESGLNA\MEVCALHFE KKC*IKSLLEL\HKL\ATDKN*PP ICVDFI*DTFTLNEQ/V*KAIKRI WGDH/V*PKLWRKMGSAPNLG FGEYLF*QSTPWGDSDNES |
| 21470 | 51838 | A | 21598 | 3 | 390 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21471 | 51839 | A | 21599 | 1 | 483 | FQLEVTPQNITLNPFGGGPVFS WRDQAVLRQDGVVVTINKKR NLVVSVDGDTFEVVLHRVWK GSSVHQDFLGFYVLDSHRMSA RTHGLLGQFFHPIGFEVSDIHPG SDPTKPDATMVGLQKDYSKDP WHGAEVSCWFIHNNAGLIDG AYTDYIVPDIF |
| 21472 | 51840 | A | 21600 | 1 | 1521 | |
| 21473 | 51841 | A | 21601 | 1 | 837 | |
| 21474 | 51842 | A | 21602 | 3 | 310 | EVRLNLSSQALRMWLDYGFVT PLTSMISIRGMADQDGLKPTIDK PSEDSPPLEMLGPRRTFVLSALQ PSPTHSSSNTQRLPDRVTGVD* VVT*PYVLCWNLC |
| 21475 | 51843 | A | 21603 | 62 | 462 | MPLPLPSAFVLSALQSPTHSSS NTQRLPDRVTGGFSVNGQLIGN KARSPGQ\HDGTYFGRLGIANP ATDFQLEVTPQNITLNPFGGGP VFS\WRDQAVLRQDGVVVTIN KKRNLVVSVDGDTFEVVLHR VWK |
| 21476 | 51844 | A | 21604 | 37 | 2883 | SMDGAMGPRGLLLCMYLVSL ILQAMPALGSATGRSKSSEKQ AVDTAVDGVFIRSLKVNCKVTS RFAHYVVTSSQVNTANEAREV AFDLEIPKTAFIGSFAVTADGNA FIGDIKDKVTAWKQYRKAAS* EKA\GLVRASGRTEQFTIHLT VNPQSKVTFQLTYEMLKRNH MQYEIVIKVKPKQLVHHFEIDV DIFEPQGISKLDAQASFLPKELA AQTIKKSFSGKKTSGSHSRF QGHVLFRTVSQQQ |
| 21477 | 51845 | A | 21605 | 1 | 1008 | |
| 21478 | 51846 | A | 21606 | 1 | 435 | |
| 21479 | 51847 | A | 21607 | 1 | 676 | IRHQGAAAEQEDAETPGSVERR GRRAGAEDGMSQAPGAQSPSP TVYHERQRLELCAVHALNNVL QPAA\FSQEADEICKRLAPDSR LNPHRSLLGTGNYDVNVIMAA LQGLGLAAVWDRRRPLVPS WPCPKGLG*ILNLPSPVSLGLL SLPLRRRHLRWPCARL\VTVS YNLDSK\LRAPGPGGLRTE/LR GLSLAAALAQGLCEVLLVVT EVEEKGSWLRTD |
| 21480 | 51848 | A | 21608 | 89 | 316 | ELLSPLL VAPGPSDLT VTGLKSF SSPSLCSLNTLLAGTSRLMVA*L YESLGQGEDLGLLTPGPEFLSIS SYCNFM |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21481 | 51849 | B | 21609 | 1 | 1920 | |
| 21482 | 51850 | A | 21610 | 1 | 1727 | LPRVLGHSGHRGGLSSRRSQGL VSRFRLRALCGAGSDMWRLPG LLGRALP\RTLGP\SLWRVTPKS SSPDGPQTTSSTLLVPVPNLDR SGPHGPGTSGGPRSHGWKDAF QWMSSRVSPNTLW\DAISWGTL AVLALQLGR\HIHFQAFLAAGP\ KRVE\HCS\WHSPL\DRFFSSP\ WHPCSSLRQHILPSPDGPAPRHT GLK/ENPRLGKE\EASAQPRNFS HNSLRGARP\QDPSEEG\PGDFG FLHASSIESEAKPAQPQTGEK EQDKSKTSLSEEA\VTSIQQLFQL SVSIAFNFLGNQMDPAPRQEGT ENMKSGDHTAAFSYFQKAAAR GYSKAQYNAGLCHEHGRGTPR DISK/SV*KAGLYYQLAASQGH SLAQYRYARCLLRDPASSWNPE RQRAVSLKQAADSGLREAQA FLGVLF\TKEPY\LDQRAVKYL WLAANNQDSQSR\YHLGICYEK GLGVQRNLGEALRCYQQSAAL GNEAAQERLRALFSMGA\ASPG APTNLTVTGLKSFSSPSLCSLNT LLAGTSR\LP\ASSTGNLGLLC RSGHLGASLEASSRAIPHPYP\ LEKN\VVRLGFG |
| 21483 | 51851 | A | 21611 | 1104 | 1680 | LATPDVRYCYLSTYTSLPNPAR RFFLFSLCKFSSH\KTATVKK YNKSEYPWDLVKAHLQGAFTS NITFDISELQNKILD\NRHTQEF QPSLEDWTEFQEGLESLNPWTY LKYHSN\LYVVLGVMLFCLCLL FIVCKIGWTANRRMRAAQPGL TFFQLIHKQGD\MQGAEGPWDV TNSAFHWRLYDQTANCLS |
| 21484 | 51852 | A | 21612 | 364 | 824 | LCIILFKQLSTWRTGCAQPTKR GYTELQTEGPMLKSMFLWLGE QVQILQL\HSNCIVILTTLV/FCV TNLE*FIVCKIGWTANQKMGA AKPGLTFFLLICK\QKGD*GA KGPWDVINS\AFH*RM |
| 21485 | 51853 | C | 21613 | 196 | 504 | |
| 21486 | 51854 | A | 21614 | 3 | 142 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21487 | 51855 | A | 21615 | 1178 | 2285 | IVWLMTTGGQCRY*LSALIKL* DR/WFQRLCIHVIQRLRPVHAH LYLQPGMEDGNSFRQMFRSTR SLHIPTRDLPLSPDTTVVLHQVY NVLLGLLSRAKLYVDAAVHGT TKLVPHYFSFMTYCLISKTEKLM FSTYFMDLWNLFPKLSEPAIA TNHNKQALLSFWYNVCADCPE NIRLIVQNPVVTKNIAFNILAD HDDQDVVLFNRGMLPAYYGIL RLCCEQSPAFTRLASHQNIQW AFKNLTPHASQYPGAVEELFNL MQLFIAQRPMREEELEDIKQF KKTITISCYLRCLDGRSCWTTLIS AFRILLESDEDRLLVVFNRGLIL MTEGKD\TFMIVCC*TTSFLIIS SIYYAELQSTVKNLLKH |
| 21488 | 51856 | A | 21616 | 1 | 436 | |
| 21489 | 51857 | A | 21617 | 369 | 508 | |
| 21490 | 51858 | A | 21618 | 2150 | 3120 | DLRALALLSVHTPKQLNPALI PTLQELLSKCRCLQQRNSLQE QEAKERKTKALALWTITFRV GGGSNTLGVTGLRVVCSAEPK YKC*KQN*LPTSPNVILMTFRE VLLACVFTDDEGATPIKRRRV SSDEHTVDSCISDMKTETREV LTPTSTSDNETRDSSIIDPGTEQ DLSPENSSVKEYRMEVPSSFSE DMSNIRSQAEEQSNNGRYDD CKEFKDLHCCKDSTLAESESE FPSTSISAVLSLADLRSCDGQA LPSQDPEVALSLSCGHSRGLFS HMQQHDILDTLCRTIESTIHVVT RISGKGNQAAS |
| 21491 | 51859 | A | 21619 | 2 | 4049 | EEENGREYKFDVSSELLEWIWH DNMQFLQDKNIFEHTYFGFMW QLCSCIPSTLPDPKAVSLMTAK LSTSFVLETFIHSKEKPTMLQWI ELLTKQFNNSQAACEWFLDRM ADDDWWPMQILIK\CPNQIVRQ MFQRLCIHVIQRLRPVHAHLYL QPGMEDGSDDMDTSVEDIGGR SCVTRFVRTLLIMEHGVKPHS KHLTEYFAFLYEFAKMGEESQ FLLSLQAISTMVHFYMGTKGPE NPQVEVLSEEEGEEE |
| 21492 | 51860 | A | 21620 | 58 | 219 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21493 | 51861 | A | 21621 | 195 | 1187 | RVPRTWLLPSFCASRSRENEGL SEFGASQTVTPSPASSVQAW MEPEFLYDLLQLPKGVEPPAEE ELSKGVCKKYLPTSRKDPKFE ELQKVQQEWINATLLPEHIVVR SLEEDMFDGLILHHLFRKWAAL KLEAEDIALTATSQKHKLTVVL EAVNRSVCSWRSGRPSGA/WEST WNKDLLSTLHLLVALAKRFQP DLSLF/D/HTNVQVEVITIEVAA NFVNQKLDRLGLSVQNLDQTQV GTGVILLLLIGQLEGFFLHKEF YLTPNSPAEMVSFVTLAELL/I GRGPAQLPC/LALKVSAT/MDA KSTLRVLYGLFCKHTQKAHRD RTPHGAPN |
| 21494 | 51862 | A | 21622 | 96 | 1350 | AAGLLPPGLVPEDPRRTRNLLP FGIQGPPFALSRLPFCVESGWA WEAMEPEFLYDLLQLPKGVEPP AEEELSKGGKKKYLPTSRKDP KFEELQKPAVLMWINATLLP EHIVRSLEEDMFDGLILHHLF QRLAALKLEAEDIALTATNQK HKLHSCWCRP*TGVCWSRSGR PSGA/WESIFNKDLLSTLHLL LAKRFQPDLSLPTNVQVEVITIE STKSGLKSEKLEEQLTEYSTDK DEPPKDVDFELFKLAPEKILNA VKEAIVNFVNQKLDRLGLSVQ NLDTQFADGVILLLLIGQLEGFF LHLKEFYLTNPSPAEMLHNVTL ALELL/IGRGPAQLPC/LALK/TI VNKDAKSTLRVLYGLFCKHTH KAHRDRTPPWSPELTLTASKAQ SLPVSPAGGPEAAGCPPTVPLFP |
| 21495 | 51863 | A | 21623 | 1 | 87 | |
| 21496 | 51864 | A | 21624 | 45 | 277 | |
| 21497 | 51865 | A | 21625 | 171 | 511 | GKFRYSPALHSWATRLRTSTAA GHCCMNSSQNKLSSKSWAMTR HALNVKRFTIFQSHQCSLSKKV NLSLFQQGAERLPSQELTHLLL QEVRC*RDFFPEEATWTGLPV LPSQ |
| 21498 | 51866 | A | 21626 | 276 | 387 | |
| 21499 | 51867 | A | 21627 | 1 | 218 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21500 | 51868 | A | 21628 | 139 | 9009 | ESSEDVSGGLPFLVDLGFRSVC VSLFHVKNPVQWDQKLPKKKK PVRSYCGSKLLQREVIQPDVME EMVVSCVIKHLNLVDALQSLIN FQYQEEHAAEYDLLCKIMGETF KKLNAMERQLQNKMKLELLC SMKEVSFDGNDLENMVLSLRE KFLQEVNSLIQKPSHPLAKTKT LVKSLMNRAELLLHVTIAAQSG LTRSISGTPAETPACKSASETKV ISHAVRQPVFLRSMAPSDEMI GNEDLEFTRANQRR |
| 21501 | 51869 | A | 21629 | 1697 | 2056 | |
| 21502 | 51870 | A | 21630 | 237 | 1545 | KPENKKSRTGRNRTKSTPGYRA /RPAAATARISARSTK*WKNSL AGRWARHICWTLWALPRITLR /HVMAAGFPQRMQKDYRDAID ALCDANRFGQKKRLGFWRYKE DSKGVGLCSYLLIGFYTDPKN GAAAMKAFVTVTRVGDVFLAFA LFILYNELGTLNFREMVELAPA HFADGNNMLMWATLMLLGGGA VGKSAQLPLQTLADAMAGPT PVSALIHAATMVTAGVYLIART HGLFLMTPEVLHLVGIVGAVTL LLAGFAALVQTDIKRVLAYST MSQIWLRCSSRLACRHGCGGSL ECLQHEGIPYSRMGRPHTTTAL RRFTSEFGMGSACTLTGYFFMY KQAVILLMLFTASVSAACTLPI AIDHGTGPAELLTVALRYNLS SYDAAYLELALRLEIPIAKGSPN FAFRRAATGNEGIMHFLRNK GILWI |
| 21503 | 51871 | B | 21631 | 1 | 1440 | |
| 21504 | 51872 | A | 21632 | 525 | 716 | PKTPAGPVEPMHQVPSSKRVPT RDKRTRGDSTRHSGQSKPTKRY NHAYEI*PRIKWFI PDAGC |
| 21505 | 51873 | A | 21633 | 8 | 136 | |
| 21506 | 51874 | A | 21634 | 1476 | 1611 | GCDPAPGLPAPPHT/QP/DH*NQ RQIGIG*FLTGTVPATHLRQLA AA |
| 21507 | 51875 | A | 21635 | 461 | 827 | AALQMRDTS DPADCGEQSVCG YSEPVPYACFHRIQDLHDTET AACFSHAGSGRTHV*SQSEHAA GSVLWSYRYRC*TG TAGYTDR FSQQRCHVRRGISPRCWPEYQS RSWCRLFPSPESAG |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21508 | 51876 | A | 21636 | 1 | 3735 | MAEASVFQTVDPWRPGFATIPD FLKERYDKTTRIHDFCFLIATGV CFLPIVLYSGALALNSLFHVGES LQISHGAAIWLLVILLGLAGILY AVIGGLRAMAVADSINGIGLVI GGLMVPVFGLIAMGKGSFMQG IEQLTTVHAEKLSISGGPTDPLP IGAAFTGLILVNTFYWCTNQGI VQRTLASKSLAEGQKGALLTA VLKMLDPLGLKPDLLAYNTAL RALIPQRLIAFDDAVRSTLKEEE KLVNSSDWGY |
| 21509 | 51877 | A | 21637 | 840 | 1064 | WSVENYHRRGYGGHIPLPAASP AVAAQWCDAGR*VPPAARRW HRHQVYLTYLITLDRGLSRARF CIPSAHCSAY |
| 21510 | 51878 | A | 21638 | 979 | 1409 | RLVVDIFHDNRHAFPRRLVSDA AAHNACTQHRGLFRGFNVFGE FLRFAFYILIVKENADQCAGFV GMRQRDKTFVFQV*GFFTTKT GRSFNGFYCGDGGRI MF/LPLFV RPSL*RW*SSWWLQSCSVLVVP ASADVLLSSRGRR |
| 21511 | 51879 | A | 21639 | 903 | 1397 | LPTLPMVCCTTPTSSRKHWM *NPSTLT/HAWVPYTNFSPYIEG KCGMSGARVEGKVIYETQSTH KLLAAFSQASMIHVKGDVNEE TFNEAYMMHTAASPHYGIVAS TETAAMMKGNAGKRLINGSI ERAIKFRKEIKRLRTESDGWFF DNAAGYIDTITLGGPS |
| 21512 | 51880 | B | 21640 | 1 | 5305 | |
| 21513 | 51881 | A | 21641 | 129 | 723 | LITARGQVADRNLRLDLLAPWV PDAPSRALPEMTLDSRVAAAV DLFVARIGHQADGRRYIPQAIA QGVAIIAEAKDEATDGEIREM HGVPDIYLSQLNELLSALAGRC YHEPSDNLRLVGVGTNGKTT TTQLLAQWSQLLGEISAVMGT VGNGLLGKKKEKAAIQYNTLC KSCTLTHPKPHNESDH/IRCRC* |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21514 | 51882 | A | 21642 | 1 | 2230 | MMRTSGGTRDNESSDDDERER ENRLSDEKSNEYANLVGGERY EPDEENPMLGFRGAGRYVSDSF LRLCSSLEIVKARETVALIQGLK H\DLLADDTALRALIPQRADRF MNAVRSTLKEEEKLVNSSDWG Y\DAQAFARWRPEYGYFAKQA GFTVKTSASLAALWQVVNQIG GKERYFFGNILWQTRALMDRAI GHKLAKGRPEREYLQTGDAVD SWKVIVVEPEKQLTLLFGMKAP GLGRLCFSLEDKGDYRTIDVRA FWHPHGNRAEREKPRFQPYSTR KFIGQNMILLPMSIMPPVFRRVI CPLGVARLGKFRDPVYLVCFVT RQIFRYYTSGDEFLQINTTGGED IDDIDDIKLFVYEESYGISKESH WREAINAKAMGAMTLNWQEK RWQRFFNSEEPGNIEPVYMLEK VENQNHAKWEVHNFTMGYQR QVTEDTYEYLLLVVGVVPVPD NIHPMTKDEAGVWSWRTPILK GNLYEYFFNVDGVRSDTGTA MTNPQRQVNSSMILVPGSYLDT RSVAHGDLIAITYHSNALQSER QMYVWTPPGYTGMGEPLPVLY FYHGFQDGRSAIDQGRIPQIM DNLLAEGKIKPMLVVPDTE AKGIIPEDFVPQERRKVIFYPLNA KAADRELMNDIIPLISKRFNVR KDADGRALAGLSQGGYQALVS GMNHLESFGWLATFSGVTTTT |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21515 | 51883 | A | 21643 | 1 | 1549 | MDASGHHVRGFASGMGCCRV RRTMKRETGGGRLAGFRLVGT LGQHLGAHRSASKGHQILAAA RHVDRLAK\LQLA\NVSCHEVD LSWPDNLPALLQDIDTVYFLVH SMGEGGDFIAQE\RQVALNVRD ALREVPVKQLIFLSSLQAPPHEQ SDHLRARQATQ\EIRSEGNVP\V TELRAEIIVGAC\S\AAL\EVMRD MVYNLPVLTTPRWVRSRTTPIA LENFLHYLVALLDHPASEHRIF EA\AGPEVFSYQQQFEHFMAVS GKR\RWFDPSPPLPTRWISVWF LNVITSVPPTTARAL\QGLKHD LLADDTALRALIPQRLIAFDDA VRSTLKEEEKLVNSSDWGYDA QAFARWRPEYGYFAKQAGFTV KTSASLAALWQVVNQIGGKER YFFGNILWQTRALMDRAIGHK LAKGRPEREYLQTGDAVDSWK MIVVEPEQQRTL\LFGMQAPGL GRL/CCFSLEDKGDY\RTID\VRA FWHPHGMGP/L*F*WLLMIPAH LFIFRGMKQIARLAVPSTDLD |
| 21516 | 51884 | A | 21644 | 201 | 363 | SLRGSRTAASPCWAVPVHVP HGAGEPAHHPGHQP*LPPHPH VLLPLQPVLA |
| 21517 | 51885 | A | 21645 | 3 | 440 | PFSLPFSLGLTASLFMNTWLAIS SNCDGFIPASPACFCSFLMSSA L*RTKAM*IMC*FSGLSGSKGV YIR*ASHSL*NCAGLSSFP*MT SESLTFVAF*APLINPSKRASLS RFSLCISSLSCGSNWGSVPGNW VLPYSWGF |
| 21518 | 51886 | A | 21646 | 359 | 543 | VVTPDSGSSH*KANSFCLSGAN LMLKKASFRSKQVNQLSSAGS NPSNMYGLGTVGCKVTVA |
| 21519 | 51887 | A | 21647 | 2 | 582 | |
| 21520 | 51888 | A | 21648 | 3 | 574 | |
| 21521 | 51889 | A | 21649 | 1 | 195 | LCVFFVLVSFFLSPLDSQLAVV C*FDGTGIGMYLTSAVSPPPRN GVVASVMYAVVTPMLNLFICS |
| 21522 | 51890 | A | 21650 | 2 | 457 | |
| 21523 | 51891 | A | 21651 | 21 | 545 | PPCTSLRPLHAFSGKMTHLNRG TSLLDSQLHNLIALQMTCKFD VEIPNFFWEPSVTPSHRNINMYF PAAVFGFLPISGTLFSYCKIVSSI LRVSSSGGKYK/AFTTCGSHLS VVC*FYGTGVGGYLGSDVSSSP RKRAVASVMYTVVTPMLNPF YSLRNRDMKSVLRRPHSSAV |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21524 | 51892 | A | 21652 | 899 | 1039 | LWTSSLTAESSPMRAA*LRETSI VSAASRAFSAAALSSSALRAFSAC |
| 21525 | 51893 | A | 21653 | 804 | 1390 | QGTIILKVLRLRWTWIPSRASL RTGYCFCLTGWTPGLTSISTGA WLTANPGGLSSAHTLGHRLAR AGLISWPGSVKKSLSHSSSRGSIR VIMTPVPGNFSSKEPCSVKEIVA LSLLSKSLPNKGKGQSGMYKN* *ITLCPPIVQVWGKQKACFAET PMAPMMSIVFLDKGATEAVTT ECSALVSTRKSMSLPPTV |
| 21526 | 51894 | A | 21654 | 84 | 730 | HLSDSKSQVRYQPSADLSFLLG HYNPQSSRRVLSVLDSQLHNLI ALQVTCFKDVEIPNFFCDPSQLP HLACCDTFTNKIIMYFPAAIFGF LPISGTLFSYSRIVSSILRVSSSG GKYKAFSTCGSHLSVVC*VYGT GVGGYLSSDDVSSSPRKA AVAS VMYTVITSMLNPFIYSLNRNDIK GVL RQPHGSTVQFQYLLICSIPF VWVWKKGSKVK |
| 21527 | 51895 | A | 21655 | 1049 | 1979 | |
| 21528 | 51896 | A | 21656 | 2244 | 2901 | LRCLSLPFLEAWKRDMLLSVM A\YDRFVAICHPLYHSAIMNLCS VGFLVLLSFFFFLSLSDSQLHN LIALQMTCFKDVEIPNFFWEPS QLSHLACCDTFTINIIMYFPTAIF GFLPISGTLFSYYKIVSSILRVSS SGGKYKAFSTCGSHLSVVC*FY GRGVGGYLSSDVSSSPRKGAV AAVMYTVVTSMLNPFIYRLGN RDIKSVLRRPTEHCLISKK |
| 21529 | 51897 | A | 21657 | 1 | 2850 | |

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|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 21530 | 51898 | A | 21658 | 1 | 1703 | KKMALTSFLPAPTQLSQDQLAE AEEKARSQRSRQPSLVSSRREPP PYGY\RKAWIPRLLED*DRGA FPEIHVAQYP\LD MGRKKKMSN ALAIQVDSEGGIKYDAIARQGG SKDKVIYSKYTDLPKEVMNA\ DDP\DWQRP\DEEAIIIEITEKA\R VAL\EKSVSQKVA\AAMPVRAA *QIGPLLQYIPIHTISGKGVAIQ T SWS*TRRVIR\MVEMQ\KDPM\AE PP\RFKINKKIPRGPPSPAPVM HSPSRKMTVKEQQEWKIPPCIS *LGKMAKGYTIPLADKRLAAD GEEGLQDSYTLNGKFSAKLAE ALYIADRKAREAVEMRAQVER KMAQKEKEKEHEEKLREMAQK ARERRAGIKTHVEKVYFSTVH TEDGEARERDEIRHRRKERQH DRNLSRAAPDKRSKLQRNENR DISEVIALGVPNPTSNEVQYD QRLFNQSKGMDSGFAGGEDEI YNVYDQ\ALIGGKYMAQSIYRP SKN\LDKDMYGDDLEARIKTN RFVPDKGVFLVQTRRQREGP \VQFEEDPF\GLDKFLEESPTAM GGS\KRPSG*PAAPREHGAWKA RKRRKE |
| 21531 | 51899 | A | 21659 | 2 | 1588 | CLRRALPGSIESAPTAPPPPSGE GSQAYISRLPATLIVLILERRQL LGVWRRARCCSLINLAHRRHC GMPTRESPCAILARRYEGRRSPS TVAQPPPPPPPIELAPSTSETPIQ ATRGAHPAQSS/VPPA/PARPPE RPPVPEQGPSGTHPDPT/PGPT NAPQRPSAP\PNNTN*PTRHMH QLPDAA*TPYPAYGSDYL*AR* DATASHQASCTN/SPDAA*TPYP AYAKIERA*ENPVPSAIKIIGRSS SSGRQASPWGMA/SPHWRSWR MGPNGSGKRPRRAAERISCCRN AQGRTHSQKAYIQQQPQCCVN VHLQPPD/PTPAQ/PSQTLSPDPS /PAPPLPAYPS/TQHPTAPPPTSSP MSS/RIVKPHPQHCGARPGQGK ERDETERKDAKERNRRTATPTT RHTDRLPRTAHGPPPP\PPPPPP PPPPPPPRDSRRRPRRREKPEQQ KEGGQTGRTOQKETARRGEER ETGRKKTRGAPPRPAAARRPH ETAETKRRPPARQHRPPRRRPS DGTERTRHQLGFIMLGLLSWN |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21532 | 51900 | A | 21660 | 2 | 192 | RVDICSTNYCWWLYPMTSGPSF SYV*GP*EEDVRE*MCGRDGL* YLSIGVVCGFICQHHRNAQ |
| 21533 | 51901 | A | 21661 | 783 | 2119 | GSEMPVTVMLTLGEPGHFMSS LGVCWCGVEDEAAPSKQSIYIQ RETQVRTPMAGVSPKKAHPCE MCGPILGDILHVADHQGTHHK QKLHRCEAWVNILYDSGNFHR RQNEHIGEKPYRGSVEEALFAN RCKLHVSG\SHLSSVRV/EKDFL LRSGLLQQEATHTGKSNSKTEC VSLFHGGKSHYSCGGCMKHFS TKDILSQHERLLPTEEHFVWCE CGKSSSKYDSFSNHQGVHTREK PYTCGICGKLFSSKSHLLVHQRI HTGEKPYECEVCQKFFRHKYH LIAHQRVHTGERPYECSDCGKS FTHSSTFRVHKRVHTGQKPYEC SECGKSFAESSSLTKHRRVHTG EKPYGCECEKKFRQISSLRHH QRVH/T/NERAYECSESLIKYW RIHT*VRSCDCSKCGK/CFTQRS ALLGYWRVHTR\KSPYK*NKFG QFCSHTSVFLQDYS |
| 21534 | 51902 | A | 21662 | 84 | 437 | KMTSTQPVKFSLFASHVPCGQ SFPGRRAFAFAMPRRRIPSSDHL PEPGQSHQHVNRQRWACRELI AAFLPSSYRL*LVETGGEIGQRN RASCHSPFPAGSSPGIFQTEIGKP CLLP |
| 21535 | 51903 | A | 21663 | 69 | 446 | |
| 21536 | 51904 | A | 21664 | 880 | 1365 | |
| 21537 | 51905 | A | 21665 | 1705 | 2196 | RQNQREGDDDDTEDQPPRPGTQ MTELFFLIQMLCFMANALRQL VHPL/MGNVHEYFADLKMPAC AVSAFLCAMHRSITSMFE*DNG PGPADADAR\LDMRIQVFMFCA NTLPARVLQRNKNPGQDHPET AERRAESQRIIEKGLKCIQGKGI VNSISMKEGVDAFIH |
| 21538 | 51906 | A | 21666 | 1 | 1147 | |
| 21539 | 51907 | A | 21667 | 254 | 557 | AADEIGGIAVETVTEDAHLLCG CTVVAIPPRICVSAGGGAGDRK SSVRFHQNLAQVHITRGV/VWT MTNSHIITCCATAFGTTTSPSPT ESTGVPCGRNRQH |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21540 | 51908 | A | 21668 | 557 | 1031 | SSRNASGAVRKISRGMPDKKW NMALT*HSR*ANFSPLPVSGLS RRKICTIPRAQRIR*PICADRLSV ASPAACGIAAYTRRYSHDGATA EKY AHLQSRFRQQCRQFHPAA YDESPHRNRRRKWRPTYRCHP APDHRTACLRSFYGNAPGCV QTERSW |
| 21541 | 51909 | A | 21669 | 572 | 825 | QARISTSFFRESLPSRHPVPRYR PLEAFWTPCTRGYYRFFFS PAR ENAEYRTLAKHWAKFLLVRASF PGASTLCCCKSPGRTISV |
| 21542 | 51910 | A | 21670 | 303 | 899 | EDNYSGSSLYCFDDVASVQMP GSNGNCRR*CAGKTSG/TWRNS LVRQWLLTAQKKTLLHAVSNL PKTWAQILFSKQVLRSPNLRH LIW*CAAVKL*LLVLYPAIRQSI SSKSI AKSLSRRYFR/LPIGDSM* NRW*RIFTIIGMYIGTAL*SDGAI VVCRLCENLPGSFHQHQRC AASLAGGSEPIAFSRAGRTPGP |
| 21543 | 51911 | A | 21671 | 1 | 1320 | |
| 21544 | 51912 | A | 21672 | 99 | 761 | IDNAPPDQTTVHAF AANSENHS PPQLPYETPDDADPTHQAFSRW RHRPQAYSADALLRERLPPTHR HRGQSPDSLTS LPYWRGRKY RAAPALT*TPPDTLFDSP*PAV PPPVAKELPVTAQRQVHNAMS ANSFVIFHPVKIRNNIVLQPAIAI QRRNGHGVTRCAAALHSRHGS LSVARHRVHLPVCRQADDKPA PAPLRPARYCLCPNQSAAVRYL R |
| 21545 | 51913 | A | 21673 | 62 | 680 | SSRNASGAVRKISRGMPDKKW NMALT*HSR*ANFSPLPVSGLS RRKICTIPRAQRIR*PICADRLSV ASPAACGIAAYTRRYSHDGATA EKY AHLQSRFRQQCRQFHPAA YDESPHRNRRRKWRPTYRCHP APDHRTACLRSFYGNAPGCV QTGPVRRSGAASASSPAVFLSG TSPWSFARTIALVRGRSRKSTRT RLWHISAHC |
| 21546 | 51914 | A | 21674 | 411 | 481 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21547 | 51915 | A | 21675 | 402 | 915 | RLASKLFTTVTPRGGV GELQAT TRNA AVAGIKRKR SNRGRPAEE PELTADRGQGENEITEAATAAK ARRTMRPKTGNQNPDKHRTRG LQICHTFNANGNRARCSAANA MAATISGLSSGLSGTGWQETIR PPLAAIF*SSCASNDIHLPKSFLA LPNGTAPLNLGPSIAS |
| 21548 | 51916 | A | 21676 | 1416 | 1832 | GSAPRQRHLAGRRPVTTTRPKHV SHHG PQENSAHRLSHVDNESTC IVCGTLRLQHSARYFPPSLPETL FLAPVNHSV/EYNWQAAVPK*I Y*HQTFPGRDCQHLLFHFVRKF GVRESI/AQVVAVRAATSAWRY SRSSAITL |
| 21549 | 51917 | A | 21677 | 97 | 300 | |
| 21550 | 51918 | A | 21678 | 756 | 1179 | RRRLPSPYCRAAAGSSPSYECF AHQRSVASSRGHTGTRQFYRE HWFLRCIRRLSGTRLLAYHRCF QPHLACSGKRAVSASSTRSADV AAWYRV/CAKPFSSSS*VQEDL SYLRFSAS*P*TVIL*PACRKPCR KRRGQRRWR |
| 21551 | 51919 | A | 21679 | 3 | 1279 | |
| 21552 | 51920 | A | 21680 | 1 | 2448 | |
| 21553 | 51921 | A | 21681 | 317 | 1985 | PNTPLTSKLPLLTHPLTLLTPSA SGWQKTTKLSCVF/PETEKYAH ERLAHHVAQGANQYAPMTGV QALREAIAQKTERLYGYQPD DSDITVTAGATEALYAAITALV RNGDEVICFDPSYDSYAPAIALS GGIVKRMALQPPHFRVDWQEF AALLSERTRLVILNTPHNPSATV WQQADFAALWQAIAGHEIFVIS DEVYEHINFSQQGHASVLAHPQ LRERAVAVSSFGKTYHMTGW KVGYCVAPAPISAEIRKVHQYL TFSVNTPAQLALADMLRAEPEH YLALPDFYRQKRDILVNALNES RLEILPCEGTYFLLVDYSALSTL DDVEFC*SLTQEHGVAAIPLSVF CADPFPKLRIRLIQTAAINLLVN HERRANAVINVDHAEIPFLRIIL PFLRQRQHHAVIDDHPNAELL FQQIFHLHRRCPRRFRHGLRHA GHRINLTVDFQRQVDGMVRPQ FTVAMPAIFRFRTAAPSASVHQ SGVRLPYQFMALIASDNFCCW VHGGYITLAVNGNDAIGSVFNN QIVKCPRTQCLGEVINTLTDLP HFTGQLW |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21554 | 51922 | B | 21682 | 160 | 312 | |
| 21555 | 51923 | A | 21683 | 80 | 452 | |
| 21556 | 51924 | A | 21684 | 158 | 1980 | REDTAHLPAVGFLPQNPFRAIR ASGEMLLPLLLLLPMCWAVEV KRPRCV\SLTNHHFYR\ESKPFT\ CLDGSATIPFDQGGRLTYCDCK \DGS*RSQATAA\CP\NGQAFHC HQTLGL*SPL**SPSKPGSNDGV CDCCDGTDE\YN\SGV\CENTC KEEGPVRRESLQQMA\EVTRE G\FRLEEDPLFEGLGKKAREEK QKKL\IELQAGK\KSLEDQ\VEM LRTVKEEA EKPEREAK EQHQK LWE\EQLAGFQGP NREQDARA ADAFKELDDMDGTVSVTELQ THPELDTDGDGALSEAEQAALL SGDTQTDATSFYDRVWAAIRD KYRSEALPT\DL PAPSAPDLTEP KEEQPPVPSSPTEEEEEEEEEE EEAEEEEEEEDSEVQGEQPKEA PPPLSPPQPASPA\EEDKMPPYD EQTQA\FIDAAQEARNKFEEAE RSLKDMEESIRN\LEQEISFDFGP NGDV\FAYLYSQ\CARDLTTNE YV/YTRLCPFQVLFFAGNPNSG VFPTSLGHLGASW/VLGPDHGQ VSVAMKF*ARHGACWQGP NPL QHP*RFWFGKET\MVTKHPQ*P SRCEYLHGS**TPAA\CPEPPAL KQPQPKD\DHDEVLSWMGARE |
| 21557 | 51925 | A | 21685 | 59 | 359 | LLRIGNDWCIPKGITPTTHIILP IGEIRQPNATLDLSQSVDNEY CLLLAKELGLNVPDAEIIKAGN/ GARVSGRTF*QALEC*ANGFTS LATGGYVSDI |
| 21558 | 51926 | A | 21686 | 1 | 213 | MSIAVTTTDPNTGVSTTSSSSL TGSNAADLQSSFLTLLVAQLKN QDPTNPMENNELTSQLAQISTV SGIEKLNTTLGSISGQIDNSQSL QASNLIGHGVMIPGTTVLGTG SEEGAVTTTTPFQVQLQAADK VTATITDKNGAVVRTIDIGELT AGVHSFTWDGTLTDGSTAPNG SYNVAISASNGGTQLVAQPLQF ALVQGVIRGNSDITTFGVNMKL AHLGRQALMGVMAVALVAGM SVKSFADEGLLNKVKERGTLLV GLEGTYPFQSGDDGKLTGFE VEFAQQ*FAHGQQRRTKQFS DFAGGAAEKPGPDQSNGKQRA DVAIGTNQHGQRD |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21559 | 51927 | A | 21687 | 1 | 2339 | MSGGQTEKQAQLIRDFQPDMI MVTPSYCLNIEELERQLGGDA SGCSLRVGVFGAEPWTQAMRK EIERRLGITALDIYGLSEVMGPG VAMECLETDDGPTIWEDHFYPE IVNPHDGTPLADGEHGELLFTT LTKEALPVIRYRTRDLTRLLPGT ARTMRRMDRISGRSDDMLVLR RRHLCRPSACQLCRPPSLPATD RVLELFAQSGAQWLVLGDVL NHGPRNALPEGYAPAKVAERL NEVAHKVIAVRGNCDEVDQM LLHFPITAPWQQVLEKQRLFL THGHLFGPENLPALNQNDVLV YGHTHLPVAEQRGEIFHFNPGS VSIPKGGNPASYGMLDNDVLS VIALNDQSIIAQVAINPAPEKEG FLIMEQRRLASTEWDIVNEEN EVIAQASREQMRAQCLRHRT YIVVHDGMGKILVQRRRTETKDF LPGICATSKVRKLLCKSAALLP VSELLLVLLTPVFVGSVIGKL GAFAIHIDGITVKRRLVRNTVL QFCGRSRQPLEYVSAGDTGPVL RALKRMAMRHYMRSQTVKG VTDTRAIDEVALSVAQVEEMY RYLAIANYEDRFVIPTSHREMA GDAFAERNCGFTFGDCCHGS DSKFNLFNSSRIDAINITEILKVI GLLMEYPDELLWECKEDALALI RRDAPMLTDFTHNLLNAPLLD KQAEWCEVFDRGRTTSLLLFEH |
| 21560 | 51928 | A | 21688 | 391 | 631 | |
| 21561 | 51929 | A | 21689 | 2779 | 3348 | LMQLHNGLPVAGLRQFCQQLV IQRLYFFTTATAHQCTRHMCHR HRSLLTAHRQMALCFQYVDDL HHAFADVLINNACYPLLMEQ GVFIYNGTQQLLHWVIIDSRQD HGFGGL*KSRIVCERRRL*SQH GQFVFRHHVPDHRIDIAFNAL *TLVIREISSVPASVGVGIDFPGG AATWAGPVVIKPGQS |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21562 | 51930 | A | 21690 | 1 | 1239 | MPNVDDVVGEMVNTMSASRSY QANVEVLNTEKAMSIAVTTTDP TNTGVSTTSSSLTGEQRRRFTK QFSDFAGGAAEKPRPDQSNGK QRADVAIGTNQHDAARILRKG TMTTLLNPYFGEFGGMYVPQIL MPALRQLEEFVSAQKDPEFQ AQFNDLLKNYAGRPTALTKCQ NITAGTNTTLYLKREDLLHGGA HKTNQVLGQALLAKRMGKTEII AETGAGQHGVASALASALLGL KCRIYMGAKDVERQSPNVFRM RLMGAEVIPVHSGSATLKDAC NEALRDWSGSYETAHYMLGTA AGPHPYPTIVREFQRMIGEETK AQILEREGRLPDACVGGGS NAIGMFADFINETN/VSVGPQH AYLNSSVRAD*VSITDDEDLQA FKTLTASYKTTTAAAKTSLHVP |
| 21563 | 51931 | A | 21691 | 32 | 1778 | WDARVFSHSGWVLYLIRQYCSI SAVSSCGSTTGSACSATSWATA TSDSVTHLRLFSYRGSDHFRMR RFNHFRRLRFGNLNGGFYDTGHF FNNWRANNRFDSGGDRDLSSH RLHMYFFLFALLFNLYILRTYN WIADPDFARGQFRRRARYGQR HWRLGWITLVTIATTTTLYAQ VTRRAARTTRHATVVTVISIVL FLLFWCSLRYDWHYCILILRSTP SVLSQYPVGNELRRRLVHLHL LCTYSDDDSRDPYRQESRTRN GVVPVIVNIDVHRFGQTGDQH GAMIIPVIFLLNVAMHERASGHI PNGNRTYYLSRSQPPVFALMVE LFEEDGVAVARYLDHLKMEYA FWMDGAESLIPNQAYRHVVRM PDGSLHRYWCDCHTSCD*SW LEDVETAKHSGRPPNEVYRDLR AGAASGWYSSRWLRDTGRLA SIRTTQFIPIDLNAFLFKLESAIA NISALKGEKETEALFRQKASAR PMREYETGEQWDKPNGWAPL QWMAIQGFKMYGDDLLGDEIA RSWLKTVNQFYLEQHKLIEKY HIADGVPREGGGGEYPLAQDGF GWTNGVVRRLIGLYGEP |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21564 | 51932 | A | 21692 | 1 | 2514 | MKTLIARHKAGEHIGICSVCSA HPLVIEAALAFDRNSTRKVLIEA TSNQVNQFGGYTGMPADFRE FVFTIADKVG FARERILGGDHL GPNCWQQENADAAMEKSVEL AVVIDLWSRAVIGWSMSPRMT AQLACDALQMALWRRKRPRN VIVHTDRGGQYCSADYQAQLK RHNLRGSM SAKGCCYDNACVE SFFHSLKVECIHGEHFISREIMR ATVFNYIECDYNRWRRH SWINS LLSQKRNTQGRIEDGRQH |
| 21565 | 51933 | A | 21693 | 1 | 1527 | |
| 21566 | 51934 | A | 21694 | 792 | 1602 | HCLSARRYELVCQPK*AFVR*L LR*IAVLR\HLNIQH LRRSHSLR HGRRHTRKGERGTINIVNGTPI HERSRNIDNRRSPSPYIRKRG AH TELRS DHPLLINQHWHHFAGM VAVTNGRIVAVIRHHDQAIWL HRLNKP GKVTVNDLQTFGITCD VFCMTSEVGFLNVGANKRRRM GVKFVEGDIHNPLAIHQILPAH AIRIVDDICH LTHQHGWHACFI QFLWHLHFFIDAIAHMDLET V VISARTRRIDTNKAPFFAFCGIE |
| 21567 | 51935 | A | 21695 | 1 | 1530 | LSQQTVNTLQAGHQTIHFFMG VIHGQRRP THRRDVVIGHQWH CAVMSGTHSNAVIEKTANIIGV VFTEIKSNNAKPVLWAIESNAA ATDGEIVFDGEILKSACEINDSD KKIEVALGHYNAEQFRNIGERS PKIPFTIPLVNC PMTGEIANILGS KPGTIFTMLRDTGGIKPHERKR AVAHLTLSEREEIRAGLSAKMS IRAIGYWR*IASPSTFSRE\VQRK GGHR\YYKAVDANIRANRMAK RPKPCLLDQNVPLRKL VLEKLE MKWSPEQISGWLRRTKPRQKT LRISPETIYKTL YFRSREALHHL NIQHLRRSHSLRHGRRHTRKGE RGTINIVNGTPIHERSRNIDNRR SLGHWEGLVSGTKNSHIATLV DRKSRYTII VRLRGKDSVSVNQ ALTDKFLSLPSELRKSLTWDRG MELARHLEFTVSTGVKVYFCD PQSPWQRGTNENTNGLIRQYFP KKTCLAQYTQHELDLVAAQLN NRPRKTLKFKTPKEIIERGVALT |
| 21568 | 51936 | A | 21696 | 2 | 140 | IITNSISRPGDPPMSDPHS*SPAS SSAKTETKSLFNAFLV |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21569 | 51937 | A | 21697 | 1817 | 4083 | KGLLTSFHYIKTPEVPNLCVEG GTRLQIWPACSSSTGSGGTCWK APPQPPRPPTSSSPS/PAPPSEAF VLSAGAMQLEAGAYSLVIKES KNNVGVDVIKRRHFCTAGGNV NQYNHYGKHCVLSCSGPASGA QPLYRMAQPPSPNMAAGIPPA ARISSITSPLLKPSWLHLLAHP VLQAHLTEEGLGRSHHVQRGQ CLVSKSVFTNACWEMQNVKRF TDFIPLHKNTRGPEPLCRRRNQ APNMACMQQHWQRRN |
| 21570 | 51938 | A | 21698 | 247 | 281 | KPGKQHSMMLK*SALLPSAHGPT S/CKEARCHPVQILPELLF*MP KKICPPLCYLWTVKAWETTFH AEV |
| 21571 | 51939 | A | 21699 | 531 | 716 | PRRLRAAPPDLGGFRLLP/LPE ASGCSP*SQRLFQKAPSPAPCS WRRSRFCVKTCVLPMMGGQ |
| 21572 | 51940 | A | 21700 | 202 | 606 | ITCLHAHVTWCQILPYLMLPAP LLRPLPTPLTVAGVGQSLPEIQL SVTLPLQGRNQGSLESRLVLS WAEP*DPVVSALPLQGRNQGS LESRLVLSWAEP*DPVVSAL PLQGRNQGSLESRLVLSWAEP |
| 21573 | 51941 | A | 21701 | 444 | 1167 | FRLHGHLERGPFYFLSPLAVQS SQSCLRRFTTRYHLPYVLNRK NSWHVAHIFRRHAKPEEQAPIY SHIHFTSDLDEVLPDVKLVV VCTHADSHFEYAKRALEAGKN VLVEKPFTPTLAQAKELFALAK SKGLTVTPYQNRFRDSCFLTAK KAIESGKLGEIVEVESHFDDYR VAETKPLPQDGAFFYGLGALFT NQQGFKSSLLSIFADSSSSVAG RSPHNLVKKRGGIVAIASAFAG |
| 21574 | 51942 | A | 21702 | 1 | 668 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21575 | 51943 | A | 21703 | 1 | 1308 | MRVYMDGRLIVSTRQRKVLAA GPMLYAA TRAPAF TMSGDNLV RSHASIYMTSCH TLLGEQAGYA VFGALLPAITLLHLNSACCIVYV SCLLADAGHRDSLQ QAGDKWT TTDSYSSSCTSETLGSACVRYA HSSRNHVRFALS DLDEV LNDPD VKLVVVCTHADSHFEYAKRAL EAGKNVLVEKPFTPTLAQAKEL FALAKSKGLT VTPYQNR RF DSC FLTAKKAIESGKLGEIVEVESHF DYYPVAETK PGLPQDGA FYG LGVHTMDQIISL FGRPDH VRL* HPGALRNKSP IWTNPFEAQLAFY GDLKAIVKTSHLVKIDYPKFIV HGKKGSFIKYGIDQQETSLKAN IMPGEPGAADDSVGVLEYVN DEGVTVREEMKPEMGDYGRV YDALYQTITHGAPNYVKESEVL TNLEILERGFEQAS PSTVTLAK |
| 21576 | 51944 | A | 21704 | 199 | 706 | SHDVCRINADRQRDRNNRRQR RSLRVYKLG NQQQNNGIGPRIL FHHFTQYALNFRHMRTEHGFC HPCDTVHRHDGDHTGTEDFVF/ WR*TRDWFWSG*YQRP GQQH KHLNNQYHRQRFAAEGWTQV RISTKKGDYSDCPEENPHCQPV AGRYHYSLVGRVSNATLARLIR |
| 21577 | 51945 | A | 21705 | 354 | 569 | SRAVCWQVGTRLW AIFGVS*E LQRHVLVV FAGFWIVKNSRNL FLVCRAEHKRSVVKGLLRQQG AGLLVPLS |
| 21578 | 51946 | A | 21706 | 373 | 462 | |
| 21579 | 51947 | A | 21707 | 1 | 1293 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21580 | 51948 | A | 21708 | 1 | 1371 | MCPIEETASSFGGKPLSMVLVIQ MFMLLTGALIIILTKTNPASISK NEVFRSGMIAIVA VYGIWMA ETMFAPACYGYYILPTPSDLA AIQFDRSGTTHIGRFVINHSFILP GLIGVSVSCVFGWIFAAIKRDA AAGRAKENVIFHHFPFQSVKAD IATNPFKRPGGAFIRITQTFRTV QTFRLSAYRLDFAGDRLRISTPR AKMRTAFKKDHLRQRRRCIRQ RAPPARHNLVGAVALPATVAG VNFTFSNVPLDSSVLSLLTDFS TAVGSIVMLAVIMGLMLAFDM GGPVNKVAYAFMLICVAQGVY TVVAIAAVGICIPPLGMGLATLI GRKNFSAEERETGKAALVMGC VGVTEGAIPFAAADPLRVIPSIM VGSVCGAVTAALVGAQCYAG WGGLIVLPVVEGKLGYIAAVA VGAVVTLFV*TC*KVWRVKM GLRLMKKKTTWIWILKLI |
| 21581 | 51949 | A | 21709 | 961 | 1116 | |
| 21582 | 51950 | A | 21710 | 228 | 388 | RRGRNRYPALQ*TMFLPADGP ARCLSRQAAILKESVLPK*GRP DVVFSPAYPY |
| 21583 | 51951 | A | 21711 | 1168 | 1851 | LHRTGQRPAQAQRTETHHPFFNH FARLQVDTVVINHHQHTVAFQ NRTFRSEI*RNNVDIFQPDVLPD ILLGPVREREDADAFVNLVP VVVPQLRALIFRIPAMEAVTER VNSLFSAGFLFVTARTTEGGIKT VFVQRLFQAFSFHNIGMFRAAV HEWINPHRHAFRVFMHQQFAA VGFSSTIAELIHLAEFPAGIDMQ QRERQRTWIKRLARQM QHDAG IFTDRVEH |
| 21584 | 51952 | A | 21712 | 1 | 2653 | |
| 21585 | 51953 | B | 21713 | 632 | 709 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21586 | 51954 | A | 21714 | 1 | 1214 | MHDQQVIDAYHPDLRRTRAAS QSIIPVDTKLAAGITRFFPQFND RFEAIAVRVPTINVTAIDLSVTV KKPVKTDVGGAGTVKLNRCQI ARISRQDVITPPGCVFEKALTLL IASGRNDTLARQNNHTKESLVE KPFRKILVIKMRYHGDMLLTTP VISTLKQNYPDADIDMLLYQDT IPILSENPEINALYGISNKGAGTF DKIKNVLSLIKTLRANNYDLVI NLTDQWMVALLVRCLPARMKI SQLYGHRQHGIWKKSFTHLAPI HGTHIVERNLSVLEPLGITDFYT DTTMSYAEDCWKKMRREDA LGVKDHVYVVIQPTARQIFKCRD NDIISKVICMIRGSPTEGRWSVF FFYPADFTFVCPTELGD/GC*PL RRTAETGRRRIRSIYRSLHPQS |
| 21587 | 51955 | A | 21715 | 25 | 1086 | |
| 21588 | 51956 | A | 21716 | 1 | 1113 | |
| 21589 | 51957 | A | 21717 | 80 | 430 | RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNDLWYCELS HYTVVLLLFRKRSRFQSNVQ RKLMTNF |
| 21590 | 51958 | A | 21718 | 1 | 2076 | |
| 21591 | 51959 | A | 21719 | 2742 | 3109 | VWTEGTGNASRRR/WKGNQL LPVSLVKRKTTLPNTQTASPR ALADSLMQLARQVSRLEKRAV SATQLMAKAVKGQSLLPVSL VKKKNHPGALIRKPPLPARWPI LLIQLARQVSRLETGQ |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21592 | 51960 | A | 21720 | 174 | 1608 | TAAKRKIPSASIRSIND*KY*VC KRT*CVGQLAAENADGTVAEY NGYHVVFALAGSPKDADDTSI YMFYQKVGDNSIDSWKNAGR VLMNPLMILVKIILSLTLACH ALLDCKTLTLTELGRNLPTKAR TKHNIKRIDRLLGNRHLHKERL AVYRWHASFICSGNTMPIVLVD WSDIREQKRLMVLASVALHG RSVTLYEKAFPLSEQCSKKAHD QFLADLASILPSNTTPLIVSDAG FKVPWYKSVEKLGWYWSRV RGKVQYADLGAENWKPISNLH DMSSSHSKTLGYKRLTKSNPIS CQILLYKSRSKGRKNQRSTRTH CHHPSPKIYSASAKEPWVLA TN LPVEIRTPKQLVNIYSKRMQIEE TFRDLKSPAYGLGLRHSRTSSS ERFDIMLLIALMLQLTCWLAGV HAQKQGWDKHFQANTVRNRN VLSTVRLGMEVLRHSGYTITRE DLLVAATLLAQNLFTHGYALG |
| 21593 | 51961 | A | 21721 | 1 | 3285 | |
| 21594 | 51962 | A | 21722 | 1095 | 1188 | |
| 21595 | 51963 | A | 21723 | 568 | 1263 | |
| 21596 | 51964 | A | 21724 | 2 | 1688 | |
| 21597 | 51965 | A | 21725 | 1456 | 2046 | SKGKVAIVSSHQEVRA SPRRSP LGSEERPGPHTSRQAAGQPHPG TCSSVHCQGSWGLQTQNSEVIH DGDVEAISVGEDAAPGPRVHG ADLGQEEEA FR*VVMGGLPDR DSALAPVPEPMHRGWAVRAAE GAVQNDPVGGSESWGAGSHS QPFSHRPAPHTRGLAQAQTEAA GEGAVPEVHRGAVLAGVRAPG WAQP |
| 21598 | 51966 | A | 21726 | 335 | 595 | AGLFSRKRKVVSSICIRFE*ILTSCL GVRISTGKLVARIHGSFADAE*I L\WTGGDNESVS/MR*FFRPLER DLYNRIWHEIGLLLVSL |
| 21599 | 51967 | A | 21727 | 80 | 428 | RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVAIRCP LYLLTGLIFVSKNGLWYCELS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF |
| 21600 | 51968 | A | 21728 | 622 | 1281 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21601 | 51969 | A | 21729 | 1066 | 1827 | VPQAKGNNVVITSYMTNRGFF EDKKATFAPSFLMNIKGNKTSV VKNSILEQQQLTWLQVAKRAG LGGGQSGRTVLRERVRIEIAST HIALQHAIVTGDAVGMDDIPQE ARQYRHNQAYAYSIIQGDGAED DDERIAFASHTIQECRSQGP GG YPFKIYSSRKDRIPISQS LLESHF TVHEETAPDLETTG*PGCKDHG NLCC/LSSVKLRYSMYRIKAGL WMTHPG*RTYWV |
| 21602 | 51970 | A | 21730 | 1 | 1326 | |
| 21603 | 51971 | A | 21731 | 1 | 1971 | |
| 21604 | 51972 | A | 21732 | 1 | 1626 | |
| 21605 | 51973 | A | 21733 | 1 | 1810 | |
| 21606 | 51974 | A | 21734 | 305 | 442 | AGLFKSRKVSSICIRFE*ILT SCL GVRISTGKLVARIHGSFADAE |
| 21607 | 51975 | B | 21735 | 1 | 1938 | |
| 21608 | 51976 | A | 21736 | 531 | 669 | AGLFKSRKVSSICIRFE*ILT SCL GVRISTGKLVARTHGSFADAE |
| 21609 | 51977 | A | 21737 | 80 | 428 | RWLATPYLTVKLSLLPNLAVTC QPKREQNITSNESTDC*VIVTST KSDSLYTVGMLALSVRAIRCPL YLLTGLISVSKNGLWYCELQSH YTVVLLLFMRKRSRFQSNVQR KLMTNF |
| 21610 | 51978 | A | 21738 | 10 | 426 | |
| 21611 | 51979 | A | 21739 | 314 | 451 | AGLFKSRKVSSICIRFE*ILT SCL GVRISTGKLVARTHGSFADAE |
| 21612 | 51980 | A | 21740 | 1 | 1139 | MWGIGSRTPIYNKILVYSSPEVS CEKPKYVKSQTSTHTGFESHKR YIFYLRLVGKNLHVSAMGLGK SQERRKKALKSQPQQPADSFPS LPTVEGLTTSGEVAAGFWLSGE ALSSC*LLSASVHLLLA CLGMG KCSCSGFWLYF |
| 21613 | 51981 | A | 21741 | 306 | 444 | AGLFKSRKVSSICIRFE*ILT SCL GVRISTGKLVARTHGSFADAE |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21614 | 51982 | A | 21742 | 189 | 1089 | HHTAHCQ*CWL*S/DHGINPLRS WVGTG*V/GVRGKVQYADLGA ENWKPISNLHDMSSSHSKTLGY KRLTKSNPISCQILLYKSRSKGR KNQRSTRTHCHHPSPKIYSASA KEPWVLATNLPVEIRTPKQLVN IYSKRMQIEETFRDLKSPAYGL GLRHSRTSSSERFDIMLLIALML QLTCWLAGVHAQKQGWDKHF QANTVRNRNGSLLTNWPSVPP TIKEEENSEEELAAATTSKEQEP IGTDLDAVRTPEPLEEFPKREDQ EGSPPETSLPYKWWVEAANLLI PAVGSSLSEALDLIES |
| 21615 | 51983 | A | 21743 | 1 | 1135 | |
| 21616 | 51984 | A | 21744 | 80 | 430 | RWLATPYLTVKLSLLPNLAVTC QPKREQNITSNESTDC*VIVTST KSDSLYTVGMLALSVRAIRCPL YLLTGLISVSKNGLWYCELQSH YTVVLLLFMRKRSRFQSNVQR KLMTNF |
| 21617 | 51985 | A | 21745 | 80 | 430 | RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF |
| 21618 | 51986 | A | 21746 | 773 | 1015 | AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADASF STDLYHGTLPASLTMSGVVLL GRMLARSARNWS |
| 21619 | 51987 | A | 21747 | 391 | 527 | AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE |
| 21620 | 51988 | A | 21748 | 671 | 1030 | AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE*I LGDGW*Q*VRVER*FFRPLERD LYNRILACPLINT*PTPVVRLKP *TVWSMGPVVGTPARPIRTSGA CWWCW |
| 21621 | 51989 | A | 21749 | 221 | 478 | AEQDCTILPVLRHFTFFKSRKVS SICIRFE*ILTSCLGVRISTGKLV ARTHGSFADDQTLFFMTLAVS GELWTPSPWRPNSIRTS |
| 21622 | 51990 | A | 21750 | 590 | 940 | RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF |
| 21623 | 51991 | A | 21751 | 473 | 613 | AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARIHGSFADADT |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21624 | 51992 | A | 21752 | 342 | 1459 | SFLWRFRRLRGGSERFCLAGIPSA SGV*NIPSASIRSIND*KY*VCKR T*CVGQLAA\ENADGTVAEYN GYHVVFALAGSPKDADDTSIY MFYQKVGDNIDSWK NAGR VF KDSDKFDANDPILKDQTQEWS GSATFTSDGKIRLFYTDYSGKH YGKQSLTTAQVNVSKSDDTLKI NGVEDHK TIFDGDGKTYQNVQ QFIDEGNYTSGDNH TLRDPHYV EDKGHKYLVFEANTGTENGYQ GEESLFNKAYYGGGTNFFRKES QKLQQSAKKRDAELANGALGII ELNNDYTLKKVMKPLITSNTVT DEIERANVFKMNGKWYLF TDS RGSKMTIDAKSTLLESTEGSMT PPMTATEPFLRFLKGEIAQPKPH |
| 21625 | 51993 | A | 21753 | 2094 | 2201 | |
| 21626 | 51994 | A | 21754 | 81 | 1080 | HHTAHCQ*CWL*S/DHGINPLRS WVG TG*V/GVRGKVQYADLGA ENWK PISNLHDMSSSHSKTLGY KRLTKSNPISCQILLYKSR SKGR KNQRSTRTHCHHPSPKIYSASA KEPWVLA TNLPVEIRTPKQLVN IYSKRMQIEETFRDLKSPAYGL GLRHSRTSSSERFDIMLLIALML QLTCWLAGVHAQKQEHPLWSL ALVRRRSPAQSPHVG TGSSGST GCSSQAPCMKSNNALIVILGTV TLDAVGIGLVMPVLPGLLRDIV HSDSIASHYGVLLALYALMQFL CAPVLGALS DRFGRRPVLLASL LGATIDYAIMATTPVLWYPLV |
| 21627 | 51995 | A | 21755 | 80 | 430 | RWLATHYLT VKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALS VRAIRCP LYLLTGLIFVSKNDLWYCE LQS HYTVVLLLFMRKRSRFQSNVQ RKLM TNF |
| 21628 | 51996 | A | 21756 | 1 | 593 | MGVNDLWQILEPVKQHIPLRNL GGKTI AVDLSLWVCEAHPVKK MMGSVMKKHLRDFADFGTTIK QDFRLLGQTSVDRLLQLSQGQ AAYPIPDQVQSVLISMLLIAL MLHLTCGLAGVHAQKQGWDK HFQANTVRNRNVLSTVRLGME VLRHSGYTITREDSLVAATLLT QNLFTHG YVLGKL*GDSLVSLSL |
| 21629 | 51997 | A | 21757 | 410 | 547 | AGLFKSRKVSSICIRFE*ILT SCL GVRISTGKLVARIHGSFADAE |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21630 | 51998 | A | 21758 | 719 | 814 | AGLFKSRKVSSICIRFE*ILTSCL GVRIFNR |
| 21631 | 51999 | A | 21759 | 1 | 1596 | |
| 21632 | 52000 | A | 21760 | 80 | 430 | RWLATHYLTVKLSLLPNLAVT CQPKREQNITSNESTDC*VIVTS TKSDSLYTVGMLALSVRAIRCP LYLLTGLIFVSKNDLWYCELQS HYTVVLLLFMRKRSRFQSNVQ RKLMTNF |
| 21633 | 52001 | A | 21761 | 1343 | 1480 | AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE |
| 21634 | 52002 | A | 21762 | 2 | 151 | |
| 21635 | 52003 | A | 21763 | 258 | 396 | AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE |
| 21636 | 52004 | A | 21764 | 1 | 3081 | |
| 21637 | 52005 | A | 21765 | 449 | 586 | AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE |
| 21638 | 52006 | A | 21766 | 563 | 2042 | |
| 21639 | 52007 | A | 21767 | 1001 | 1093 | |
| 21640 | 52008 | A | 21768 | 1814 | 1870 | |
| 21641 | 52009 | A | 21769 | 2760 | 3723 | HHTAHCQ*CWL*S/DHGINPLRS WVG TG*V/GVRGKVQYADLGA ENWKPISNLHDMSSSHSKTLGY KRLTKSNPISCQILLYKSRSKGR KNQRSTRTHCHHPSPKIYSASA KEPWVLTATNLPVEIRTPKQLVN IYSKRMQIEETFRDLKSPAYGL GLRHSRTSSSERFDIMLLIALML QLTCWLAGVHAQKQGWDKHF QANTVRNRNVLSTVRLGMEVL RHSGYTITREDLLVAATLLAQN LFTHGLFGPSVDAPPPKRGFKR PKLPELRLQRFFGGVITPPLESY SLPSDPVHLFPPRRPPRQLTASP LRARAPYECSSCKDA |
| 21642 | 52010 | A | 21770 | 860 | 3503 | |
| 21643 | 52011 | A | 21771 | 4597 | 6030 | |
| 21644 | 52012 | A | 21772 | 1513 | 3464 | AGLFKSRKVSSICIRFE*ILTSCL GVRISTGKLVARTHGSFADAE |
| 21645 | 52013 | A | 21773 | 1 | 453 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21646 | 52014 | A | 21774 | 1 | 1526 | MSSSHSKTLGYKRLTKSNPISC QILLYKSRSGRKNQRSTRTHC HHPSPKIYSASAKEPWVLATNL PVEIRTPKQLVNIYSKRMQIEET FRDLKSPAYGLGLRHSRTSSSE RFDIMLLIALMLQLTCWLAGV HAQKQGWDKHFQANTVRNRN CKMATLKEKLIAPVAEE\EANS\ PNNKITVVGV\GQVGMA\CAISI LGKVS WPDEL\ALVGCFWEDK LKGGNDGSFQHGELIFFQTPKN CGQDKGLFWGPPNS*RFVSW*L AGSPVQPRRGRIRLKS WVPEK WLMVFQIPLFLKIV\KYSP*FAS* LVVSHPV\DIPTYVT\WETKVGL PKHRVIGSGCNLDSARFRYLMA EK\LGIHPS\SCHGW\IFWGEHG DSSVAWCWNGVNVAGVSLQE LNPEMGTDNDSENWKEVHKM VVESAYEVIKLGKGTNWAIGLS VADLIESMLKNLSRIHPVSTMV KGMYGIE NEVFLSLPCILNARG LTSVINQKLKDDEVAQLKKSA DTLWDIQKDLKDL |
| 21647 | 52015 | A | 21775 | 2 | 355 | |
| 21648 | 52016 | A | 21776 | 2 | 178 | |
| 21649 | 52017 | A | 21777 | 1 | 888 | |
| 21650 | 52018 | C | 21778 | 127 | 255 | |
| 21651 | 52019 | A | 21779 | 1 | 1824 | |
| 21652 | 52020 | A | 21780 | 330 | 476 | |
| 21653 | 52021 | A | 21781 | 452 | 500 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21654 | 52022 | A | 21782 | 3 | 1584 | DAWAAVSRGDEPGWGSWSR LLQHWGVSCWSDPKRFSSALQ GYIITDWCAPFNKRIWKREQPE ETFPNTETNGEFGK\ RPAEDME EEQAFKRSRNT\ DEMVEL\ RILL\ QSKNA\ GAVIGKGGKNIKALRT DYNASVSV\ DSSVPERILCISA DIETIGEILKKIIP TLEEGLQLPSP TATSQLPLESDAVECLNYQHYK GSDFDCELRLLIHQSLGREGIIG GQRCLKSKELRG GTLQTTIKLF QECCPHSTDRVVLIGGKPDRFV\ ECIKIILDLISESPIKGR\ AQPYDP NFYGVKPMDDY\ GFTMMFDD RRGRPVGFPMRGRGGFDRMPP GRGGRPMQPYRRDYDDMSPRR GPPPPPPGRGGRGGSARNLPL PPPPPPRGGDL MAYDRRGRPGD RYDGMVGFSADETWDSAIDTW SPSEWQMA YEPQGGSGYDYSY AGGRGSYGD LGGP IITQVTIPK DLAGSIIGKGGQRIKQIRHESGA SIKIDEPLEGS EDRIITITGTQDQI QNAQYLLQNSV\ KQYSGKFF |
| 21655 | 52023 | A | 21783 | 211 | 1635 | KNMETEQPEETFPNTETNGEFG KRPAEDMEEEQAFIRSRNTDEM VELRILLQSKNA\ GAVIGKGGK NIKALRTDYNASVSV\ DSSGPE RILSISADIETIGEILKKIIP TLEE GLQLPSPTATSQLPLESDAVECL NYQHYKGSDFDCELRLLIHQSL AGGIIGVKGAKIKELRENTQTTI KLFQECCPHSTDRVVLIGGKPD RVV\ ECIK IILDLISESPIKGRAQP YDPNFYDETYDYGGFTMMFDD RRGRPVGFPMRGRGGFDRMPP GRGGRPMPPS\ RRDYDDMSPRR GPPPPPPGRGG/ RGLGSARNLPL LPPPPPPRGGDL MAYYKGRPV\ GDPYDGMVGFSADETWDSPID TWSP\ SEWQMA YEPQGG\ SG\ Y DYSY/ AQGGRGSYGD LGGP IIT QVTIPKDL/ ALGSIYWKKGQR\ IKQIPS* VGELSIKIDEP\ EGSED RIITITG\ TQDQIQ\ NAQYLLQ\ N SVKQYADVEGF |
| 21656 | 52024 | A | 21784 | 860 | 1201 | TISEPPALILLPIAVPSFSTTCRLP EDIIVVSFAFPPLLIFCVPLLILVP VAMP* LLIFCVPLIMVFVAFPA TSITPPLSIRVASALALVKTDIVP LSLIIVLFAEPYAFMSK |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21657 | 52025 | B | 21785 | 1 | 3750 | |
| 21658 | 52026 | A | 21786 | 1 | 1350 | |
| 21659 | 52027 | A | 21787 | 189 | 1939 | TAMAGRMPCAEVISGSATRPD GPKALFKPIGRPHQAI RPINKPP AAPPKQAVTNGFMRGRVPPKT LTVPSESSLAPMTLVVIVVKEA LPPAKIFSTPVYPQPTRRAPDAE PLSASKTPSVYLVNFVVSPEL RKLTVDVLPALRANTRALWQV EVSAPFSFMTQATPATQPLINAE PAVAAPTEQNPQVGPVMPGVQ GADAPVVAQNGPSRDVCLKTFA PIAPPPGSMVLRGLNPNGSLEFG MRSDEVVTKAMVQLELTPWH GYGCQCPFLPVKYLYAAIGFSV MIEALNQLAIFNRRRFLSANQT LRQRTTEAVMRLLSGQKEDAE LDAETASMLVDHGNQQIFNPQ ERRMIERVNLNLQRTVSSIMTS RHDIEHIDLNAPEEEIRQLLERN QHTRLVVTGDGDDAEDLLGVVH VIDLLQQSLRGEPLNLRVLIRQP LVFPETLPLPALEQFRNARTHF AFVVDEFGSVEGIVTLDVDTETI AGNLPNEVEEIDARHDIQKNAD RSWTGN/GLLPLGDCRL*QASP TGCINRRGS\HYGYPTLYEFRKR FLTPGTVCRCRCDQRGDAMRVQ VQWVFYTYILPLANE |
| 21660 | 52028 | A | 21788 | 558 | 1563 | TNNRL*K*GNN**LTNQKKSRT RWIHSRILPEAGC/GIASVGRNN CGLWRFTPAKAISWGKIHPVFQ RQILRVLSQTLFPN/MSLGRNLG YGLKMFGVPRAELKPRFKEALP MVNLEGFEDRFVDQISGGQQQ RVALARALILKPKVLLFDEPLS NLDANLRRSMRDKIRELQKQF DITSLYVTHDQSEAFVSDTVL VMNKGHIMQIGSPQDLYRQPA SRFMA SFMGDANLFPATFSDG YVDIYGYHLPRPLHFGTQGE MVGVRPEAITLSDRGEESQRCV IRHVAYMGPQYEVTVEWHGQE ILLQVNATRLQPDVGEQYYLEI HPYGMFVLADAA |
| 21661 | 52029 | A | 21789 | 201 | 312 | CSWHDRFPDWKAGTHLLARG* QLSLPVWLCPVLKLS |
| 21662 | 52030 | A | 21790 | 925 | 2388 | |
| 21663 | 52031 | A | 21791 | 1 | 759 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21664 | 52032 | A | 21792 | 1 | 1086 | MEKKITGYTTVDISQWHRKEHF EAFQSPAQCTKNQTVQLDITAF LKT VKKNKHKFYPAFIHILARL MNAHPEFRMAMKGVPGGDSV KNTSRVWSGNERDQKLLTENA LNDLIPSFLTGTGQTPALGRRVS GVIEIADGSRRRKAALTESDY RVLVGELYDEQMPPLSRLGND YRPTSAHPQKRRYASRLQNEFA GNISALADAENISRVRDYNLLL EVLGVDSVEKTRVWSGNERD QELLMEDALDDLIPSFLTGTGQ TPAFGRRVSGVIEIADGSRRRK AAALTESDYRVLVGELDDDEQM AALSRLGNDYRPTSAYERGQR YASRLQNEFAGNISALADAENI SRKIIPRCINS\AKLP |
| 21665 | 52033 | A | 21793 | 1 | 935 | MLRDLLKNVDLKGFEVDVRIIL TKYSNSNGSQSPWMEEQIRDA WGSMLVKNVVRETDEVGKGQI RMRTVFEQAIDQRSSTDNEGAP VIPKHTLNTQPVEDTSLSTPAAP MVDSLIARVGV MARGNAITLP VCGRDVKFTLEVLRGDSVEKTS RVWSGNERDQELLTEDALDDLI PSFLTGTGQTPAFGRRVSGVIEI ADGGSSRSKKRRRGCEGGRR/V RQGCPDQKHAAFSVSGGKIHL SGRTPVEKRPRLPQPRDLGARA FAACRGSRGPRWNWLPAA LRL HADLGCVRGGGGGWPGANPY PAPASSTC |
| 21666 | 52034 | A | 21794 | 181 | 923 | QHAIVTGDVGMHHIPQEARQ YRHNQAYAYSIIQGDGAEDDDE RIVRFHTRCLTEAFEKLQCGGV VNQLSRRGNQHHISSTYDINRA DTQVRRAVNNYDIIVMSNSFN ASRSIRCGSVGSLPSSNLPINSVS IRCRAR/SG/EE*CQAPASKWAL LHK*HRPFQDRKAGECLLHEY EDLVPIRDTLRLFPGGRYLPRA KHVAPSEPDPQDEQKLRFCKR HLYGQQPRSPVEIRLQHVAIAY PTHAYD |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21667 | 52035 | A | 21795 | 178 | 798 | IRLEPFKINVLEQITKHIEKLQCG GVVKQLSRRGNNQHISSTYDIN RADTQVRRVNNYDIIVMSNSF N\ASRSIRCGSVGSLPSSNLPINS VSIRCRAR/SG/EE*CQAPASKW ALLHK*HRPFPQDRKAGECLLH EYEDLVPIRDTLRLFPGGRYLPR AKHVAPSEPDPQDEQKLRFCR RHLYGQQPRSPVEIRLELVAIA YQTHHA |
| 21668 | 52036 | A | 21796 | 499 | 972 | |
| 21669 | 52037 | A | 21797 | 3 | 1141 | SRVKLGQSSSQVAALKTREPM NIATLEVLVLKGLRVCFVKVNH PKGPAZMYPGWVPILYIHAEDP LLPFYLGEKEDVTYAIKPTCWP GLDIIPSCALPRIETELMGKFD EGKLPTDPLMLRLAIETVAHD YDVIVIDSAPNLGIGTINVCAA DVLIVPTPAELFDYTSALQFED MLRPLLKNVDLKGFEVDVRIIL TKYSNSNGSQSPWMEEQIRDA WGSMVLKNVKEFAGNISALAD AENISRKIITRCINTAKLPKSVV/ ALFSPGELSA\GDALQKAFTD KEELLKQQASNLHEQKKAGVIF EAEVITLLTSVLKTSSASRTSL SSRHQFAPGATVLYKGDKMVL NLDRSRVPTECIEKIEAILKELE |
| 21670 | 52038 | A | 21798 | 1 | 617 | LEPASLSIPNLLLHPRGLRAITIA VFGKQNTYIRLEPFKINVLEQIT KHIEKLQCGGVVKQLSRRGNN QHISSTYDINRADTQVRRVNN YDIIVMSNSFN\ASRSIRCGSVGS LPSSNLPINSVSIRCRAR/SG/EE* CQAPASKWALLHK*HRPFPQD RKAGECLLHEYEDLVPIRDTLR LFPGGRYLPRAKHVAPSEPILSC |
| 21671 | 52039 | A | 21799 | 181 | 953 | QHAIVTGDVGMDDIPQEARQ YRHNQAYAYSIGDGAEDDDE RIVRFHTRRLTFKINVLEQITKHI EKLQCGGVVKQLSRRGNNQHI SSTYDINRADTQVRRVNNYDI IVMSNSFN\ASRSIRCGSVGSLPS SNLPINSVSIRCRAR/SG/EE*CQ APASKWALLHK*HRPFPQDRK AGECLLHEYEDLVPIRDTLRLFP GGRYLPRAKHVAPSEPDPQDE QKLRFCRHLYGQQPRSPVEIR LQHVAIAYQTHHAYD |
| 21672 | 52040 | A | 21800 | 1 | 798 | |
| 21673 | 52041 | A | 21801 | 1 | 1782 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21674 | 52042 | A | 21802 | 666 | 1131 | KGRGTYGNERDQELLTEDALD DLIPSFLTGGQTPAFGRRVSGV IEIADGSRRRKAAALTESDYRV LVGELDDQMAALSRLGNDYR PTSAYERGQRYASRLQNEFAG NISALADAENISRKIITRCINTRQ LPKSVVGGFFSHPGELSARSGDA |
| 21675 | 52043 | A | 21803 | 1 | 3297 | |
| 21676 | 52044 | A | 21804 | 1 | 898 | |
| 21677 | 52045 | A | 21805 | 1 | 1977 | |
| 21678 | 52046 | A | 21806 | 1 | 1929 | |
| 21679 | 52047 | A | 21807 | 181 | 755 | QHAIVTGDAVGMDDIPQEARQ YRHNQAYAYSIIQGDGA\GMTM SALLDFIHGA***YIRCGSVGRL PSSNLPINSVSIRCRAR/SG/EE*C QAPASKWALLHK*HRPFPQDR KAGECLLHEYEDLVPIRDTLFL FPGGRYLPRAKHVAPSEPDPEQ DEQKLRFCRHLVGGQQRSPVE IRLQHVAIAYQTHHAYD |
| 21680 | 52048 | A | 21808 | 181 | 456 | QHAIVTGDAVGMDDIPQEARQ YRHNQAYAYSIIQGDGAEDDDE RIVRFHTRCLA*SRRVNNYDII VMSNSFNGQSEHQVWIGGQFT FIKFAH |
| 21681 | 52049 | A | 21809 | 1 | 780 | |
| 21682 | 52050 | A | 21810 | 1 | 1050 | |
| 21683 | 52051 | A | 21811 | 5 | 735 | PPAAP/MGNLLMARVGVKARG KAHYLPLLRGESVRKTSRVGSG NERDQELLTEDALDDLIPSFLT GGQTPAFGRRVSGVIEIADGSR RRKAAALTESDYRVLVGELDD EQMAALSRLGNDYRPTSAYER GQRYASRLQNEFAGNISALADA ENISRQIITRCINTAKLPKSVVAL FSHPGELSARSGDALQKAFTEK RTLKQQALTSEQKKRGI/YEAE EVSSSLSPQGRLSNRSASKDMY |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21684 | 52052 | A | 21812 | 1 | 887 | MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKETK AVGSGNERDQELLTEEAWNDL ILSFLTGTQQTTPAFGRRVSGVIEI PDGSRRRKAAALPKSDYRVLV GELDDEQMAALSRLGNDYRPT SAYERGQRYASRLQNEFAGNIS ALADAENISRKIITRCINTAKLP KSVVALFVSHPGELSARS GDALQ KAFTDKEELLKQQASNLHEQK KAGVIFEAEVITLLTSVLKTSS ASRTSLSSRHQFAPGATVLYKG DKMVLNLDRSRVPTEC/IEKIEA ILKELEKPAP |
| 21685 | 52053 | A | 21813 | 345 | 921 | RWRLQNLSCSSCSGSGSEGAT CFARGSA YELGQRYASRLQNA FAGKISALADAEIFSRKIITRCIN TAKLLKSVVALFVSHPVELSARS GDALQKAFTDKEELLKQQASN LHEQKKAGVIFEAEVITLFTSV LKTSSASRTSLSSRHQFAPGAT VLYKGDKMVLNLDRSRVPTEC IEKIEAILKELEKPAP |
| 21686 | 52054 | A | 21814 | 1 | 1989 | |
| 21687 | 52055 | A | 21815 | 6 | 311 | |
| 21688 | 52056 | A | 21816 | 3 | 848 | PGGDSVKNTSRVWSGNERDQK LLTENALNDLIPSFLTGTQQTTPA LGRRVSGVIEIADGSRRRKAAA LTESDYRVLVGELYDEQMPPLS RLGNDYRPTSAHPQKRRYASRL QNEFAGNISALADAENISRVRD VNLLLEVLGVDSVEKTFRVWS GNERDQELLMEDALDDLIPSFL LTGTQQTTPAFGRRVSGVIEIADG SRRRKAALTESDYRVLVGEL DDEQMAALSRLGNDYRPTSA YERGQRYASRLQNEFAGNISALA DAENISRKIIPRCINS\AKLP |
| 21689 | 52057 | A | 21817 | 1 | 969 | |
| 21690 | 52058 | A | 21818 | 1 | 1614 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21691 | 52059 | A | 21819 | 1 | 832 | MDDIPQEARQYRHNQAYAYSI QGDGAEDDDERIVRFHTRVTV DSDTLASDAARLTCRHGLARD VKFTLEVLRGDSVEKTSRVWS GNERDQELLTEDALDDLIPFFLL TGQQTPAFGRRVSGVIEIADGS RRRKAAALTESDYRVLVGELD DEQMAALSRLGNDYRPTSAYE RGQRYASRLQNEFAGNISALAD AENISRKIITRCINTAQLAKSG VALFSHPGELSAPSGDAL*KAF TD*EEFL*PQGSNLYEQKKAG\ VIFGS*KKFSLFLTSVV |
| 21692 | 52060 | A | 21820 | 678 | 1338 | TLRQTKPDNSAEIADGSRRRKA AALTE\SDYRVLVGELDDKQM AALSRLGNDYRPTSAYERGQR YASRLQNEFAGNISALADAENI SRKIITRCINTAKLPKSVVALFS HPGELSARSGDALQKAFTDKEE LLKQQASNLHEQKKAGVIFEAE EVITLLTSVLKTSSASRTSLSSR HQFAPGATVLYKGDKMVLNLD RSRVPTIEKIEAILKELEKPAP |
| 21693 | 52061 | A | 21821 | 1 | 1809 | |
| 21694 | 52062 | A | 21822 | 2 | 1010 | |
| 21695 | 52063 | A | 21823 | 284 | 2177 | |
| 21696 | 52064 | A | 21824 | 1 | 1296 | |
| 21697 | 52065 | B | 21825 | 1 | 1044 | |
| 21698 | 52066 | A | 21826 | 637 | 1073 | IRLEPFKINVLEQITKHIEKLQCG GVVKQLSRRGNNQHISSTYDIN RADTQVRRVNNYDIIVMSNSF NASRSIRCGSVGSLPSSNLPINS VSIRCRAR/SG/EE*CQAPASKW ALLHK*HRPFPQDRKAGECLLH EYEDLYPSVIH |
| 21699 | 52067 | A | 21827 | 1 | 2403 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21700 | 52068 | A | 21828 | 1471 | 3186 | LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFTPVI GVAAIKTGTTVHIVSSSSLLGG DHGPSRIGGLLLVCDYGPLVSS SGISGPTRIVGLIISLPGYHLCF RSDYRTGITDPLYIGDATIRVSL RVYSLPSRSRIEHVVANCGMIP KQQQNEKYQVPQFDQSTIKNIE SAKGLDVWDSWPLQNADGTV AEYNGYHVVFALAGSPKDADD TSIYMFYQKVGDNSIDSWKNA GRVFKDSDKFDANDPILKDQQT EWSGSATFTSDGKIRLFYTDYS GVMARGNAITLPCGRDVKYT LEVLRGDSVEKTSRVWSGNER DQELLTEDALDDLIPSFLTGTQ QTPAFGRRVSGVIEIADGSRRR KAAALTESDYRVLVGELDDEQ MAALSRLGNDYRPTSAYERGQ RYASRLQNEFAGNISALADAEN ISRKIITRCINTAKLPKSVVALFS HPGELSARSGDALQKAFTDKEE LLMQQASNLHEQKKAGVIFEA EEVITLLTSVAKTSSASRTSLSS RHQFAPGATV\LYKGDKMVLN LDMSR\VQLECLDRLHACRSTL |
| 21701 | 52069 | A | 21829 | 158 | 926 | AGPVIQNYVNTQPV/EETSYSTP AAPMVDSLIRVGVMAPGNAI TLPVCGRDVKFTLEVLRGDSVK KTSRVWSGNERDQELLTEDAL DDLIPSFLTGTQQTAFGRRVSG VIEIADGSRRRKAAALTESDYR VLVGELDDEQMAALSRLGNDY RPTSAYERGQRYASRLQNEFAG NISALADAENISRKIITRCINTAK LPKSVVALFSHPGELSARSGDA LQKAFTDKEELLKQGGSSRV GDNSIDSWKTRGRVL |
| 21702 | 52070 | B | 21830 | 1 | 3774 | |
| 21703 | 52071 | B | 21831 | 1 | 1495 | |
| 21704 | 52072 | A | 21832 | 556 | 1622 | |
| 21705 | 52073 | A | 21833 | 1 | 2616 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21706 | 52074 | A | 21834 | 1412 | 3310 | SVTSCLKVTSVCLTSAAASCRS VLMRSTAELQCASHTLRKRKA ARRLISLMMTARKARKITRRW RIGEAADLVGVSSQAIRDAEKA GRLPHPDMEIRGRVEQRVGYTI EQINHM RDVFGTRLRRAEDVFP PVIGVAAHKGNDPQGTASMYH GWVPDLHIHAEDTLLPFYLGEK DDVTYAIKPTCWPGLDIIPSCLA LHRIETELMGKFDEAQPNLGIG TINVVCAADVLIVPTPAELFDY TSALQFFDMLRDLLKNVDLKG FEPDVRILLTKYSNSNGSQSPW MEEQIRDAWGSMLKNVVR DEVGKGQIRMRTVFEQAIDQRS STDTSLSPTAAPMVDSLIRVG VMARGNAITLPVCGRDVKFTL EVLRGDSVEKTSRVWSGNERD QELLTEDALDDLIPSFLTGTGQQT PAFGRRVSGVIEIADGSRRRKA AALPE\SNYGVLVAELDDEQMP AYPRLGNDYRPTSAYERGQRY ATRLQNEFAGNISALADAENIS IITRCINTAKLPKSVVALFSPG ELSARSGDALQKAFTDKEELLK QQASNLHEQKKAGVIFEAEVI TLLTSVLKTSSASRTSLSSRHQF APGATVLYKGDKMVLNLD RSR VPTECIEKIEAILKELEKPAP |
| 21707 | 52075 | A | 21835 | 783 | 2371 | |
| 21708 | 52076 | A | 21836 | 3236 | 4718 | |
| 21709 | 52077 | A | 21837 | 1 | 2481 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21710 | 52078 | A | 21838 | 2450 | 3963 | LLTAPITGGIGTINVVCADDVMI VPTPAELFDYTSALQFFDMLRD LLKNVDLKGFEVDVRIILLTKYS NSNGSQSPWMEEQIRDAWGSM VLKNVVRETDEVGKAAPMVDS LIARVGVMARGNAITLPVCGRD VKFTLEVLRGDSVEKTSRVWS GNERDQELLTEDALDDLIPSFLL TGQQTPAFGQRVSGVKEIADGI RRRKAALTEASDYRVLVGELD DEQMAALSRLGNDYRPTSAYE RGQRYASRLQNEFAGNISALAD AENISRKIITRCINTAKLPKSVV ALFHPGELSARSGDALQKAFT DKEDLLKQQASNLHGAEKSW GCYFEAEVITLLTSVLKTSSA SRTSLSSRHQFAPGATVLYKGD KMVLNLDERSVPTEYRYGVFL NVLLPATKYFQLHDP SLRNMEL NYSLASEDLVLKGLRVLLVEG NDPQGTASMYHGWVPDLHIHA EDTLLPFYLGEKDDVTYAIKPT CWPGLDIHPSCLALHRIETEYNG |
| 21711 | 52079 | A | 21839 | 1573 | 2858 | EPVFEQAIDQRSSTDTSLSPTAA PMVDSL IARVGVMARGNAITLP VCGRDVKFTLEVLRGDSVEKTS RVWSGNERDQELLTEDALDDL PSFLLTGQQTPAFGRRVSGVIEI ADGSRRRKAALTESDYRVLV GELDDEQMAALSRLGNDYRPT SAYERGQRYASRLQNEFAGNIS ALADAENISQ*ICWKYFCAG*C GKYFRKIITRCINTAKLPKSVV ALFHPGELSARSGDALQKAFT DKEELLKQQASNLHEQKAGV ISPPEEVITLLTSEIKTSSASRTSL SSRHQFAPGATVLYKGD KMFIT VKIAKRSQAPCMKSNALIVIL GTVTLDAVGIGLVMPVLPGLLR DIVHSDSIASHYGVLLALYALM QFLCAPVLGALSDFGRRPVLL ASLLGATIDYAIMATTPVLWIY PLVNSPSC |
| 21712 | 52080 | B | 21840 | 63 | 368 | |
| 21713 | 52081 | A | 21841 | 189 | 204 | SLPSGIKPOSSSKASSRIQVAPT M*SLPRQPLAWSPGHEACPQG |
| 21714 | 52082 | A | 21842 | 153 | 370 | LIAGAFRKASGGNNIFRRPKTL* LRRQPR*PQKSTPRRNKLGHYA IHKFPLTTESAVK KIEETNTLVFT VLV |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 21715 | 52083 | A | 21843 | 842 | 1770 | CTPEKCLPAVHRRNWLRNAEPP VWKRHLSPICRKRQGRATKPK RRPWYTTPTTRRVRDVALRPYS RH/GRQPHAKKKIRMSLTFRRP KTLRLRRQPRYPRKSTPRRNKL GHYAIKFPLTTESAVKKIEENN TLVFTVDVKANKHQIRQAVKK LYDSVAKHTEERRHDEQNNIL TREAKNRNDNTRNRARTETNT ETQKNSGYQALISFHSYSDTS DNKAHLVSYQSGQCTYDRLG WNLLIRMTCRSLQHTYDIQSTQ IASCFHPVSVRVNRLRYCANYG GISAVFMPLRKELLILTRSSNSK VSQRLI |
| 21716 | 52084 | A | 21844 | 353 | 605 | EMAPKAKEAPAHPKAEAKAKA LKAKKAVLKGVRSHTRKKKIR MSLTFRRPKTLRLRRQPRYPRK STPRRNKLGHYAIKFPLTT |
| 21717 | 52085 | A | 21845 | 301 | 946 | PGSYLKPLSWTVALSRLPGFMS RWPCQRLTWQRRSVTQASGAS GASLCASRLPRDKTAPKAKEAP APPKAEAKAKALKPKKAVVER CPHTHAKKRIRMSPTFRRPKTL RLRRQPRYPRKSTPRRNKLGHY AIKFPLTTE\SAGKKNNKNNTP LVHCGC*RPTRHQ\IRQAVKK\L YDSVAVKVTTLICPDKEKKAY VRLAPDYDALDVANKIGII |
| 21718 | 52086 | B | 21846 | 12 | 115 | |
| 21719 | 52087 | A | 21847 | 1397 | 1489 | |
| 21720 | 52088 | A | 21848 | 519 | 747 | SGSVISPIAAT*YRIFAVL*SVQ* **AGPGDLSGDGELP*SVAIQPN VFIAVSSITCNWLPFGKCGSTY WMCQSM |
| 21721 | 52089 | A | 21849 | 185 | 456 | QHQPLeVASQWKVCSVSVKLL SQSSDVTRVPLEGLDRLSERSG SLSVL*SGILWALDAASQLVSL LP*LTRYHDP RVSSL/SSTYV*SP |
| 21722 | 52090 | A | 21850 | 789 | 1086 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21723 | 52091 | A | 21851 | 1 | 766 | SGRKEANYYGSLTQAGTVSLG LDAEGQEVFVPFSAVLPMVAP NDLVFDGWDISSLNLAEMRR AKVLDWGLQEQLWPHMEALR P/LGLAVYIPEFIAANQSARA\D N\LIPGSRAQQLEQIRRDIFRS SAGLDKIVLWTANTERFCEVI PGLNDTAENLLRTIELGLEVSP\ STLFVAVASILGGLCLSFNGSPQ NTLVPGALELAWQHRILVGGD DFKSGQTKVKSVLVDFLIGSL KTMSIVSYNHLGNNDGEN |
| 21724 | 52092 | A | 21852 | 2 | 2122 | WKSWMVFTAMKLVKAHRLK LRLKGYLPVTCLEGTRNQRIAA TIRHNRARGRHQITAMSEIVRE LSQLGWDDNKIGKELGMDSD VLRLKQINGLQELFADRQYSRA WTLKLAQAFSCCQQRFLGK TETNQFMWEGIGAKHRQRNRR YAVLLRQPLAKLNIIQARYPNQ HRQHAGECNPHCQAGGDIVDR CPARCFTKGDSKDGSPQATWP FHNSATMTAKRLSEASQCGSK KSILRERHIYRPSITRYPFQSTMN HPLPEQTLGCIATDYGSSPSPDR SPGPAHYWTDHSTANIRYQV AAEENGEYTYVERVKIPLDHGT LLIMERATQADWQLEQIRRDIFR SSAGLDKIVLWTANTERFCEVI PGLNDTAENLLRTI/D/RSV WEVSPSTLFVAVASILEGCAFLN GSPQNTLVPGALELAWQHRVF VGGDDFKSGQTKVKSVLVDLI GFRLQRP/SSIVSYNHLG\NNDG ENLSAPLQFRSKEVASRSNVVD DMVA\SNP\VLYTPGEEPDCV VIKYVPYVGDS*RAL\DEYTSEL MLGGTNTLV\HNTC\EDSL\A APIM\DLGAA*PSCCQRTFLA LDIGTPSRPFHPVLVPAQAFF KGATLSPPGKP/VLVNAAFSAS AAAIENILRACVGLPPQNHMLL EHKMERPGPSLKRVTWPLPP YPMLNKKGPGSRCQPMAPVD |
| 21725 | 52093 | A | 21853 | 1 | 1908 | |
| 21726 | 52094 | B | 21854 | 1 | 1833 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21727 | 52095 | A | 21855 | 1 | 749 | MFQLMKASSGGEAACMPAGL MENYKHTTVLLDEAVNGLNIR PDGIYIDGTFGRGLGEEGRLLA IDRDPQAIAV/AKTIDDPFRFSIH GPFSAIGEYVAERDLIGKIDGIL LDLGVSSPQLDDAERGFSFMRD GPLDMRMDPTRGQSAAEWLQT AEEADIAWVLKTYGEERFAKRI ARAIVERNREQPNPDEEEIEQA LKSSLNVLAPGGGVSIISFHSLE DRIVK/RFMREHQFCVVVRSGV GLKT*SVR |
| 21728 | 52096 | A | 21856 | 532 | 1418 | CFASGFIGELRKNIVGFIEQDHT RGLVFRLTPGRTLRAESLNLVIC LPMNFQPYDSDADWVITGVPF DMATSGRAGGRHGPAAIRQVS TNLAWEHNRFPWNFDMRERLN VVDCGDLVYAFGDAREMSEKL QAHAEKLLAAGKRMLSFGGDH FVTLP LLRAHAKHFGKMALVH FDAHTDTYANGCEFDHGTMFY TAPKEGLIDPNHSVQIGIRTEFD KDNGFTVLDACQVNDRSVDDV IAQVKQIVGDMP/VYLTLYNCG GPS*QFHSLRPAQSPLDRCRAR YLAPQCVPDFRTLQR |
| 21729 | 52097 | B | 21857 | 64 | 1842 | |
| 21730 | 52098 | A | 21858 | 1 | 503 | MRWLVSPIEDTGHKALLFACL ALHRACVSGHCLSPKCVGVDG RSHENVAPGLFLDWLLDGTGV WDGTSTNVEGAQEHAVLILLII TDGVISDMEETGMPWCRLPSCP CPSSSGRGQCGLRCHGVPGWG RRMLRSHTGEEAARDIVSSFPF ESSATMSEEVYDPRSLYERLQE QRTGSSRTARQEA VVGSKVTV SQPGHRQETT VLEHLVQY/FILL IITDGVISDMEE/TRHAVVQASK LPMSIII/VGVGNADFAAMEFLD GDA/GMLRSHTGEEAARDI/VQ FVPFREFRNNVRGGL*PSISI |
| 21731 | 52099 | A | 21859 | 2223 | 2363 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21732 | 52100 | A | 21860 | 3 | 693 | GDDGKWMLVHRTEVIKYTLDP VWKPFTVPLVSLCDGDMKPIQ VMCYDYDNDGGHDFIGEFQTS MSQMCEARDSVPLEFECINPK KQRKKKNYKNSGIIILRSCKINR DYSFLDYILG\GCQLHVSPGLID F\TASNG\DPDLPSSLHYINPMG TNEYLSAIWAVGQIIQDYDSK MFPALGFGAQLPPDWKVSHEF AINFNPTNPFCSGVDGIAQA\YS TCLPHIRFYGPT |
| 21733 | 52101 | A | 21861 | 1 | 2231 | MYSQEGNQFCNRTDCQELLPPP PAPMAHIPSGGAPAAGAAPMG PQYCVCKVELSVSGQNLLDRD VTSKSDPFCVLFTENNGRWIEY DRTETAINNLPASFKKFVLDY HFEEVQKLKFALFDQDKSSMR LDEHDFLGQFSCSLGTIVSSKKI TRPLLLLNDKPAGKGLITIAAQE LSDNRVITLSLACRRLDKKDLF GKSDPFLEFYKPGDDGKWMLV HRTEVVIKYTLDPVWKPFTVPL VSLCDGDMKPIQVMCYDYDN DGGHDFIGEFQTSVFKMCEAR DSVPLEFECINPKKQRKKKNYK NSGIIILRSCKVNQRGQARARG QVSGHTEGTDRALEDLEPARPVF KSRLCHILALWPSELHLTRPQSP HLWNGDINEAEHVQGYSSLTFL CGGQGRHELTFQGLSWWENCH CELLPPTVGMQGAEDIGWGHP VLSGISVTVTPMINRDYSFLDYI LGGCQLMFTVGIDFTASNGNPL DPSSLHYINPMGTNEYLSAIWA VGQIIQDYDRPRSFLKPDPWAG TEAVTGQHVMFVSVEYETHVEWG RQIGLPDVANQNTRHPVKFEFQ VSHEFAINFNPTNPFCSGVDGIA QAYSACLPHIRFYGPTNFSPIVN HVARFAAQATQQRATQYFILL IITDGVISDMEETRHAVVQASK LPMSIIIVGVGNADFAAMEFLD GDSPHAALPTRGRRQPRDIVQF |
| 21734 | 52102 | A | 21862 | 694 | 825 | QPGLSINIEAGAVPRPFARRYW GNLG*FLFLGVLCFSSPGSPH |
| 21735 | 52103 | A | 21863 | 1032 | 1127 | FYAKAEAGDRTVA*PHKPKMF LSIHHRVAKI |
| 21736 | 52104 | B | 21864 | 1 | 564 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21737 | 52105 | A | 21865 | 43 | 617 | PIIQKVRSHTPKRAPTACTYTVS GSFSLPSPGFFSPFPHGTGSLSVS QEYLALEEWSPHISARDCTCSG LLIELPSTGIFVYGAVTLYRAPF QTLPVTHALIQALGCSP\FARRY WGNLG*FLFLGVLRCSFSSPGSP H*PMDSVNDSVSKHT/EVSPFG N\PGYNGSYHLTDAYRRLARPS SPLTPGHPPLYG |
| 21738 | 52106 | A | 21866 | 2969 | 3593 | |
| 21739 | 52107 | A | 21867 | 1219 | 1503 | HFTDGQNNRQHGCQVRRQAG KQVVCKVEHQNQYNHRCVW* ESFQVRTHGTGEPVNKTRTSQA VSHHNQSCQVDQCVPCAVIAG NVFPRHNQVQGH |
| 21740 | 52108 | A | 21868 | 193 | 378 | |
| 21741 | 52109 | B | 21869 | 1 | 1473 | |
| 21742 | 52110 | A | 21870 | 3536 | 3926 | PKMVRWLARKCWNTVSTVRC FWMAMPTPVFAPCAAIKTASA R*MSWASSR*PNRGCVKSATLR QFS*VAAMK*PPVAQ*WWLGR NASTAGGDSGAGRSLDDGEPTP CGMGLEQKRHGNPAGCVAPSR WS |
| 21743 | 52111 | A | 21871 | 140 | 901 | MAMSKVKSITRESWILSTFPEW GSWLNEEIEQEQVAPGFTFMW WLGCTGIWLKSEGGTNVCVNL WCGTGKQSHGNPLMKQGQQM PPMAGVKKLQPNLRTTPFVLDP FAIRQIDAVLATHDHNDHIDVN VAAAVMQNCADDVPFIGPKTC VDSWIGWGVPKERCIVVKPGD VVQVTALEIHAPDAFDRTAPIT WLADQKRRRTVKG/MDDAPL* QVSYRPSTPPRCCYWSLLSSSV YYSKRPFAGHYARLCIPFMD |
| 21744 | 52112 | A | 21872 | 287 | 392 | |
| 21745 | 52113 | A | 21873 | 1 | 492 | |
| 21746 | 52114 | A | 21874 | 569 | 1061 | SGTVLDM/SEYSRVQIRKQPYLS KGYIPVRQKTKAAWLLKAVTFI DLTTLSGDDTSSNIQRLCYKAK YPIREDLLKALNMHDKVAAGF PAGQTHLKTRLEEIRLAVEDGA TEIDVVINRSLVLTGQWEG/LYS PVVYSALPCNI*HSRLFLPSGNA LLLWLWCLHS |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21747 | 52115 | A | 21875 | 2 | 1072 | ARSNIRMVTAFRSLPAGSSGAA RA\MSAHNRGTDLDSWISIKQ VNHPAVL\RRAEQIQARRTVK KDWQAAWLLKAVTFIDLTTLS GDDTSFNI*RLCYKAGYPIREDL LKALNMHDKGIT\TAAVCV\YP ARV\CDAVKGTSRPAG/CVNIPV GISRAAGF\PAG\QTH\LKTRLEE \RLAVEDGSLQKIDV\VINRSLG A*QAQWE\ALYDEIRQF\RKAC GEA\HLKTLA\TGELGTLTNVY K\ASMIAMMAGSDFIKTSTGKE TVNATFPVAIVMLR\AIRDFFWK TGNKIGFKPAGGIRSAKDSLAW LSLVKEELGDEWLK\PELFRIGA ST\LLSDIER\QIYHSCGLGRYGS LFMDLSQCL |
| 21748 | 52116 | A | 21876 | 3 | 221 | |
| 21749 | 52117 | B | 21877 | 49 | 342 | |
| 21750 | 52118 | A | 21878 | 1 | 828 | |
| 21751 | 52119 | A | 21879 | 1362 | 2405 | RPPWRHWDGNSSVLVHFQLHF LLRPLQTLSLGLEELLQRGIRA RLREHGISLAA YGTIVSAELKG GSRPCAVWWPSEPGAGRCPGN SFSCGNSQCVTKNPECDQED CSDGSDEAHCECGLQPAWRMA GRIVGGMEASPGFEPWQASLRE NKEHFCGAAIIN/DQPLRS*NHR FQDPTKWVAYVVRPTSAARRP APCGPSKKA/WISGWGYLK/EG LP*ASRPAMVKPEVLQKA/DW ELLDQALCASLYGHSL/TDRMV CAGYLDGKVDSCSVLFLFRGTI SFFFSEDRNLIRYVLLYSIFVVN CISGKPQPGPPVLRALCQHPHQI DAGPQYRASCWVTVPKLQGIF |
| 21752 | 52120 | A | 21880 | 600 | 904 | SVSLLDEETALPFSWDELRLSA LLDT*AAFQEIELAFQDPQCVG LLTAP/YADAAFGSTDIAMFLL VPILSARKPASPRSS*TFSHLATE PLPASIK*AAA |
| 21753 | 52121 | A | 21881 | 393 | 572 | |
| 21754 | 52122 | A | 21882 | 165 | 432 | PGMAVSYEKISKYPVEFLPAQA NIAGHNDAPEEREFPQW*LWLL LPNF*LQEKCSPTLCHFLSRRTQ SEFPSSTAAGNLSVSLLYPCKS |
| 21755 | 52123 | B | 21883 | 1 | 1011 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21756 | 52124 | A | 21884 | 783 | 1234 | YYRRCGAASPHGRDPVQIG*TS SQPR*SA YRN/PASVIPVARHSA RAPAILRP*VVVAERSERSIPGL RATPAEIRTTAPSSAGVASSPE KPLIFTAIDSHTGSHWSDIIHVC AKKLQNYVPKLNASLLLTPSIY VTRTTRSGPIPPARQ |
| 21757 | 52125 | A | 21885 | 249 | 398 | GYFDIFS YDTAIPGQSAEQDAR ED*AF*MPDRAYSQPCSSLVFP KGCKK |
| 21758 | 52126 | A | 21886 | 309 | 845 | CGAREERGRGCHHVHSQLRGP GPAPGQVQQPQLVPAPVPELP GLRGLSWQARRTRARHRQGQV QDHQPDPTVHAQLRGVQLGEA PLQLHHGD*DHRAP*GYFDIFS YDTAIPGQSAEQDARED*AF*M PDRAYSQPCSSLVFPKGCPVPG RGCAAGVQAAGAAHPPLDHPA LQPLQGR |
| 21759 | 52127 | A | 21887 | 1236 | 2100 | DLLCGRGCQGRRPRHLQPQTEL EAEVPAERPGRGPAVAARSDP RAQAEDVPGYNPLSGKPAKQQ VHEGHHPGAPGHRRPGGAAPV AGGPHRCLPAQPARPCGGAAEP RGGPAGAH*ARGSRAAGEGQP WWPSRLGAGPPAAPVHAAPG SHLLPGHHLPTQPSALAAAQ\PL AEEPREQ/PGAGGPQPGSPTLRG VEVVPLPHAAGGAGAVPVGGA ACPTAPHPAASAPAVLLSQLG TQHPPRRDPPHCSCAGIQDSGW AGPPALWSLLHVAKPAQARRP CALLHPGV |
| 21760 | 52128 | A | 21888 | 1931 | 2185 | AKAFSFFRYISRVSRTCLSR SMRRSFDSSNADAAFGST MFLLPILSARKPASPRSS*TFS HLATEPLPASIK*AAA |
| 21761 | 52129 | A | 21889 | 1254 | 1760 | |
| 21762 | 52130 | A | 21890 | 1 | 2001 | SIRRPKRARPIRIKKIPEQQG/PQ PAVLVPQTVATRDRELPM/P VGPETLKRDPVVRAMTIPATAA VYKPYWGATPLPIA\KPSPAG*Q *SRFSKGYFGFD |
| 21763 | 52131 | A | 21891 | 195 | 545 | HSPGSFYSSRRDAQSPAPAIRAA V*AEVQ*TPLCHDRITHFPEDW RGWQRS*F*PAACRVAGSLPVP VSPQIQHPYCRSSAQYLPAGAG LPLPGFDRLCPRSLFQGLAVTG GSCGPS |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21764 | 52132 | A | 21892 | 825 | 1299 | YSCRTEHPPRLATAEYRHHQRA ADAGR*RHAGVAFYPIKERYR QPEPAFSYQ/PRRWSASRNRPS R*RMRRFPANSSTPFPPAPPLRR KRVASLIGGRMLRLTGAGIAEE RMIAPQLPECILHELTERPHFPF LGIDLILTCGERLLAIPRTTHVE |
| 21765 | 52133 | A | 21893 | 1460 | 1810 | RATHVLTWVRGTPKRAEMILG SSRSMSAAAVTVLISPATAQRW ITRAP*PSPIRSPSVSRLTATRPSS ITKARALSPMAAPALRSTVTTTP PRITVEKPLLMEKIPRVPKSRAI SAL |
| 21766 | 52134 | A | 21894 | 231 | 704 | QSQKPDTRGRLFVAKAPPCVQR HKVRWLRLVMITSAHYLPLRR* *PAHPASGGCCPNRAKYTORPA E*ISYRPD*EAVR*SRAPAKVTQ SNPASRVALRRPAPRAVHQATII PVDESTLLPAPLAVSARQKVRQ AIPLRDSVRRPTLDVRHRATG L |
| 21767 | 52135 | A | 21895 | 1291 | 1925 | RQLLRWSNR*IAR*SLTQPARRF PAYHYAHPAAAAAPGDPLGAD LQLCARHYHRQRHCVPRHAGY PRSDGLHPQPRGRWRIRCSACL RVPF |
| 21768 | 52136 | A | 21896 | 1 | 445 | MFISGLDDFFIDVVYVWRRIKR KLSVYRRYPRMSYRELYKPDE KPL/DDYGSGVE*NGRHRQYGR AGGDHARLRKLSYLCWHLRQR PRYSA*C*RSVRSLEPCA*GSLR ASWP/HPAKPTV*TTCTWTPSPN LSVAPISLLLVLFCMTPKM |
| 21769 | 52137 | A | 21897 | 79 | 377 | SRKSGISIGAVKRPTH*GS*KAR SIC*NAAVYSKKAESLSSFPEKS ESTQRVKAVLSS**ASQCGDT AQYVLLSFKGSQQA*QVCGR* KAY**DLSRE |
| 21770 | 52138 | A | 21898 | 1282 | 1535 | GSTYEIASATPSPSAKPSNRSPSP MSRPQSNPKPNSLHSC*P*GNL RSTPESGK*ATPPPPAYTLVLF KLANPQLPEESPWAF |
| 21771 | 52139 | A | 21899 | 3775 | 4031 | CRRTAASRTPRKRTQTAPTHAT NKPQKPQTSTDRGNRREPEKTE PS*HLRPNPQEPGRRGQTQQEP APRHQPPKPQGEPTTPQKQ |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21772 | 52140 | A | 21900 | 1 | 2595 | MESHTVTDYNFGRLLNESFAN CETDRNYLGIFKCGFWLSGTRK SAFLTKSQVTLTRPVDHTLRNE VLGSTKYQVPGYRRKTNTNLE ESNVLIGYDVAPGGGKQIDGKK AEGRELMVPVAGRPLCRSSSM ELLLLLPLHIPREQMLLADAYW NLHQSCQSKTSPDTAKCPLDRC PRVFKSQSYKASTFDGLSMDTE VIKSNGKQGWRQRRLANMKDI DKQTQAATFVLSQGMQRSGND RIILVTGASDGIGREAAMTYAR YGATVILLGRNEEKLQRVASHI NEETGRQPQWFILDLLTCTSEN CQQLAQRIAVNYPRLDGV LHN AGLLGDVCPMSEQNPQVWQD VMQLFRAGIINADPGAFFVTGF RRYCCFTLCCRSFRFGFYRRRF RHRSCRQRAMRHSGTGQGQGN EQCFNSVFHTVFSLFVNSGITLT AVKTVNKWQCSEMEKAAKAT FSCYSCNAFFCEAASGLLLFQRI ANFDRLFTQVTHQSFKDDLGI KMETTKPSFQDVLEFVRLFRRK NKLQREIQDVEKKIRDNQKRVL LLDNLSDYIKPGMSVEAIQGIIA SMKGDYEDRVDDYIINKNAELSK ERRDISKKLKAMGEMKNGEAN RKERSMFRDRPLKRMKSKRD DDSYDEDVEDDEGVGEVRVHR VNHAPANAQEHEAARPSQHQ YQPPYASAQPRQPVPQPPEAQV |
| 21773 | 52141 | A | 21901 | 1 | 96 | |
| 21774 | 52142 | A | 21902 | 105 | 430 | ASIFVMLVRGAEPMEKRQQRG LFTVPGLLLAFCSHVLSCVNPLI PVDNPPYYPPLSELIPAPPQNDR AQRVSERGSGRAPNTQTASPR LADSLMQLAR/QVSRLESGQ |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21775 | 52143 | A | 21903 | 843 | 2055 | HHRMAQNLSRYGNDKRPEESQ FRVVNVKPVTLTYDVAEYAGVS YQTVSRVVNQASHVS\AKTREK \VEAAMAELNYIPNRVAQQLAG KQSLIGVATSSLALH\APSQIV AAIKSRADQLGASVVVSMVFR SGLVACHTAPHNLL\ARKRGPA GLIINYPLDD\QDATAVEA\ACT NVPALFLDVSDQTP\NSIIFSHE DGTRLGVEHL\VALGH\QQI\AL LAGPLSSVS\ARLRLAG\WHNFL TGN\QIQPIA\ER\EGDWSAMSGF QQT\QLQMLNEGIVPHWRLLVAQ RSRMALG\AMRRHYPESGLRV GADILRVGGNTTIPED\SSCYIP AL*PPIKQDFRLLGA/QTSVDR\L LQLSQGQAVKGM\QLLPVSL\V KRKTTL\APNTQTA\SPRALPRF H*MQLA\RQVSRLESGQ |
| 21776 | 52144 | A | 21904 | 1 | 1201 | |
| 21777 | 52145 | A | 21905 | 1 | 492 | |
| 21778 | 52146 | A | 21906 | 646 | 934 | |
| 21779 | 52147 | A | 21907 | 1 | 1713 | MLCTKWDLGLEKNAGKNKN AYKWYGW PANAPDEPHIEQLV GECRVMRQLKRLISRIAPSPSSV MVVGESGTAIPVVSHAFFKGGF ADIGVHYLDWTSRTTEKSSTKS HKDDFGYLEFEGGANFSWGEM YGFFDWENFYNGRHNKPGSEQ RYTFKNTKPYLSWVDTGFSLYL HAYGTYGSANRVNFLDDMFL AGFGFQF*PAGGW/WGSNPFFA K\RYTRSKPYT\GDNGYV\AG WVAGYNFMLGSEKFTLTNWN EYEFDRDATYAADFLPLYDVD CQDNGNLEYDTYSQPEWKHNL FDHYLA VLYRFKDESGKEQFSG AVVKTREATPGKEIEAITRML DFSPRLKKLADCPSPRPVFEALC ICSM LDALLLCPLDYHASCDN YSYALLDPQGFPLPHRRLWGPY IDVDVPMLHLIQHAWAQDALL SCLYSDLLYMSSFPYPAGTLTR LMGVTSYNHKNTLLTYCITLMS TIRFAYDGDDEEIAMKYTDFLKG ELSMNIRPLHDRVIVKRKEVET KSAGGIVLTGSASAKSTRGEVL AVGNRILENGEVKPLDVKIGD IVFFNDGYRGEI |
| 21780 | 52148 | A | 21908 | 2060 | 2404 | |
| 21781 | 52149 | B | 21909 | 1 | 1377 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21782 | 52150 | A | 21910 | 52 | 1719 | IGQVVVDVDTCTFTRIHLVFNFD NDTGSIHVLNDTTTFSYRSYTG VNGNSTFHTSTNQRLISAQSRN GLTLHVRTHQCTVGVVVFQERD QGRTDGYHLLGGYVHVNLV AAEQAGFAFATASYQVFYEVA FFIQVGVRLGDNVVAFFDSRQV VNFVSYNTVGHFTIRSLKEAVF VSLCVHGQRVDQTDVRTFRGF DWTDATVVSRYVVSNEACTF TGQTAWAECGDTTFVRNLRQR VVLVHKLRQLAGTEELFHCCG SQDPQQPWGWNLRVNPLAQT GHAHEAQRKQWHKGNEEADD PEPERAFTPGFVQFETERFRPPV GHPCEAAEDHAADDHVMEVR NQEQAVMQNEVRARYGQQA SHPAHREGDDKTDGPQHRRME HDAALIHGEQPVEDLHPGRDG DNHCGDTKEGVYVRARTHRKE VVQPNDERQHGD TDGCPYQRG ITKQFTTREGCRNFGEHTENRQ DQDVNFRVAPGPNQVDVHHH VATHIVGKEMGAQIAIQGQHAT YRQNGKDL*SNRGVASGNPQC RHRAHRRATDCQTVIKQPVFFG |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21783 | 52151 | A | 21911 | 608 | 2508 | YITATSCSGWMIRWCAKAAKCA/CSRGPGGKLR RHKGAEETL CGNTRVLIAPQLPAVIAATLSGS RSQTGRREGPTPTTVMIQDHTG SSTDDECSANVQRIFNRIMLC SI VSRPRTIPFHDLAQSFRQFRNVK CLWCAFEQAQLMRIQPAIVMV KTIHRERLNSGQFRCHQEARNI PPHRQSRFLASRGLLAELMFML YGIGELPEIVTLPKEIRGNVDNS RHAVFLANSMPPELRFIRTHGS RFTSQDCTLFNWLARIITPVLQS WLNDEEQQVALRLLEKDRDHH RVLVDITNAVLSHLDLDDLIAD VAREIHFFGLASVSMVLGDHR KNEKFSLWCSDLSASHCACLP R CMPGESVLLTQTLQTRQPTLTH RADDLFLWQRP LLLLLLASNG CESALLIPLTFGNHTPGALLAH TSSTLFSEENCQLLQHIADRIAI AVGNADAWRSMTDLQESLQQ ENHQLSEQLLSNLIGIGDIYQSQ AMEDLLQQVDIVAKSDSTVLIC GETGTGKEVIARAIHQLSPRRD KPLVKINCAAIPASLLESELF GH DKGAFTGAINTHRGRFEIADGG TLFLDEIGDLPLELQPKLLRVLQ EREIERLGGSR TIPVNV RVIAAT NRDLWQMVEDRGVI |
| 21784 | 52152 | A | 21912 | 147 | 2699 | MTIRAICSCCPLPDA*NVLM* IY MSTFQASGNGQQLQIARIVIQNI TG |
| 21785 | 52153 | A | 21913 | 432 | 1016 | FCPSSCLAATAPAA*AGWSFLP SPAEQNRWRFP LSRFCQIPAPL/ LGTLIISLSVFCSILAASAAEIPG SVDGIYNKSPSLI\WVKIPRQLY *AAREPSAPKAPPPAAWFSASA VLSATA\MINTNQKAIERVTAFR RNFATDPVAHQDRDHYDRQQR RTRHRIRFGERQRAKQTPFLPFQ GEDRDKRQRDNQQQTDK |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21786 | 52154 | A | 21914 | 1 | 1146 | MTTSM LNAKLLPSAPSAAVVV VRVVVVVGNAPTSRKVGPEEK DWSMASSGTTSTRKRFTGAEFI VHFLEQ/PGH*DCDRHSG/S/CSI LPVYDALSQSTQIRHILARHEQ GAGFIAQGMARTDGKPAVCMA CSGPGATNLVTAIADARLDSIPL ICITGQVPASMITGDAFQEVDT YGISIPITKHNYLVRHIEELPQV MSDAFRIAQSGRPGPVWIDIPK DEQTAVFEIETQPAMAEKAAAP AFSEESIRDAAAMINAAKRPVL YLGGGVINANARVRELAEKAAQ LPTTMTLMALGMLPKAHPLSL GMLGMHGVSTNYILQEADLLI VLELAGVQTVDDTNASKPAS ATRHIAFQVTIGCDRNLADSV VFPHSVDDIGKVAA |
| 21787 | 52155 | A | 21915 | 1001 | 1037 | MVGMASSCMPAFTRLELYSVIS QSTQIRH/ILARHEQGAGFIAQG MA/RTDGKPAVCMACSGPG/AT NLVTAIADARLDSIP/LICITGQV PASMIGTDA/FQEVDTYGI/STM TLMALGMLPKAH/ALSLGMLG MHGVRSTNYFCQEADLSIVLG ALFDAGQIGKTSSFCPNAKI/IH VDIDRAE/REFPCPIPKACDLS H/YGLINAVAACVDDNAIITD VGQHQMWTAQAYPLNRPRQW LTSGGLGTMGFGLPAAIGAALA NPDRKVLCFSGDGLMMNIQ* MIIAIPITGVKIFNWCSPCIRPHR VPFCDAVAIGFIVTFSDVIQIASI YEIPCRDPTGVASTEYSSSSCRR RRNTTLCDPGSPAQRQSPQAGQ NPSCPAHRRSATGVGD |
| 21788 | 52156 | A | 21916 | 135 | 449 | |
| 21789 | 52157 | A | 21917 | 5 | 214 | |
| 21790 | 52158 | A | 21918 | 2 | 337 | IGIAKHAQQLLLNVMQTRAVG AEVQTVSATGSAVRQALANNL QPFAIFFQINA/W**RAGRYPDD HGISPETALYGWHTSATGTAG MR*SVRPWLQSGQGCSGWRRQ QPRWSP |
| 21791 | 52159 | A | 21919 | 1 | 774 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21792 | 52160 | A | 21920 | 2 | 914 | RHIRTPAHLERFIVDIALNVADG HRAKLIVQSAGTFAQTVLRADS SANFRQGVGLVRQFRFRKNTPL VGELQPV RDVVVYRAFPLAVW VAARQAAVSLRFGLAFGKRLV NFNKLNFADLQRFLWRINAAQ LSCATTT/ADPAVLLHHWTSV* PAQI*WR\S*PVRQNLFTALRAG MLHMLGDKTTQMLFMDRQSV NA*DLDQFRVNAFAEIAAFIEN VSETAGHARTEVNAGFTQNAD DTTRHIFTTVVANAFYHGDSTG VTHAETFTRAACGIQTTTGRAI QAGVADNACFMAAEGGTNRR TNGD |
| 21793 | 52161 | A | 21921 | 204 | 371 | PGPAGAQSAALYRWSPGQAVS RADWFRFADC*IYPENRRNAGS AYRPRLSPAYCG |
| 21794 | 52162 | A | 21922 | 2664 | 2970 | TPDTAPAGCRSRAPDGPSPRQ MPRRRG*FHTARYCRTPRAITA *R*TE*STCPARTGEWYAHARY APGTSRQTATMPPTMPRRRASS YSSTQPDGRRQNC |
| 21795 | 52163 | A | 21923 | 318 | 459 | |
| 21796 | 52164 | A | 21924 | 577 | 888 | TNSSNQQLAEGNRERLIGRNTA GPERITAGRRL*LFSCQNRPCGW RFNKCHIGMPVVVIWRIIVMGI QHDDLVPFGRVNRVNMQF AKTLGQRALLLRNSLIA |
| 21797 | 52165 | A | 21925 | 3 | 711 | AGAHSGPSHPALATTAARQSV AGNRSGISGFSGHSRNPTRMSA RCL*SSALERLMRRLNGGEIQI SDVTTTTPS\LPQVYCSAMSRN LCTRATPRWQSAGHPYCRWTA SYCAIYSDRSIRGNYSTQSFAS GRRV\PTGSWQKTESEKDCSTC CANWANDRTPLPTSTSSANCST NVQTSVVPVLRRWIWLTSLRV VLTVSLKSV CARGTSPQASCWF VKRAASSATSPVVITTC |
| 21798 | 52166 | A | 21926 | 244 | 535 | TRYPDDHGISPETALYGWHTSA TG TAGMR*SVRPWLQSGQGCS GWRRQQPRWSP**RSC**CSVY PATL*FCRLYNQTS GPGHSDLP AFPDSDRRKI |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21799 | 52167 | A | 21927 | 869 | 2923 | PKKDLKIATSAMMEAAYSV*SR TLFW/SPVRDSQVTDQTQWQGL MSQLRLQGFDLVLQWTRYGD AFTQPEQRTLLFKRAAAQA GLKLIVGLNADPEFFMHQKQSS AALESYLNRLLAADLQQARLW SAAPGITPDGWYISAEIDDLNW RSEAAQPLLTWLNNAQRLISD VSAKPVISSFFAGNMSPDGYR QLLEHVKATGVNVWVQDGSG VDKLTAEQRERYLQASADCHD GAAPHGK\VFKLIIA*RARR |
| 21800 | 52168 | B | 21928 | 72 | 690 | |
| 21801 | 52169 | A | 21929 | 1 | 2241 | |
| 21802 | 52170 | A | 21930 | 1607 | 1893 | NKRIFPSDVKVAEPDHSCV*SFR IGSLASNLSSLKTRPAFFQLLIK HVD/SMCHQRLSGSRKSKHNVI AVVFSYCSVSVFSASCPHQVL LQTQYF |
| 21803 | 52171 | A | 21931 | 1 | 3960 | |
| 21804 | 52172 | A | 21932 | 1 | 1281 | |
| 21805 | 52173 | A | 21933 | 1 | 1491 | |
| 21806 | 52174 | A | 21934 | 1 | 1254 | |
| 21807 | 52175 | A | 21935 | 1 | 723 | |
| 21808 | 52176 | A | 21936 | 740 | 880 | NKRIFPSDVKVAEPDHSCV*SFR IGSLASNLSSLKTRPGFFPTVN |
| 21809 | 52177 | A | 21937 | 1 | 1191 | |
| 21810 | 52178 | A | 21938 | 1033 | 1248 | |
| 21811 | 52179 | A | 21939 | 1 | 1425 | |
| 21812 | 52180 | A | 21940 | 1 | 2784 | |
| 21813 | 52181 | A | 21941 | 676 | 1467 | |
| 21814 | 52182 | B | 21942 | 1 | 3288 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21815 | 52183 | A | 21943 | 145 | 1929 | VSGVIEIADGSRRRKAAALTES DYRVLVGELDDDEQMAALSRLG NDYRPTSAYERGQRYASRLQN EFAGNISALADAECDNLKTCHT SHGSVMAETA VINHKKRKNSP RIVQSNDLTEAAYSLSRDQKRM LYLFVDQIRKSDGTLQEHDGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEEDAG DEKGYESFPWFIK/RPSRGLYSV HINPYLIPFFIGLQNRFTQFRLS ETKEITNPYAMRLYESLCQYRK PDGSGIVSLKIDWIIERYQLPQS YQRMPDFRRRFLQGFCRFRNH HQTGFSPAGANQRGPLAATLSG PGGEGQSAVARLTGEKKNHPG AQYANRLSPRVGRFINAAGTTG FPTWKAGSERNAINDDVTYAIK PTCWPGLDIIPSCALHRIETEL MGKFDEGKLPTDPHMLRLAIE TVAHDYDVVIDSAPNLGIGTIN VVCAADVLIPTPAELFDY TSA LQFFDMLRDLLKNVDLKGNSN GSQSPWMEEQIRDAWGSMVLK NVVRETDEVGKGQIRMRTVFE QAIDQRSSTGAWRNALSIWEPE CNEISIGVSLDQDGGSNSVLRK |
| 21816 | 52184 | A | 21944 | 1790 | 2947 | TDFSVRCKGCRTGPFLRLIFQDR IVGVELIAVF*NTGPRFSSCRLS WRRPFDKTCRMRWHQRLSGFP QEQNDGKQQPILC |
| 21817 | 52185 | A | 21945 | 1 | 888 | |
| 21818 | 52186 | A | 21946 | 252 | 1863 | RKNPFILH*LFR*TLRQTKPDDS AGKGVKI**HTQNQRSGRSQND F*RRLW |
| 21819 | 52187 | B | 21947 | 1 | 1794 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21820 | 52188 | A | 21948 | 138 | 341 | PNPRGLLNTITPEHFKSKLHIPT TYRQSNGITASHYSYARN*RVG VMARGNAITLPVCGRDVKFTL EVLRGDSVEKTSRVWSGLLELL KAAASLVFLEQHKPYEEIGTSF GSVLVSVVGEGPFVEEDLRKSF PGRWDKKHKMFDAIEEPKKDS DKFDANDPILKDQTQEWGSA TFTSDGKIRLFYTDYSGKHYGK QSLTTAQVNVSKSDDTLKINGV EDHKTIFDGDGKTYQNVQQFID EGNYTSGDNHTLRDPHYVEDK GHKYLVEANTGTENGYQGEE SLFNKAYYGGGTNFFRKESQKL QQSAKKRDAELANGALGIIELK YDYTLKKVMKAADHFQTPVTD EIERANVFKMNG |
| 21821 | 52189 | A | 21949 | 761 | 916 | NKRIFPSHVKVAEPDHSCV*SFR IGSLASNLSSLKTRPAFFQLSIE LSPT |
| 21822 | 52190 | A | 21950 | 1 | 1437 | |
| 21823 | 52191 | B | 21951 | 50 | 1690 | |
| 21824 | 52192 | B | 21952 | 1 | 1032 | |
| 21825 | 52193 | B | 21953 | 1 | 1974 | |
| 21826 | 52194 | A | 21954 | 878 | 1202 | SVYNKRIFPSDVKVAEPDHSCV *SFRIGSLASNLSSLKTRPAFFQ LSIE\FRRPFDKTCRLMCHQRLS GFPHEQTQRDSTCIQLLFRQRF AAASCPHQVLLQTQYF |
| 21827 | 52195 | B | 21955 | 7 | 1702 | |
| 21828 | 52196 | A | 21956 | 527 | 665 | NKRIFPSDVKVAEPDHSCV*SFR IGSLAFNLSSLALKTPARVFSTVD |
| 21829 | 52197 | A | 21957 | 469 | 687 | |
| 21830 | 52198 | A | 21958 | 2 | 1018 | EGSDSRAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDNSIDSWKNAGRVFKDSD KFDANDPILKDQTQEWGSGATF TSDGKIRLFYTDYSGKHYGKQS LTTAQVNVSKSDDTLKINGVED HKTIFDGDGRKTYQNGQQFIDEG NIPPATPYAERPYYFEDKGLKY LGKPTVEPSVCGGRLESPWQTA GVSPTVQKLKSLKFDVARGQES VWEKDEAALANWTPNHTCD NLKTCHTLHGSMVAETAVFNP KKLKNSPRIVQSNHLI |
| 21831 | 52199 | B | 21959 | 7 | 1113 | |
| 21832 | 52200 | B | 21960 | 1 | 1188 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21833 | 52201 | B | 21961 | 1 | 1414 | |
| 21834 | 52202 | B | 21962 | 1 | 1515 | |
| 21835 | 52203 | A | 21963 | 1652 | 1916 | RKNPFILH*LFR*TLRQTKPDNS AGKCVKI**HTQNQRSGRSQND F*RR |
| 21836 | 52204 | A | 21964 | 1 | 1353 | |
| 21837 | 52205 | A | 21965 | 1 | 1507 | MAAQDAMVTRTSSQTDCKEPG LKWAGVVLMLLLCWLMFQVL WEACQKKTGEHKTMLQMILCN KSYQQLRLVITPMYMLGDWL SKNCGQNSTPSLGDNPPTQTQ EWSGSAFTSDGKIRLFYTDYS GKHYGKQSLTTAQVNVSKSDD TLKINGVEDHKTIFDGDGKTYQ NVQQFIDEGNYTSGDNHTLRDP HYVEDKGHKYLVFEANTGTEN GYQGEESLFNKAYYGGGTNFF RKESQKLQQSAAKKRDAELANG ALGIIELNNDYTLKKVMKPLITS NTVTDEIERANVFKMNGKWYL FTDSRGSKMTIDDLHIHAEDTL LPFYLGEKDDVTYAIKPTCWPG LDIIPSCALHRIETELMGKFDE GKLPTDPHMLRLAIETVAH*P AEK*HQNHSSPF*PRFFAVSLRT GSSYHCILSSH |
| 21838 | 52206 | A | 21966 | 729 | 843 | NKRIFPSDVKVAEPDHSCV*SFR IGSLASNLSLLINM |
| 21839 | 52207 | B | 21967 | 1 | 1416 | |
| 21840 | 52208 | A | 21968 | 1 | 1794 | |
| 21841 | 52209 | B | 21969 | 1 | 1171 | |
| 21842 | 52210 | A | 21970 | 1108 | 1250 | NKRIFPSDVKVAEPDHSCV*SFR IGSLASNLSLSLKTRPGGASRVP K |
| 21843 | 52211 | A | 21971 | 1 | 2535 | |
| 21844 | 52212 | A | 21972 | 743 | 898 | NKRIFPSDVKVAEPDHSCV*SFR IGSLASNLSLSLKTRPAFFQLSIE LSAT |
| 21845 | 52213 | B | 21973 | 1 | 1605 | |
| 21846 | 52214 | B | 21974 | 1 | 1873 | |
| 21847 | 52215 | B | 21975 | 1 | 2946 | |
| 21848 | 52216 | A | 21976 | 1419 | 1498 | |
| 21849 | 52217 | A | 21977 | 1 | 2314 | |
| 21850 | 52218 | A | 21978 | 1 | 1215 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21851 | 52219 | A | 21979 | 1 | 1851 | PWISAPVPVDVVEGAMDSVTV LSFGGLMLYFCAGWPPARRWC FPESISCGSMERDQWWGLQVA KRAGLAGGQSGRTVLRERVRIE IASTHIALAARHSDWRCCRNGR YPARGPAALQNFQRYTGIQHV HRIGMAERMWCDNRNRERTVS SSGGNRLPNPGPDRSCDNLKTC HTSHGSVMAETA VINHKKRKN SPRIVQSNDLTEAAYSLSRDQK RMLYLFVDQIRKSDGTLQEHD GICEIHVA\KYVEIF\GLPFAEAS KDIRQALKSFAGKEVVFYRPEE DAGDEKGYESFPWFIKRAPSPS KGLYSVHINPYLIPFFIGLQNRL TQFRLSETKEIPNPYAM/RLYTN TLCQYRKPDGSGIVSLKIDWIE RYQLPQSYQRVWTPGINCPEPC PGVWTPGINCPGAWGIHGPFGS AENTGPLHPGQTS AQLETSLP SLRSARELELAQLSPRRKQNR LQNIGVTPSLRVPWPKASNVQQ FIDEGNYTSGDNHTLRDPHYVE DKGHKYLVEANTGTENGYQG EESLFNKAYYGGGTNFFRKESQ KLQQS AKKRDAELANGALGIE LNNDYTLKKVMKPLITSNTVTD EIERANVFKMNGKWYLF TDSR |
| 21852 | 52220 | A | 21980 | 3197 | 5376 | |
| 21853 | 52221 | A | 21981 | 543 | 5690 | RKNPFILH*LFR*TLRQTKPDNS AGKCVKI**HTQNQRSGRSQND F*RRWSRSY |
| 21854 | 52222 | A | 21982 | 2241 | 2614 | ETLTTLKTKAINTLYSKPTREQ KTDTKAKNLYLTKRTTAAART SSVKKAISFNRA LKNAMLS*RT APSVS*IRHRV*NL TMRSSSSA PSPWML*A*AWLCRYCRASCGI SSIPTASPV TMAACC |
| 21855 | 52223 | A | 21983 | 31 | 892 | |
| 21856 | 52224 | A | 21984 | 548 | 855 | |
| 21857 | 52225 | B | 21985 | 1 | 1825 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21858 | 52226 | A | 21986 | 1 | 3146 | MEWGKFKRLVLP SQGKSKPEQ RCQYRHTVGDQATLPLRSRVE KRNGEAEGRIRKLWDVALLC CVQEVINGERKPLRALTEVKSG FRLREDSKFDANDPILKDQTQ EWSGSATFTSDGKIRLFYTDYS GKHYGKQSLTTAQNVOQFIDE GNYTSGDNHTLRDPHYVEDKG HKYLVFEANTGTENGYQGEES LFNKAYYGGGTNFFRKESQKL QQSAKKRDAELANGALGIIELN NDYTLKKVMKPLITSNTCDN |
| 21859 | 52227 | A | 21987 | 1 | 3107 | MNEMKREEKFREKRRENEQI LQEIRDYVKRSNLHLIGVSKSD GENGTELENTLQDHIQENFPNLA RQANIQIEIQRMQLQRYSSRRTT PRHIVRFTKVEMKEKMLRAAR EKGRVTHKGKPIRLTADLSAET LQATKEWRPIFNILKEKNFQPRI SYPAKLSFISEGETKYFTDKQM LRDFVTTRPALKELLKEALNME RNNRLVKSLAWASQNGFRSPA LLPLSLMLCAPLQEADGTNLG WLAHCGLLCTGDH |
| 21860 | 52228 | B | 21988 | 239 | 2825 | |
| 21861 | 52229 | A | 21989 | 7533 | 11119 | |
| 21862 | 52230 | A | 21990 | 1 | 3718 | MEVIPEGYRLSELKKCSKWIVV MVARLYEYTKNQIIHLKWVN HMLGCLLDRNDPLRDVDEAAV PVLICISADDPVCGPPDHTLTTE LFHSNPYFFLLLSRHGGHCGFL RQEPLPAWSHEVILESFALTEF FRTEERIKGLSRHRASFLGGRRR GGALQRREVSSSNLEEIFNWK RSYTRLMAAAAGAAAAPGSRE PQDRPECGAGHPGPRYYRHPER WLLRPEAFLGPLRTRAPSAEDS QREPAARSGPEM |
| 21863 | 52231 | A | 21991 | 1 | 697 | |
| 21864 | 52232 | A | 21992 | 1 | 978 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21865 | 52233 | A | 21993 | 145 | 1929 | VSGVIEIADGSRRRKAAALTES DYRVLVGELDDEQMAALSRLG NDYRPTSAYERGQRYASRLQN EFAGNISALADAECDNLKTCHT SHGSVMAETAVINHKKRKNSP RIVQSNDLTEAAYSLSRDQKRM LYLFVDQIRKSDGTLQEHGIC EIHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRPEEDAG DEKGYESFPWFIK/RPSRGLYSV HINPYLIPFFIG\LQNRFTQFRLS ETKEITNPYAMRLYESLCQYRK PDGSGIVSLKIDWIERYQLPQS YQRMDFRRRFLQGFCRFRNH HQTGFSPAGANQRGPLAATLSG PGGEGQSAVARLTGEKKNHPG AQYANRLSPRVGRFINAAGTTG FPTWKAGSERNAINDDVTYAIK PTCWPGLDIIPSCALHRIETEL MGKFDEGKLPTDPLMLRLAIE TVAHDYDVIVIDSAPNLGIGTIN VVCAADVLIPTPAELFDYTSA LQFFDMLRDLLKNVDLKGNSN GSQSPWMEEQIRDAWGSMVLK NVVRETDEVGKGQIRMRTVFE QAIDQRSSTGAWRNALSIWEPE CNEISIGVSLDQDGGNSVLRK |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21866 | 52234 | A | 21994 | 1184 | 2229 | RSSVATVALLHAVINHK/KRKN SPRIVQSN DLTEAAYSLSRDQK RMLYLFVDQIRKSDGTLQEHD GICEIHVAKYAEIFGLTSAEASK DIRQALKSFAGKEVVFYRPEED AGDEKGYESFPWFIKRAHSPSR GLYSVHINPYLIPFFIGLQNRFT QFRLSETKEITNPYAMRLYESL CQYRKPDGSGIVSLKIDWIIERY QLPQSYQRMPPDFRRRFLQVCV NEINSRTPMRLSYIEKKKGRQT THIFFDMLRDLLKNVDLKGFEF DVRILLTKYSNSNGSQSPWMEE QIRDAWGSMVLKNVVRETDEV GKDTSLSTPAAPMVDSLARVG VMARGNAITLPVCGRDVKFTL EVLRGDSVEKTSRVWSGAVSQ GGESFIYMPLTGAAFLSEMP PERRNLKKQCGYSGFAACGYQ SQERKNSPRIVQSN DLTEAAYS LSRDQKRMLYLFVDQIRKSDGT LQHDGICEIHVAKYAEIFGLTS AEASKDIRQALKSFAGKEVVFY RPEEDAGDEKGYESFPWFIKRA HSPSRGLYSVHINPYLIPFFIGLQ NRFTQFRLSETKEITNPYAMRL YESLCQYRKPDGSGIVSLKIDWI IERYQLPQSYQRMPPDFRRRFLQ DHNSSPEREQNWMEFDELT EVGFRRWVITNSSELKEHVLTQ CKEAKNLDKRLQELLTRISNLE NIDDLMEKNTAQELHETYTSI |
| 21867 | 52235 | A | 21995 | 82 | 325 | |
| 21868 | 52236 | B | 21996 | 220 | 1173 | |
| 21869 | 52237 | A | 21997 | 1 | 1599 | |
| 21870 | 52238 | A | 21998 | 188 | 421 | |
| 21871 | 52239 | A | 21999 | 1 | 596 | MGMTDMGKSKKKSQGPPSFPP GGAPPPAIGAPAGRERPPGTGD PFNQRPCDNLKTCHTSHGSVM AETA VINHKKRKN SPRIVQSN DLTEAAYSLSRDQKRMLYLFVD QIRKSDGTLQEHDGICEIHVAK YAEIFGLTSAEASKDIRQALKSF AGKEVVFYRPGEDAGHEKGYE SFPW/FIKRSPE*RRGKFPFTQM GQD |
| 21872 | 52240 | A | 22000 | 1 | 1527 | |
| 21873 | 52241 | A | 22001 | 2 | 870 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21874 | 52242 | A | 22002 | 1 | 4304 | MAETAVINHKKRKNsprivQSN DLTEAAYSLSRDQKRMLYLFV DQIRKSDGTLQEHDGICEIHVA KYAEIFGLTSAEASKDIRQALKS FAGKEVVFYRPEEDAGDEKGY ESFPWFIKRAHSPSRGLYSNRFT QFRLSETKEITNPYAMRLYESL CQYRKPDGSGIVSLKIDWIIERY QLPQSYQRMPDFRRRFLQCINA GHEMTKAIAIAQFNDDSPARK ITRRWRIGEAADLVGVSSQAIR DAEKAGRLPHPD |
| 21875 | 52243 | A | 22003 | 740 | 1159 | SLPNLDNSAICSSSSSPTTR*SL SVSAAALRRRLPSAISMTPTDL RPNAGVC*PVSRKEGMRSSSAS SVSSWSRSLPDHTREVFSTLSP RSTSRVNFTSRPHTGKVMALPR AITPTRAINESTIETAGEDNEVSS TG |
| 21876 | 52244 | A | 22004 | 664 | 1844 | SGNLKACHPSHGSVMAETA\VI NHKKRKNsprIEQ*KDGYQQA YLSRDQKRMLYLFVDQIRKSD GTLQEHDG\I\CQIHGAQYR*QIS D*PFAEASKDIRQALKSFAGKE VVFYRPEEDAGDEKGYESFPW FIKRAHSPSRGLFSGHIPP\YLIPF FIGVKNRLTQ\I\RLFETKEIPHS ALARYYESLGQDRK\PDGSSIGS LK\IDWIIERYQLPQSYQRMPDF RRRFLQHFLAHAGCPKGTQNT FRMKFIIFSIIKKVLPVDTILAH PVIHTCHLRESFGSVSPSPKSN RLPCPEVILFHYGESWNLLRAD QRLIFAKSWPRASRYQQGHQD LFILRSDLPSQVFIRDKLMERN RRTGRTEKARIWGSDDGQNGQE PGYVEAGCPPLLLTV |
| 21877 | 52245 | A | 22005 | 3 | 272 | |
| 21878 | 52246 | A | 22006 | 1 | 528 | |
| 21879 | 52247 | A | 22007 | 461 | 831 | LLNLATWRYLGTLTRGTAS\VA VAGILAAALRITNNKLSNHVFVF QGAGEAAMGIAHLLVMALRRK K\GTERTTATRKIWMVDSK\GLI CQGEGLN/HHEKEMFAQDH PEVNSLEEVRLVKPTAM |

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|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 21880 | 52248 | A | 22008 | 3 | 1894 | EGEDRGLPRTMGAALGTGTRL APWPGRACGALPRWTPTAPAQ GCHSKPGPARPVPLKKRGYDV TRNPHLNKGMFTLEERLQLGI HGLIPPCFLSQDVQLLRIMRY ERQQSDLDKYIILMTLQDRNEK LFYRVLTSDVEKFMPIVYTPTV GLACQHYGLTFRRPRGLFITIHD KGHLATMLNSWPEDNIKAVVV TDGERILGLGDLGCYGMGIPVG KLALYTACGGVNPQQCLPVLL DVGTTNEELLRDPL\YIGLKHQ RVHGKAYDDLDEFMQAVTD KFGINCL\QFEDFANANAFRL NKYRNKYCMFNDDIQGTASVA VAGILAA LRITNNKLSNHVFVF QGAGEAAMG\IAHLLVMALE\K EGVPK\A\EATRKIWMVDF\KGL IVKGRSHLNHEKEMFAQD\HPE SNSLDEVVRLVKPTAIGVAAIA EA\FTEQILRNMAFRRAPIIFA LSNPPRKAECTA\EKCYRVTEG PRGFFASGKSFLRSVDL/ESMGK TFIPGGRGNNA*RVPRGWQLG VHSPGGDPGHIP\DEIFLPDSRA KLPQEVSEQHL\SQGRLYP\PLS T\IRDVSLRIAIVLDYAYKHNL V\SYYPEPKDKEAFCKIPGSYTP DYDSFYT/VDSYIWAQ GKAMN |
| 21881 | 52249 | A | 22009 | 322 | 567 | |
| 21882 | 52250 | C | 22010 | 338 | 603 | |
| 21883 | 52251 | A | 22011 | 127 | 417 | |
| 21884 | 52252 | A | 22012 | 253 | 424 | |
| 21885 | 52253 | A | 22013 | 124 | 1235 | YLCLLPKGQGDRLSRTSQWP QMSQSQACGGSEQIPGIDIQLN RKYHTTRKLSTTKRFTACWR KKVGAF TKIIEAMGFTGPLKYS KWEDLRLRALRIVY*LCGRKLD FEGFFSK\CS\MPDTFNSWFLINP YFHVWMCLVRMKQEGRSGKY MCRIIVHFMWEDVQQRGRVM GVNPIYILKKNMILMTNHFYA\A ILGYDEGILSDDHGLAAALWK NLL\N\RKCEDPRHLELLVEYVR KQIQYLD S\MNGEDLLLTGEVS WRPLVEKNPQSILKPHSPTYND RGTFDGLGPPHGPPAGFRGTSR EEKCLVGPRT PARKWPELDLLN KHL SKYLAPICVEFPLSPQESD LLGYRAWENPLALPGCPSSLRG |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21886 | 52254 | A | 22014 | 282 | 435 | GGGASPAACSGSPDSSVHSATA GTGCRRPARPPPAPPTPTPWSR RQQGSRAS |
| 21887 | 52255 | A | 22015 | 3 | 399 | IVALPFGHHHSQTSPLPNLLQTA ACLLHFLLLSGVETGRPGPWQ PRIRARGPPAPPGPAPPAKPRRR /GCRGPAREACWYGCRPARPP PAPPTPTHGAAGSREAERASEL/ C*GARPLRLGSAGTİMVSACVP |
| 21888 | 52256 | A | 22016 | 279 | 872 | KIPIISLSLKLQGASSKIPTPQNP HLSPGTRKRDSSFQWLSAFIIT GQCCSYIVRWGLWKPRLLVV KKYAALSAEMLLVKVEEPSA ACSGSPDSSSFCNCW*PAAAGR L/ASAAQRPPTPNAHKRSRQQG SRASERAS/CKGRGRYGLGALG GRGGRALGGSRWPPPLPGETLF SGCKHRRRRRGSDAAPGEEAG |
| 21889 | 52257 | A | 22017 | 106 | 398 | NAAPFSRHAAFQGSWAVCIFR LPAERALRLFPASCLVLPGPS GVAPHGWPLPTTAPPLLQGVW RVEVGEHEMAEIFSSAKKEAAG ALQRPCIPVW |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21890 | 52258 | A | 22018 | 1 | 1806 | MRGNTAGGPGDEKPDSTHPPW EGTLQEAQEMKKVVRFMWTS GGPDPQHWRGSGLYGQLVAQ MLHIDVAQVYMDSWWPRCST LAWLRFIWTAGGPDAPHWLRS GLGGQLVAWMLHVGVAQVYV DSWWPSCSASMWLSFMEHKQ CLTLGYEVALFLQHFLSRAFLV VWVPRKEKAQVLRQGLSLTFR ENPGVCVMSSYRPWLITAAAD MQPSKPGGTGSYCSYWSPTDN TPRLAAACTWNLGSSHGSAAG VRTFIEAGFSPFLAPKALATL SDSDSRWGNPNVYAQPQP/PEP AWGNPNV*GQPQPRNRPQ\PEP CVCSTPTAEPWGNPNVSTPTA EPAWGNPNVYA/PTPTAEPWGN PNPV*GQPQP/REPAWGNPNVY GQPQPRNRPQS\PPQGNLYCSA ALGATDPSQSWHQCSQNLLPA DKGAKREAPW/PRPPSGEVDHQ VWHLHGWPLPTTAPLLQGVW RVEQTPASHHRQPRPRQSSPST KAPPVITVNQGPASHHRQPRPR QSSPSTKAPPVITVNQGPASHH RQPRPRQSSPST/TGPASHHRQP RPRQSSPSTKAPPVITVNQGPAS HHRQPRPRQSSPSTKAPPVITVN QGPASHHRQPRPRQSSPSTKAP PVITVNQGPASHHRQPRPRQSSP STKAPPVITVNQGPASHHRQPR PRQSSTLTKAPPVITVNQSPASH |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21891 | 52259 | A | 22019 | 27 | 1367 | RILAGPARAEAGSASDRSTGHL FPRGVGMDLCHPQPAELSSGET DELPRI*WHRKQLLEDIQKLKD EIADVFAQIDCFESAGDSRMAH KENELCIGRKKFNMDPRQGRW LWRARATGCGGCMGAPAWFL SGEGLNKTAIGTYLGER*ERVE P*RGRK*RCAGVYRCVDVQAL R*VVLGQGPQPQGWHSPSGWG CRDPRYCLCNPGVFQSTGARRG VGPRAPGPLQHCQA*ISQTRPPF ERFVSMNRRGINNGSDLPEDQLR VREAQPTQPGPGESRRDLSLDG WPFNPDREGWLLKLGERPTD TRRRTHTHARAGTHRCMHTTV SRVLLGLPLPPPLPAQPTSQ/PPT SRC/LRLQDPE/CWSHWEIS*TE RGESRVVEGKHESYRISATSAE ERDQWIESIR*GVPRSGDGFSP SRRPCFFWVLRDSWRWHWGL VTLRVPSAAPGDP |
| 21892 | 52260 | A | 22020 | 140 | 356 | |
| 21893 | 52261 | A | 22021 | 2 | 1147 | APARGPAVASGSPGPAAEPVQ NTETAAMTTHVTLEDALSND LLEELPLPDQQPCIEPPSSIMYQ ANFDTNFEDRNAFVTGIARYIE QATVHSSMNEMLEEGHEYAV MLYTWRSCSRAIPQVKCNEQP NRVEIYEKTVEVLEPEVTKLMK FMYFQRKAIERFCSEVKRLCHA ERRKDFVSEAYLLTLGKFINMF AVLDELKNMKCSVKNDHSAY KRAAQFLRKMA DPQSIQESQNL SMFLANHNRTQCLHQQLEVIP GYEELLADIVNICVDYYENKM YLTPSEKHMLLKVMGFGLYLM DGNVSNIIYKLD AKKRINLSKID KFFK/HAAGGAPFRRHADRAGQ IH*DQCSL*REQVQVDVHPEQH QPPVQYL RADGSDPG |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21894 | 52262 | A | 22022 | 47 | 1581 | ALVLMYLASSICMSPKRGTTCSCLERGSRCPPTSEPPPPPEPPGGRS SRCRPGLGPGYGGGGEKMADDP SAADRNVETWKIKKLIKSLAA RGNGTSMISLIIPPKDQISRVAK MLADEFGTASNIKSRVNRLSVL GAITSVQQRLKLYNKVPPNGLV VYCGTIVTEEGKEKKVNIDFEP FKPINTSLYLCDNKFHTEALTA LLSDDRQVWDFIVIGG/SVGALF GHTPKGNTRGGPWHKFTVGIFP K\KHG*EGGQ\SALRFARLRME KRHNYVRKVAETAVQLFISGD KVNAGLVLAGSADFKTELSQ SDMFDQRLQSKVLKLVDISYG GENGFNQAIELSTEVLSNVKFIQ EKKLIGRYFDEISQ/DLTGKYCF GVEDTLKALEMGAVEN\LIVYE NL\DIMRYVLHCQGT\KEEKILY LTPEQEK\DKSPFH\DKETGQEL ELIESMPLLEWFANNYKKFGA\ TLEMFTDKSQKGSPV**KDLGG IGG\ILRYQSRFPGEWNTKKET MNFLTLMTTR |
| 21895 | 52263 | A | 22023 | 1 | 296 | VEDERVCAQPAWERQAGQERP ARKVQGAPEAEGKHGCLLDI LVCTYLAEGKLSGSCGLTEALV AFGEGSSLGRKNCRDPWGLSR QEPHWSDP/WSGPPERCKGKPQ RRRGSTDAFWTSWSART*PRRG SLAAVG*QRHWWPLGRAAV*E ERTAETPGAPSGRSLTGQTLGS LHV |
| 21896 | 52264 | A | 22024 | 5 | 309 | LPDADLFCPACGAAAGRARS GMRPVFAVSARTPSPR/PPPAE PQFPRLPCGSIGSPFFRDIDTIQK FPDMLSSFFRDIDTIQKFPDML VFNCCLLNQSR |
| 21897 | 52265 | A | 22025 | 1 | 258 | RGRSRIARSASGPRPALVRPPAR PPAP*TPRSWSCWSSC*PRASA TGSPSA*ATDAHADSSKAMLPE PTSSISKFSTLQTVPFRL |
| 21898 | 52266 | A | 22026 | 119 | 692 | PSSHVSRTATYSSLRQSAVSTRT STTTTLAFMARAGGRAGGRAR VGGRTPSGQCGCPACGAAAGR ARSAGMRPVFAVSARTPSPR/ PPPAEPQFPRRPQR/GAPAPSGG GASLPAPRALASSIPAQLMKPG RAKGSAGNLHPG\EGRPGARRS DPAGAARSLACP*IWPQKTPSP LASSSSFFLSETPECAH |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21899 | 52267 | A | 22027 | 2 | 246 | |
| 21900 | 52268 | A | 22028 | 1 | 927 | |
| 21901 | 52269 | A | 22029 | 251 | 1077 | VTMGKVLAVSSLPAGPPPPVP ALVGLPPPP*HPGFRLPPLGGG LGARTSVGRGLERTPGAATASA AGGAEDGACRCLPNPCTFECH RKCKEL*MEGVKFTENKAL/SS KMAIQTQQSKFVKWQVDGEYR GSDFTVDVTLWNPVLMGSG! LVAHYLKSITPCLALGSELVYH RRPGEEGTVM SVAGKYTLNNW LATVDVEFEASTRMQDTNVSF GYQLDLPKANLLFKGSVDSNW IVGATLEKKLPPLPLTLALGAFL NHRKNKLRSGFGLTIS |
| 21902 | 52270 | A | 22030 | 1 | 1171 | GGSGFGCAWRTGWERSPGRE QAPPPATMGNVLAASSPPAGPP PPPAPALVGLPPPPSPPGFTLPP LGGSLGAGTSTSRSSERTPGAA TASASGAAEDGACGCLPNPGTF EECHRKCKELFPIQMEGVKLT NKGLSNHFQVNHTVALSTIGES NYHFGVTYVGTQQLSPTEAFPV LVGDMDNSGSLNAQVIHQ GLRSKMAIQTQQSKFVNWQVD GEYRGSDFTAAVTLGNPDVLV GSGILVAHYLQSITPCLALGGEL VYHRRPGEEGTVM SLAGKYTL NNWLATVTLGQAGMHATYYH KASDQLQVGVEFEASTRMQDT SVSFGYQLDLPKANLLFKGSVD SNWIVGATLEKKLPPLPLTLAL GAFLNHRKNKFQCGFGLTIG |
| 21903 | 52271 | A | 22031 | 14 | 434 | CYCQGILSPPPCPPFLGSAQTS AICSWVRGVPAESSTSSFPKAP* VALESRGEAPTLHLPVTSRFLQ CVSSEQECVPWKP/HSSPRPRFL DISPSPTCVRL*APGPVPFDPHQ KTWRSPLGTRAQGVGPRDRDS CRIVPG |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21904 | 52272 | A | 22032 | 989 | 1859 | VYGDSRWSLALSPRLECSGAVIS AH*NLCLPGSSDSPASRITGISG ARHHAQLI/L/YVFLVEMRFHH VGQAGLKLLTSGNP/HHLGLPK CWDYSRKPPPPRPIIFSFFFL RWSLALVAQAGMQWDDLSSL QPLPPGFK*FSCLSLLSWDYD CPPRLANFVCVCVCLV/VDG GFTMLARLGLELLTSGDLPPFG LPKCLGFTGMSHCARPIFFFE MESCFATQAGVQWCDLSSLQP LPPRFK*FSCLSLLSWDYRHM PPCLANF/CFGIFSRDRVSSCW GRSQTPDLK |
| 21905 | 52273 | A | 22033 | 157 | 376 | SHQDFMRTAANLLQTGWCTGS NTGAGARWGLCRASLSRCRCA APSAPCSGSRCS*RSWKGTHPS LPPRCRGRS |
| 21906 | 52274 | A | 22034 | 298 | 399 | |
| 21907 | 52275 | A | 22035 | 1 | 185 | |
| 21908 | 52276 | A | 22036 | 311 | 516 | WKAERRTRHLLQTGWCTGSNT GAGARWGLCRASLSRCRCAAP SAPRSGSRCS*RLWKGTHPSLPP RCR |
| 21909 | 52277 | A | 22037 | 1 | 1487 | MMGHSSAIPLTATPGELKGQSP TKMPDPELGCGGAKSQGCSR ARHQKARSMPLQDQHLALAIL LELAVQRGTLSQLSAILLLLQ LWDSRAQETDNERSAQGTSTL LLSLLQTFQSIICSKDTPPSEGN MHLLSGPLSPSESFLRESFFTQ NCRNNEEVTCLICKADLENHNK DGGFWIVIDEKVYDIKDFQTQS LTGNSILAQFAGENPVVALEAA FEFEVTRESMHAFVCVQYLEVR LYALSDAEDGRGHPLMASVIHL LWRLQTSQIHYSYNEEKDEDH CSSQWAHLPANRDCSHRWALG DHSQAFLQAIADNNIQDHNVKT HQQEGRSYKEVCTPVIERLRFL SNELRPAVGNDLSIIEFKLLSSL PRWRRIAQKIIRERRKKRIPKKP ESTADEEKIGNEESDLEEACILP HSPINVDKRPIAIKSPKTITSEN LG/REPGEHPASPLPPDDAQHA HPAAQRKQPRPPAQFRHAGPHS DGTAPDWPQL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21910 | 52278 | A | 22038 | 263 | 375 | AGPRRMRRISAWAVSTPLTDSP SPGHQPA/GEVAGAGSF**HPP/P PCPSRYCPQMTPPPPPPAPPPAL PPPPPPAPASPLPPAPSPPPHAP PQALPPPPALPPPPASPLLP LSPPLAPP/PPSAPPASPPAPPP PPAPPPSPPPAPPPSAPSSAPLPP APASPPSPAPPPAPPPAPHPPSP PAPPCPLPRPRGPSVPQEKVHQ V*IPVP/PAGEGGPAPGRIWPQG WRRAGKPPTWEEALAAFPPWT ALPPASAVPAQPPRAH*VAPAL *WALHRRSDSDSDSSNLSPRIPG TGGQRRQPR*DS*APACSEVAG AGSF |
| 21911 | 52279 | A | 22039 | 1 | 2001 | |
| 21912 | 52280 | A | 22040 | 1846 | 7725 | PEPFCHRAAHWSNQYCPFQFQ DTDSPRQTLTVLIKDNGEPSLST TATLTVSVTEDSPEARAEFPGS APREQKKNLTFYLLLSLILASV GFVVTAFGVIIFKVYKWKQSRD LYRAPVSSLYRTPGSLHADAV RGGLMSPHLYHQVYLTDSRR SDPLLKKPGAASPLASRQNTLR SCDPVFYRQVLGAESAPPGQIR YPVPEESQEGTFVGNVAQDFLL DTDSLARSRLQVAGEVNQRHF RVDLDSGALLIKNP |
| 21913 | 52281 | A | 22041 | 108 | 340 | PQPSQVMSFHGDSGSCRRWAT AGT*ATSPPCSSIFLRRMHSGH WCSCWPVRGTPCRDFTAQMAG PSRGSKTNRSMW |
| 21914 | 52282 | A | 22042 | 275 | 752 | EKTHKTCRCGRGCGKRGTL*H CWWEENLLQPLWKMVWKLWL KELKVELLCDLA/VPL/LGINPEE KKSLEYKDTCT/R/LFMAAQLAI AKKWNQPKCPSINKWLQKLW YIYMMEYSAIKRNLTAFAAT WMRLETILSQGDPLESTCSRSQ ANRQEITSVPKA |
| 21915 | 52283 | A | 22043 | 25 | 202 | DAEAWAMELADVGA*ASSQG APQPEEPAASLGVNEKGGAGG RSGRRPLGRDRPRPTRLL |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21916 | 52284 | A | 22044 | 1 | 2290 | MEKLGVEPEEEGGGDEEDAE AWAMELADVGAASSQGAPQ PEEPAASLGVNEKGVHDQVLPT PNASSRVIVHVDLDCFYAQVE MISNPELKDKPLGVQQKYL VV TCNYEARKLGVKKLMNVRDA KEKCPQLVLVNGEDLTRYREM SYKVTELLEEFSPVVERLGFDE NFVDLTEMVEKRLQQQLQSDDEL SAVTVSGHVYNNQSNLLDVLH IRLLVGSQIAAEMREAMYNQL GLTGCAGVASNKLLAKLVSGV FKPNQQT VLLPESCQH LIHSLN HIKEIPGIGYKTAKCLEALGINS VRDLQTFSPKILEKELGISVAQR IQKLSFGEDNSPVILSGPPQSFSE EDSFKKCSSEVEAKNKIEELLAS LLNRVCQDGRKPHTVRLIIRRY SSEKHYGRESRQCHIPSHVIQKL GTGNYDVMPPMVDILMKLFRN MVNVKMPFRLTLLSMCFCSLK AVNTATTRLIDYYLMPTISITSR SGKHSFKMKDTHMEDFPKDKE TNRDFLPSGRIESTRTRESPLDT TNFSKEKDINEFPLCSLPEGVDQ EVFKQLPVDIQEEILSGKSREKF QGKGSVSCPLHASRGVLSFFSK KQM QDIPINPRDHLSSSKQVSS VSPCEPGTSGFNSSSSSYMSSQK DYSYYLDNRLKDERISQGPKEP QGFHFT\NSNPA\VSFAHS\FPNL QSEQLFSRNHTTDSHKQTV\AT |
| 21917 | 52285 | A | 22045 | 2 | 141 | |
| 21918 | 52286 | C | 22046 | 278 | 489 | |
| 21919 | 52287 | A | 22047 | 130 | 426 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21920 | 52288 | A | 22048 | 357 | 1579 | QRRPRPFPSQGISMTFCFLPPTSS PSEHRRVEHGSLTRTPSSEEIS PTKFPGLYRTGEPSPPHDILHEP S*SNGLMDEKDHGKKKGNFKK KEKRTEGYAAFQEDSSGDEAE KLMPRFEEAYGRTTETEKVQEF QRLLKELPEGNYLLISLFVVMH DHVITKELEAKMNIQNIYIVVSP TVQISNLVLYVFFTHVQELFGN VVLKQVTKTRRWSNVATMPTL PETQAGFKKEIRIQELLLNCLHQ DLQGGIKDLSEEERLWEEKEL TKQEELLGMEQFLRRQIASEKE EIECLRAETAIEIQSHQQQGLSET EEYSSSESESEDEEELQIILEDLQR QNEELEIKNNHLNQAIHESEA VIEPRMQPWLLQLQPDRAKQQ AQEDEEPEWRGGAMQTPKNGI |
| 21921 | 52289 | A | 22049 | 182 | 2212 | VTEKTSSLPSQGISMTFCFLPPT SSPSEHRR\VEHG\SAGLTPGPPA SEEIQLPKFPGLY\RTGEPHPHP P*HPSHEPSLM*CPDDEKDHGK KKGKFKKKEKRTEGYAAFQED SSGDEAESPSKMKR\SKGIHVFK KPSFSKK\REKDFKIKEKPKEEK HKEEKHKEEKHKEKKSKDLTA ADVVKQWKEKKKKKKPIQEPE VPQIDVPNLKPIFGIPLADAVR TMMYDGIRLPV\FRECIDYVEK YGMKCEGIYRVSGIKSKVDELK AAVDREESTNLEDYEPNTVASL LKQYLRDLPENLLTKELMPRFE EACGRTTETEKVQEFQRLKEL PECNYLLISWLIVHMDHVIKE LETKMNIQNIIVLSPTVQISNR VLYVFFTHVQELFGNVVLKQV MKPLRWSNMATMPTLPETQAG IKEEIRRQEFLNCLHRDLQGGI KDLSKEERLWEVQRILTALKRK LREAKRQECETKIAQEIASLSKE DVSKEEMNENEEVINILLAQEN EILTEQEELLAMEQFLRRQIASE KEEIERLRAEIAEIQSRQQHGRS ETEEYSSSESESEDEEELQIILE DLQRQNEELEIKNNHLNQAIHE EREAIHEL RVQLRLQMQRKA EQQAQEDEEPEWRGGAVQPPR DGVLEPKAAKEQPKAGKEPAK |
| 21922 | 52290 | B | 22050 | 34 | 322 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21923 | 52291 | A | 22051 | 137 | 1546 | QMLGGRPPPRWLQLAKARALA RRRPPPSLHLTLPTALSLKS/RTP VPKSIPISETPNIPPVSQPPASIG PPLGVPP/PEPSHGDDQPRGP\PL PIFMEQQIMQQIRPPFIRGPP\PM PPTPTAPCPTPCFPASGPRPVAP ETWAPLPAPCTGPCY\PPHPPPE/ PPPP/SPGNPPGLLPPPPGAPLPS LPFPVSMMPNGMPVPQMMN FGLPSLAPLVPPPTLLVPYPVIV PLPVPIPIPIPIPSATSPPTGSP ATGRTSFRTPLATPRRRAASQA DTPCPPGTSPRARPSRTRPPAA RARP*AWRPRPPSMAGARWWT *RGAPA\PPGPPGRGRPARLPRR AAGPAGRRHRPDRGPPSPAQR DPPRAA/PRTSRRSASRAPRSAG PAAAAGTATAARPPPATQARA PRRAPRRRPATSS*TARAAPPP/ SGAKSAEPPPEQPPPPPPAPPK KLLSPEEPAVMRARVGQGE |
| 21924 | 52292 | A | 22052 | 762 | 2049 | RSSFSMGADLLACST/SGLGNM PYDLLRGMEPTLGCSFEDLAL A*PGGITQE\KINEMRVAPEQQ MI\ADIHFMIAAGQDLWDIDAQ GATLLHIAGANGYLRAAELLDD HGVRVDVKDWDGWEPLHAAA FWGQMQMAELLVSHGAN\LNA RTSMDEMPIDLCEEEEFKVLLL ELK\HKHDVIMKSQLRHKSSLS RRTSHRQAS/SVGKVVRRTQPV GTGPNL\YRKEYE/GEEAILWQR SAAEDQRTSTYNGDIRETRTD QENKDPNPRLEK\PVLLSEFPTK IPRGELDMPVENGLRAPVSAYQ YALANGDVWK\VHEVPDYSMA YGNPGVADATPPWSSYKEQSP QTLLELKRQRAAAKLLSHPFSL THLGSSMARTGESSESGKAPLI GGRTSPYSSNGTSVYYTVTSGD PLLKFKAPIEEMEEKVHGCCR |
| 21925 | 52293 | A | 22053 | 2 | 306 | SKEAFAIGLGGGSASGKTTVAR MIIEALDVPWVVLSSMDSFYK/ NAFDLDLIISTLKKLKQGKSVK APIYDFTTSLRKMDWKTLYGA NVIIFEGIMAFADKTL |
| 21926 | 52294 | A | 22054 | 2 | 379 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 21927 | 52295 | A | 22055 | 352 | 1227 | GDVSPQLSPRQKSGPLCTSCCA WPVCSPHSDAQPSGEGGLWE KTPFLSVPHRFVPRAALASAHQ CHPLPRTL SVLKSTPQVRGMHT IIRDKETSRDEFIFYSKRLMRLLI EHALSFLPFQDCVVQTPQGQD\ *RITGVSILRAGETMEPALRAVC KDVRIGTILIQTNQLTGEPELHY LRLPKDISDDHVILMDCTVSTG AAAMMAVRVLLDHDVPEDKIF LL\SLMAEMGVH\SVAYAFPR VKKSSPRRWDKAGQLTFFRIIP GIGNFGDRYFGTDAVPDGSDEE EVAYTG |
| 21928 | 52296 | A | 22056 | 72 | 2746 | FLVETGLHHVQGAGLKLTSN DPPASASQSTGITGMSHHAQPR QSSYVPPMSLPASAMPVEGVG GDALWAGHASGYLGGGQLWA TSEYIPLCSSNAESLDRLLPPVG TGRSPRKRTTRQCKSEPPLRTS KRTIYTAGRPPWYNEHGTQSKE AFAIVPVEQEKEAGQPQAAAA GWAPLGPICAGSLPVPHRGSPL PPAGLGGGSASGKTTVARMIE ALDVPWGGSSLSMDSFYKVLT EQQQEQAAHNNCNFDHPDAFD FDLIISTLKKLKHGKSVKVIYD FTTHSRKKDWKTLYGANVIFE GIMAFADKTLLEGPGPAPCTGP EDSIIRHIAAPSLHKASSRANYC VLSMGTDPKLATSPIPQCVGAS YPKQRCPEVALARPTDQAAS VQGLVPVSPCPLLASGHSLARC LHQLLDMKIFVDTDSDIRLVRR LRRDISERGRDIEGVIKQYNKFV KPSFDQYIQPTMRLADIVVPRG SGNTVGHPR*LLQHVSQLEEV SGVPRPHGLAPSPSTHFSAAATP SWPVHLIPLRSLSPASSSSQPAQ LCQQELGNCSKKLGLGRGRIPL SLPKGRHAGGAALASAHQCHP LPRTL SVLKSTPQVRGMHTIIR DKETSRDEFIFYSKRLMRLIEH ALSFLPFQDCVVQTPQGQDYA GKCYAGKQITGVSILRAGETME PALRAVCKDVRIGTILIQTNQLT |
| 21929 | 52297 | A | 22057 | 61 | 341 | |
| 21930 | 52298 | A | 22058 | 1 | 1086 | |
| 21931 | 52299 | A | 22059 | 1 | 498 | |
| 21932 | 52300 | A | 22060 | 104 | 3395 | |
| 21933 | 52301 | A | 22061 | 1 | 1653 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 21934 | 52302 | A | 22062 | 1 | 1717 | |
| 21935 | 52303 | A | 22063 | 172 | 13375 | EDLFKCIMAHAAASQLKKNRDL EINAE EEPKRRKHKRKS RDRK KKSDANASYLRAARAGHLEKA LDYIKNGVDINICNQNLNALH LASKEGHVEVVSELLQREANV DAATKKGNTALHIASLAGQAE VVKVLVTNGANVNAQSQNGFT PLYMAAQENHLEVVKFLLDNG ASQSLATEDGFTPLAVALQQGH DQVVSLLENDTKGKVRLPAL HIAARKDDTKAAALLLQNDNN ADVESKSGFTPLHIAAHYGN I |
| 21936 | 52304 | A | 22064 | 1 | 360 | |
| 21937 | 52305 | A | 22065 | 1 | 2577 | |
| 21938 | 52306 | B | 22066 | 323 | 3154 | |
| 21939 | 52307 | A | 22067 | 93 | 791 | IRMSYAEKPDEITKDEWMEKL NNLHVQRADMNRLIMNYLVTE GFKEAAEKFRMESGIEPSVDLE TLDERIKIREIDT*KGQIQEAIRL *FNSLHPEL/LWDTNRYLYFHF ASNSILIPS*FRQ\GKTRGRRWG VAQTQLAD\RGESRECLTEME RTLALLAFDSPEESPFGDLLHT MQRQKVWSEVNQAVLDYENR ESTPKLAKLLKLLLWAQNELD QKKVKYPKMTDLSKGGD |
| 21940 | 52308 | A | 22068 | 171 | 426 | |
| 21941 | 52309 | A | 22069 | 5 | 655 | LLQPSVQLPNGTANTSLSFAAV SAVSPPPCRTSTATTLPPPMPSF FCVFPSPSPSPSEFLSCIASVS RVHSLSSSSSGSSSTASSLNFSAI MGSSSATASWVLSTTSTPPCPS ALPSSPAQES*SLAASSSAWLSE HPSFSSFTLSWASGAFCDEVSL FSGSKLSFLSSKGDGIPFI*TSA CPSSLDFSPCFSSSTSKSSSYSEI GKSPQPI |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21942 | 52310 | A | 22070 | 87 | 1180 | NQASLEVLPSVPDSDPSIPSLPP/ SDNPNRNFSAAPVSCLPSPLPVA ASWSPDPSSCSCPSPEVFRSRAP GVPTPASVVYVTVISSAAGTSSP LRANSSTTTFPAAAVFPTNSSC WCQVSSSATSEKEEALFAIVFSS AVSEPANTSLSSAAVSAVSPPPC RTSTATTLPMPSPFFCVFPSPS MSPSPSEFLSCIASVSRVHSLSSS SSGSSSTASSLNFSAIMGSSSAT ASWVLSTTSTPPCPSALPSSPAQ ES*SLAASSSAWPVAGISPSGAC TFPAGSASGAAPSPSWRCPS FRALFSLLDSSSLSLCSVSLASL SLSPPPSFLRAVMFPATFKSRRC FKYGNHCLFSDLLWLEVCAL |
| 21943 | 52311 | A | 22071 | 841 | 1052 | IGEVLLDNVLKSVF*LGSVLPIT SLKLLP/SGSKRDPKMSHSH AG*VTTGAFPRCGRWRLQPAA PPPPS |
| 21944 | 52312 | A | 22072 | 817 | 866 | HANPVSPPTSWPKE*SWP*CSG **RTFQSVSFAGGRRRGSWLKP PPATAWKSSSCHLPSGVRMAHF CRIPFGPRGRDFADFGTTIKQDF RLLGQTSVDRLLQLSQGQAVK GNQLLPVSLVKRKTTLAPNTQT ASPRALADSLMQLARQVSRLES GQ |
| 21945 | 52313 | A | 22073 | 2 | 3238 | TTFPAAAVFPTNSSCWCQVSSS ATSEKEEALFAIVFSSAVSEPAN TSLSSAAVSAVSPPPCARTSTATT LPPMPSPFFCVFPSPSPSPSEF LSCIASVSRVHSLSSSSSGSSSTA SSLNFSAIMGSSSATASWVLSTT STPPCPSALPSSPAQES*SLAASS SAWPVAGISPSGACTFPAGSAS GAAKAPSPSWRCPSFRALFSL DSSSLSLCSVSLASLSLSPPPSFL RAVMFSSDFSNPGVASNMGTT VSF |
| 21946 | 52314 | C | 22074 | 88 | 4374 | |
| 21947 | 52315 | A | 22075 | 73 | 616 | VKESLTQKSKRFQNKLINRRG WERPRSGASWTQRRALGGRGC VDRWLGI/WHRIIPGARLRGFP ALNPTPQTAPSPSPDPRPRPP/CP SDPGPRTEAQCSL\PPPP\PSPRH LDPGPEPTPLTQGGQKGTRAP RPRCPRSQK*ATSGPAVRRREA RGSASLRTRAPSRDSTHAGIQG NVALQP |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21948 | 52316 | A | 22076 | 1 | 421 | GTVVMGLPKYFISLSTKFPLSFS LSADELHIASLFLWPRSKPFGVI QRSCASQLNALPEVLKNPGDPD KMLRFAESPRNLPAGVL/GDIW TDGKGSVSLQEQQVYHFPLIRPT PGS*ARASFLSCG*EEFRRHGLT FSSTRE |
| 21949 | 52317 | B | 22077 | 211 | 2041 | |
| 21950 | 52318 | A | 22078 | 200 | 1525 | IMASAHLATSAFCTRSSSSGRSG SCKRGSWDSEQALIRAWTTLPS SLHAADGSFAGGRGIPSKRWS WRAGQQSSSLCLIMQTSSNCGNS FQLVSEGASWRGLPHCSAELQ DSLNFSYHPSGLSLSVRPSSPGN SPKEQPFQVLRPEPPDPEKLPV PPAPPSKRHCRSLSVPVDLRW QPVWRPAPSKLWTPIKHRGSGG GGGPQVPHQSPPKRVSSLRFLT SSQCLFSMCPSSQTLQPSFLQPG PGP\SSSRPCAASPQSGSWESDA ESLSPCPPQRRFSLSPSLGPQAS RFLPSARSSPASSPELPLAT*G/L SATFPESRSQPCDL DARKTGVK RRHEEDPRRLRPSLDFDKMNQ KPYSGLCLQETAREGSSISPP WFMACSPPLSASCSPGSSQ VLSESEKEEEGAVRWGRQALS KRTLCQRDFGDLNLNIEEN |
| 21951 | 52319 | A | 22079 | 1 | 117 | |
| 21952 | 52320 | A | 22080 | 3 | 632 | |
| 21953 | 52321 | A | 22081 | 1 | 448 | MQSETETVHLFIPALSVGAIIGK QGQHIKQLSRFAGASIKIAPAEA PDAKVRMVIITGPPEAQFKAQG RIYGKIKEENFVSPKEEVKLEA HIRVPSFAAGRVIGKGGKTAST *QNLCSGMKGKALKAKPSTYN CVGCGWSPRPRCSLN |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21954 | 52322 | A | 22082 | 233 | 2096 | RREDEGNKTSWIHPSPWVVLIF RFFSLFFFFKQPLFTMNKLYIGNL SENAAPS\DLKSIFKDAKIPVSG PFLVKTGYAFVDCP\DESWA\LR AIKAFSGKIELHGKPIEVEHSVP KRQRIRKLQIRNIPPHLQWEVL DSLLVQYGVVESCEQVNTDSET AVVNVTYSSKDQARQALDK/L LDKLNGFQLENFTLKVA YIPDE MATQQNPFLQPRGRRGLGQRG S\SRQGSPPSVSKQKPCDSPLRL LVPTQFVGAIIGKEGATIRNITK QTQSKIDVHRKENAGAAEKSIT IPSTPEGTSAACKSILEIMHKEA QDIKFTEEIPLKILAHNNFVGRLI GKEGRNLKKIEQD\TDKITISPL QELTLYNPERTITVKG\NVETCA KAEEEIMKKIRESYENDIASMN LQAHLPGLNLNALGLFPPTSG MPPPTSGPPSAMTPPSPQSEQSE SETVHLFIPALSVRALISKQGQH IKQLSRFAGASSKIAPVEAPDAK VRMVMIAGSPEARFKAQGRIY GKIKEENFVSPKEEVKLEAHIR VPSFAAGRVIGKGGKT\NELQ NLSSAEVVVPRDQTPDENDQV VVKITGHFYACQVAQRKI*EFL TQVRQHQQQKALQSGPPQSRR |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21955 | 52323 | A | 22083 | 8 | 1675 | TASCRLAMALHVPKAPGFAQM LKEGAKHFSGLEEA VYRNIQAC KELAQTTRTAYGPKGMNKMVI NHLEKLFVTNDAATILRELEVQ HPAAKMIVMASHMQEQEVGD GTNFVLVFAGALLELA EELLRI GLSVSEVIEGYEIA CRKAHEILP NLVCCSAKNLRDIDEVSSLLRT SIMSKQYGNEVFLAKLIAQAC\ YLFFLIP AISMLITSEFVK/FLGS GISSSSVLHGMVFKKETEGDVT SVKDAKIAVYSCPF DGMITETK GTVLIKTA EELMNFSKGEENLM DAQVKAIADTGANVVVTGGKV ADMALHYANKYNIMLVRLNSK WDLRRLCKTVGATALPRLTPP VLEEMGHCD SVYLSEVGDTQV VVFKEKEDGAISTIVLRGSTD NLMDDIERAVDDGVNTFKVLT RDKRLVPGGGATEIELAKQITS YGETCPGLEQYAIKKFAEAFE IPRALAENSGVKANEVISKLYA VHQEGNK NVGLDIEAEVPAVK DMLEAGILD TYLGKYWAIKLA TNAAVTVLRVDQIIMAKPAGGP KPPSGK*NWLN FYCR |
| 21956 | 52324 | A | 22084 | 175 | 278 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21957 | 52325 | A | 22085 | 208 | 1976 | GPSPLKEHFSGLEETAYM\NILT CMELAQTTTRTAYGPNGMNKM VINHLEKLLVTNDAATILRELE VQHPAAKMIVMASHMQEQEV\ GDGTNFVLVFAGSFPVNYLKN L\WRIGLSVSEVIEGYEACRKA HEILPNLVC\CSAKNLRDIDEVS SLLRTS\IMSKQYGLMKVFLAK PYLLQACRIYFSWIPAISMLITSE FVK/FLGSGIRSS*VLAMVFK KET\EGDVT SVKDAK\IAVYS\C PFDGHG*QET*GEQCLDKRTAL KDLDGIFR*GEQENLHG/AATSP KAIADTGANVVVTGGKVADM ALHYANKYNIMLVRLNSKM/W DLRRLCKTVGATALPR\LTPSL SLKEMGHCD\SVYLSEVGDTQ\ VVVFKHEKEDGAISTIV\LRGST DN/L*LDDIER\AVDDGVNTFQ GSLQRDKRLVP\GGGSRNLN* PKQITSYGET\CPGLEQYA/ILK KFA*GHLKAIPPAHWQKYSGE NSGVKAQWK*SPKLYAVHQEG \NKNV\GLDIEAEVP/SLVKDML EAGIPRYLTGKYWAIPLATNA AVTVLRVDQHTLV*FFMQIIM AKPAG/GGPKPPKWGRKTWGD DQNGLKIGFNFYCR |
| 21958 | 52326 | A | 22086 | 1 | 346 | PF*CTPSCLWAF*TARSAQTWS APSTRWCSEWPKSLPSPTWLR *FRKVSSYSWSQSWSPTASTD SSRPPHSLGASCHPGHQSLMP PSR*RATSTAYASLSSSHRPNTQ PSPS |
| 21959 | 52327 | A | 22087 | 3 | 484 | RSSQPRVGLCGKSLQP/SSEGSC HLQGWCSFPRSVSSIMAEA*RT *PRVSSSMHGRGPTQNREATKK ASSSETSV/QVTAQEAQAEPGA AGVAG/SPASAPQDSAGACWPA QVL*GGSDRSCRGSHPGNTEPP SVLRTGTAPGA*G/SSPFSPTTQS GSCCFPFSS |
| 21960 | 52328 | B | 22088 | 181 | 359 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21961 | 52329 | A | 22089 | 290 | 2014 | STCTPLPTASSQSRPHPPPTPTPP APWRSSNGQVPTLT*PGSTLPP G/SGKSPV/VASGGPARAKPHRA VHVSPAPSGGSPGDVAELPAAV AVRA*QAGSGQRLPAPVCVGE MGTLCPGEPADVHQVVCGLSE PRAPHRPGQPQARAHGVPSGQS LCPAQPG*DDS/AKVSSYSWSQ SWSSPTASTDSSRPPHSLGASCH PGHQ RSLMPPSR*RATSTAWRA RTASTPRCLGPRPAPWSCASLSS SHRPNTQPSPTSVRRLATP SSHGWALAPWTPMAPTQPTTW TRWGKTVSGRQMNTWRRPWS TCARYSGSAKRSSGSSHSPWAP PRMRMEKSNSTASWVRTDSS LRPWGGTRSSMGCEGLKLSTR GTRSCSPSGAMRSPAWSAHLG CRLPSTTDLQDRWRLCVPGMT SSAASVATTSQLGWPAATC*A LWGGGRWPATPAA\QAQPALP GQLPTRWSRCCWPSSWPLCSAS GPSHARCCSPWAMSSTPLP*HC *PSGGSCTSPEGVSCLOSRLEGF ATQPHPWAERTWEAPPGNTV ILGLLERGSCSRRIWRKRNQE RKAGRPAKE |
| 21962 | 52330 | A | 22090 | 363 | 487 | |
| 21963 | 52331 | A | 22091 | 234 | 282 | |
| 21964 | 52332 | A | 22092 | 742 | 990 | |
| 21965 | 52333 | A | 22093 | 1 | 206 | LFPAFSDSRECKLMKKLLEA/H EEQNVD\SYTEA\VKEYDSIFPG WTQWLTTL\LLRIKKTIQG\DEK DLR |
| 21966 | 52334 | A | 22094 | 128 | 1062 | KPFEAAMYNSGKEAEAMALLA EAER\KVKNSSQSFSGLFSGSS KIEEACEVIYARAANMFKMAKN WSAAGNAFCQAAQLHLQLQSK HDAATCFVDAGNAF\KKADPQ GGPFNCFDCVAFEIYTDMDGR\F TIAAKHHISIC*DLLRQKLVDIE KAIA\HYRALADYYQGEESNS\S ANKCLLKVAGYA\ALLEQYQK\ AIDIYEQGWGPNNAHWTSPPPSK Y\SAKDYFFKAALCHFCMDML QA\KLAFQKYEEFPVFSDSRE CKLMKK\LLKA\HGEQNVD\SY TE\SVKGITDSISRL\DQWL\TTH CLRI\KKTIRGD |
| 21967 | 52335 | A | 22095 | 1 | 1038 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21968 | 52336 | A | 22096 | 20 | 2482 | RVCSSSASTASQAVMADAWEE IRRLAADFQRAQFAEATQRLSE RNCIEIVNRLIAQKQLEVVHTL DGKEYITPAQISKEMRDELHVR GGRVNIVDLQQVINVDLIHIEN RIGDIIKSEKHVQLVLGQLIDEN YL\DRVGQEVNDKLQESGQVTI SELCKTYDLPGNFLTQALTQRL AIIIGHIDL DNRGVIFTEAFVAR HRARIRGLFSAITRPTAVNSLIS KYGFQEQLLYSVLDELVNSGRL RGTVVGGRQDKAVFVPDIYSR TQSTWVDSFFRQNGYLEFDALS RLGIPDAVSYIKKRYKTTQLLFL KAACVGQGLVDQVEASVEEAI SSGTWVDIAPLLPTSLSVEDAAI LLQQVMRAFSKQASTVVFSDT VVVSEKFINDCTELFREL MHQ KAEKEMKNNPVHLITEEDLKQI STLESVSTSKKDKKDERRRKAT EGSGSMRGGGGGNAREYKIKK VKKKGRKDDSDDESQSSHTG KKKPEISFMFQDEIEDFLRKHIQ DAPEEFISELAEYLIKPLNKTYL EVVRSVFMSTTSASGTGRKRT IKDLQE\EVSNLYNNIRLFGKRG WKFF\ADDTQGWL LPKHLLEV QCVLISLNL\FNFLGFGILMDG Q*DDPGRPFTSEL RKEI LSKLS EETKVALTKLHNSLNEKSIEDFI FC\DSAAEACDIMVKRGDKKR ERQILFQHRQALAEQLKVTEDP |
| 21969 | 52337 | A | 22097 | 1 | 711 | VLSLFDGIATGYLV LKELGIKV GKYVASEVCEESIAVGTVKHEG NIKYVNDVRNITKKNIEEWGPF DLVIGGSPCNDLSNVNPARKGL YEGTGRLFFEFYHLLNYSRPKE GDDRPF FWMFENVVAMKVG D KRDISRFLECNPMIDA I KVSAA HRARYFWGNLPGMNRPVIASK NDKLELQDCLEYNRIA\RIFGFP VHYTDVSNMGRGARQKLLGRS WSVPVIRHLFAPLKDYFAC |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21970 | 52338 | A | 22098 | 406 | 2885 | GRGILVNGACSDQSSDSPPILEA IRTPEIRGGWAVGTGVVSGADI VSGHCRQWSLLSLFQSGTSL AFITWAFRETRTRSESPAVSSHT SSQSTCGQHST*HT*HARGRQG RNVHDESPVEFPATRVGSPDAQ TPARSL*LGDMPHSLTIDLTDDT EDTHGTPQSSSTPYARLAQDSQ QGGMESPPQVEADSGDGSSEY QVDGREGLLPRV/I*GP*TRGKTS YAMVYSWKATSKRQAMSGMR WVQWFGDGKFSEVSPGKGKGF CRPEAVPACLPLNKLVSRYKA MYHALEVTWDEGMRAKP*EQ G*SKRPTLEDQLKPMLEWAH GGFKPTGIEGLKPNNTQPGGNE SPWQHPLPLLVGPLLGRVRLKT NCYNNKGKDRGDEDQSRGDCW VPGIMGQMGGGRCRSGIDVIPL TPWLGL*ACLVQCQTCRVSPPTT ALDLPPLASSNSPLLPCGRELL LCSNTSCCR*ALGPVGWMWVG PQGSYVPAV*EPWSCYMCLPQ RCHGVLRRRKDWNVRLQAFFT SDTGLEYVSHRLPPLPPQIPGAQ GVGKLWFDGIATGEFGEHLET LSCHNRVARESEESIAVGTVKH EGNIKYVNDVRNITKKNVRAV CTLRASSLPVFFPSPPHPNPARK GLYGEHPSLWQSLESCHLTG PGAGNK/RGLGWRWFQMPALS SFLSTGVQRDISRFLEVRESGD |
| 21971 | 52339 | A | 22099 | 729 | 896 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21972 | 52340 | A | 22100 | 1 | 2672 | MAYKQGFLKVMVHFRKAEVT GKNHTSVHEGYTLISPAAQVLT ISCKKSILLQEQVSFKDVCVDFT QEEWYLLDPAQKILYRDVILEN YSNLVSVGYCITKP\EVIFKI/ES KGEEPW\VLEKGIPQAQCPPQK RKWKV/EMNVVREQPRKMKM TIFGEPIPTTNKTVSVENGDRG SKTFNLGTDVPSLIKLSL*NM*L \SEMNLKNISGLIITKKNC SRKK PDEFNVCEKLLDIRHEKIPIGE KSYKYDQKRNAINYHQDLSQP SFGQSFEYSKNGQGFHDEAAFF TNKRSQIGETVCKYNECGRTFI ESLKLNISQRPHLEMEPYGCSIC GKSFCMNLRFHQALTKDNP YEYNEYGEIFCDNSAFIIHQGAY TRKILREYKVSDKTWEKSALLK HQIVHMGGKSYDYNENGSNFS KKSHLTQLRRAHTGEKTFECGE CGKTFWEKSNLTQHQRTHTGE KP\L*CTEC\GKAFCQKPHLTNH QRTHTGEKPYECKQCGKTF CV KSNLTEHQRTHTGEKPYECNA CGKSFCCHRSALTVHQRTHTGE KPFICNECGKSFCVKSNIIVHQR THTGEKPYKCNCGKTFCEKSA LTKHQRTHTGEKPYECNACGK TFSQRSVLTKYQFIHTRVKAL* TS*MLEAFIHL/SKLVIQFQKRRS EKAKECQKFVE\KTSCLNM*KL SRKIKTFH*KICKLTVKNKG NK |
| 21973 | 52341 | A | 22101 | 1 | 2817 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 21974 | 52342 | A | 22102 | 474 | 2766 | NQTALYNQAQLLHGSRFANMS AEGYQYRALYDYKKEREEDID LHLGDILTVNKGSLVALGFSDG QEARPEEIGWLNNGYNETTGERG DFPGTYVEYIGRKKISPPTPKPR PPRPLPVAPGSSKTEADVEQQA LTLPDLAEQFAPPDIAPLLIKL VEAIEKKGLECSTLYRTQSSSNL AELRQLLDCTPSVDLEMIDVH VLADAFKRYLLDLPNPVIPA YSEMISLAPEVQSSEYIQLLKK LIRSPSIPHQYWLTLQYLLKHFF KLSQTSSKNLLNARVLSEIFSPM LFRFSAASSDNTENLIKVIEILIS TEWNERQPAPALPPKPPKPTTV ANNGMNNNMSLQNAEWYWG DISREEVNEKLRDS\ADGTFLV RDASTKMHGDYTLTLRKGNN KLKIFHRDGKYGFSDPLTFSSV VELINHYRNESLAQYNPKLDVK LLYPVSKYQQDQVVKEDNIEA VGKKLHEYNTQFQEK\$REYDR LY\EEYTRTSQEIQMKRPAIEAF NETIKIFEAEQCQTQERYSKGNY HLEKFKP*AMEKEIQRMHNY DKLKSRISEIIDSRRRLE\EDLKK Q\AAEYREIDKRMNSIKPDLIQL RKTRDQYLMWLTQKGVRQKK LNEWL\GNENTEDHYSLV\EDD EDLPHHDE\KTWECLGSS/RTRN QSLKNLFARGSRDGTFLVRESS KQGCYACSVVVDGEVKHCVI\ |
| 21975 | 52343 | A | 22103 | 3 | 392 | |
| 21976 | 52344 | A | 22104 | 168 | 404 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21977 | 52345 | A | 22105 | 49 | 1760 | YQSPA WQSHWHQKLQVRKEN MAKRVAIVGAGVSGLASIKCCL EEGLEPTCFERSDDLGLWRFT EHVEEGRASLYKSVVSNSCKE MSCYSDFPFPEDYPNYVPNSQF LEYLKM MYANHFDLLKHIQFKT KVCSVT KCSDSAVSGQWEVVT MHEEKQESAIFDAVMVCTGFL TNPYLP LDFSFGINAFKGQYFHS RQYKHPDIFKDKRVLVIGMGNS GTDIAVEASHLAEKVFLSTTGG GWVISRIFDSGYPWDVMVFMTR FQNMLRNSLPTPIVTWLMERKI NNWLNHANYGLIPEDRTQLKE FVLNDELPGRIITGKVFIRPSIKE VKENSVIFNNTSKEEPIDIIVFAT GYTFAFPFLDES VVKVEDGQA\ SLYKYIFPAHLQKPTL\AIIGLH/ IKPLGLP*LPTGETQVRWAVSG S*KVLTRLPPPSVMIEEINARKE NKPSWFGLCYCKALQSDYITYI DELLTYINTKPNL/FSLWLLTDP TSGLWTVFFGPA\SPYQFRLTG P\GKMGKGAQEIALHGPQWDP NISRVH SKVRSCYKEFSIFPGK FFLKVF SFGFGLWLFFLIFPYK |
| 21978 | 52346 | A | 22106 | 262 | 969 | EWSSVRRSLVEKRALRRPHPQC LCFRMKTIL\SNQTVDIPE\NVDI TLKGRTGIREGPPEGTLR\RDFA\ HIN\VELSLLWKEKKRGSRVDK\ WWGNQKRNWPTSRD*FVSHV QN\MIKGWLHWGFR LQG*GPV YAHFPHQPLLSRKNGVSWLKIR KFLWGEKY\RRVSG*RPGCCLL VSVSQGPRKDEINPLKG\NDIEL VSK/SSAGF*FQQATTS*KTRNI RKFLADGIFCLLEKGLFRQA |
| 21979 | 52347 | B | 22107 | 211 | 457 | |
| 21980 | 52348 | A | 22108 | 1 | 159 | KEAENQCLDISSPGMSGHRQGH DSLEHDELREIFNDLSSSSEDED ETQH QDEK*LDISSPGMSGHRQ GHDSLEHDELREIFNDLSSSSED EDETQH QDEK |
| 21981 | 52349 | C | 22109 | 167 | 367 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21982 | 52350 | A | 22110 | 754 | 1950 | VKGKDDAPHELGE/SQFILRLPP VEYASTVRRRAVQSGHVNLDRL TIELHPDGRHGI\VRVDRVPLAS KLVD\LP\CVMEEPENPLLKKPF SKTAIIGQMLVSTVDGDLFPPV EESPCLALDPKAS\KKKDKDKE KK\FIW\NHGITLPLKNVRKRRF RKTAKKEIYLNLPDV*KKELKR VLEVPDA\EA\STRWGIICPKV ETKGAENQGLDISSPGMSGH R\QGHDSLEHDELREIFNDLSS SEDEDETQHQDEEDINIIDTEED LERQLQDKL NESDEQH QENEG TNQLVMGIQKQIDNMKGKLAQE TQDRAK\RQEDLIMKVGNLGS PRTDFQAVLGMSFNQREDREK EQLASSLQEELESLLREVKKNL M FNFQSFRLVQHLGKFFGLLLL GYLRPCSS |
| 21983 | 52351 | B | 22111 | 227 | 355 | |
| 21984 | 52352 | A | 22112 | 121 | 486 | WGPALCIGGYLASFLASVHLM P LR*GEMLS P*GLSFSFRFP GFKE VRLVPGRHDIAFVEFDNEVQAG AARDALQGFKITLSPLKVS PPL GAFLEPCVSEWSPHSIVPRV CPQ TLHLALLGRN |
| 21985 | 52353 | B | 22113 | 8 | 165 | |
| 21986 | 52354 | A | 22114 | 1 | 218 | |
| 21987 | 52355 | A | 22115 | 566 | 1412 | TLHSMAMPETRPNHTIYIN\NLN EKIKKDELKKSLLRPSFF/SSLG QILGYSWG IHGRP*RMEGARPF SIFKEVSSGTNALR\SMQGF PFY\ DKPMRIPVLPRTLQDIHLPRIE RAPFIGSRDPKAGERGRPKSQG DPGPPKEGLCKGGGSHPRGGG LSRGP GPGHCPPMT\KAPRI\MH HMPG\QPPLTAAPLDMIPPPG\L APGQIPPG\AMPP\QQLMPGQMP P\AQ\PLWRNPP\NHILF\LTNLP\ EET\NELMLSHAFSNQVPPGFKE GPVWVPRAGNEHRPSVEV |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21988 | 52356 | A | 22116 | 2 | 1176 | FGELSTFD AVRGP RRCPDAD PRAPGLALPGRLLVSNRRTHS RESRAPPAPHLLGARAGMAPPQ VLA\FGLLLAAATATFAAAQEE CVCENYK\LAVNCFCE*INRQC Q\CTSVGAQNTVICSKLGCQMF W*MKAEMNGSKLGRRAKPEG GLQ\NNDGLYDPDCDESLFKA KQCNG\TSTC\WCVNTAGVVRT HKDTEVTCSEVRITYWIIELKH KAREKPY\DSKS\LRT*LQKEITT RYTLGSKFLSRVFWYENNVITI\ DLFQNFSSKLLRNDVDIADVAY YF\EKDVK\GESLFH\SKKMDLT VNGEQLDLDDLIPGQTLIYNVD EKAP*/DFSMQGLK\AGVIAVIV VVVITSCCWKLLVLVISQKGRE WQKYEKAEIKGDGCRCHRELQ |
| 21989 | 52357 | A | 22117 | 3 | 257 | AKALQWPLGRGGGGTPRGSRP PGPH*SERGAVQPRSLPRQAA* RVPSGPADGQ*DGHGAADPGS RQRCKPWSEAADLHSECYSS |
| 21990 | 52358 | A | 22118 | 1467 | 1748 | SEYNCCCEIGCPQPSWGPWGRG\ TDVRQQQVGEEVHG/ECGGG SQG*RPG**AGSPAP*PGTWTGT AQQGPAAVLDPLRV*GGGIERH PLHSVGL |
| 21991 | 52359 | B | 22119 | 1 | 1461 | |
| 21992 | 52360 | A | 22120 | 29 | 417 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21993 | 52361 | A | 22121 | 616 | 1671 | TATCKPWSMRTTISSSQPKLT NSVKLPPSAKCISVSRIGGFLVS LTSRMKLRLLICSKLLPSGGV RGLAGSGVKLQFTFTVSVTALK AACLELFTSPGGFMVLLASEVK LQTFSGAGSDCLGQGRRAQRRP GPGVSAVGASGQQRAPESNERP AEEPTPAPMPSSAPRGPTPEALR RPSSADRPLAPGACRAPGAMAS PSGSSKATGKPRGRDGRPRREE DDVTPEEKRLRLLEECSAQPD DGEDAPRPRGKETGTQTGGDG RGAARAALLAVGGIRAPLPSLG VAPGC\PMSPRRRHPGATPR/P GQGGSDAAHGEEGCPCCSSAV ATCLGAGLLP\PGRGASSPSSGC ALPSSSNSRSLFSSGVTSSSSLLG RPSLPRGLPVALELPEGLAMAP GALPAPGASGLSAELGRLSAGS VGPRGA\G*ASGRAWAPPRAAR CSLAPSAG\PRAHRGHAGPWPA LSSP/GPGPSSRCPLPRRSAASLL KPAR/AINPPGEVNNRHAALR AVTLTVKVCSTPEPARPRTPE GRSFEHRRVRSFILEVSETKNP PILDTLIHLALGGSFTLFVNFCG WDELIVVLIDQGLHVAV |
| 21994 | 52362 | A | 22122 | 892 | 1931 | CTWNENQRMEIVWEVLFLQA NFIVCISAQQNSPKIHEGWWAY KEVVQGFNFVPVPSFWGLVNSA WNLCVSGKRQSPVNIETSHMIF DPFLTPLRINTGGRKVS GMTYN TGRHVSLRLDKEHLVNISGGPM TYSHRLEEIRLHFGSEDSQGSEH LLNGQAFSGEVQLIHYNHELYT NVTEAAKSPNGLVVVSIFIKVS DSSNPFLNRML\NRDTFTRN*H FKNDGIFYRGL*YRGELLFQG TSSFITYDGDGLFPTPGY/SRT ASWII MNKPV*YNPGCKMHSLR LL\SQEPAISRSLSMSDNFRPV QPLNNRCIRTNINFLQKDCP NNRAQKLQYRVNEWLLK |
| 21995 | 52363 | A | 22123 | 17 | 417 | |
| 21996 | 52364 | A | 22124 | 63 | 449 | CHPALLGPTGHGAWPRHRAPD TLRASAGGRDP*GRRSAPA*ER QP*PPVYCAGISQYD*TALSSCL RRSVRTSTDFRSLDKSNYSVF LCFLQLAGRRYFAMWTRPEFFL ARDPRSLSWGLEWRPLSL |
| 21997 | 52365 | B | 22125 | 1 | 1131 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 21998 | 52366 | A | 22126 | 359 | 548 | |
| 21999 | 52367 | A | 22127 | 755 | 1031 | TRGVLEHMAALGKGTLDKPSGP AP*NHPE\VSAASTQEAAGPP AGRPGHSGCLALPASSTSLEP GLRQDHDLLLQLLWREQEVFH DVIQLL |
| 22000 | 52368 | A | 22128 | 1 | 277 | |
| 22001 | 52369 | A | 22129 | 1 | 933 | |
| 22002 | 52370 | A | 22130 | 339 | 863 | PSPVPARPVCPSSAPISMRPPCP WREAEAADLRPEAPGHRDGED VGFLSSGQLSGLCSKRKLQPTR AALTTPSAVNKIK\HFLKNNPE HVGKVGVRTRGCNGLSYTLE YTKTKGDSDEEVIQDGVRVFIE K\KAQLTLL*TEM DYVEDKLSK GVGVITPNIKGTGCGGESFNI |
| 22003 | 52371 | A | 22131 | 16 | 419 | QIQHRPWP/SRSYTNVLGRKVV YLP SFFTYAKYIVQVDGKIGLF RGLSPLMMSNALYTATRCFMK KDLPPDEIEQVSNKDDMTTSLN KVANDTSYEMMMHCVSRMLP HPLHVISMRCMDQIVGREAKYS GVLSSIG |
| 22004 | 52372 | A | 22132 | 3 | 441 | RSYTKFVMGIAVSMLTYPFLLV GDLMAVN NCG LQAGLPYPSPV FKSWIHCWKYLSVQ\GASTGRR RPFLFFATSF S*NGFVDASLHAK GQLFRGSS\CFSAGCHQDHALP WSNLNHLKNTVSTWPPWVRPD HLGTPARRLQPNNNQM |
| 22005 | 52373 | A | 22133 | 1 | 1232 | MAGAGAGAGARGGAAAGVEA RARDPPPAHRAHPRHPRPAAQP SARRMDGGSGGLGSGDNAPT EALFVALGAGVTALSHPLLYV KLLIQVGHEMPPTLGTNLGR KVLYLP SFFTYAKYIGQRD GARE GLVPRLSPRLMSNALSTVTRGS MKKVFPDEIEQVSNKDDYEDF P*RKLLKETS YEMMMQCVSRM LAHPLHVISMRCMVQFVGREA KYSGLSSIGKIFKEEGLLGFFV GLIPHLLGDVVFLWGCNLLAHF INAYLVDDSVSDTPGGIGKRPE SRFPFSQALALRSYTKFVMGIA VSMLTYPFLLVGDLMAVN NCG LQAGVPP\YSPVFKSWIHCWKY LSVQGG\LFRGSS\CFSAGCHQD HALPW\SNLNHLKNTV\STWPP WV\RPDHLGTTARRFQPNNNQ |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22006 | 52374 | A | 22134 | 3 | 1156 | PRHPRPAAQPSARRMDGGSGG LGSGDNAPTTEALFVALGAGV TALSHPLL YVKLLIQVGHEPMP PTLGTNVLGRKVL YLP SF FTYA KYIVQVDGKIGLFRGLSPRLMS NALSTVTRGSMKKVFPPDEIEQ VSNKDDMKTSLKKVVKETS YE MMMQC VSRMLAHPLHVISM R CMVQFVGREAKYSGVLSSIGKI FKE\EGLLGFFVGL\IPHLLG\DV VFLWG\C\NLLAHF\INAYLVDD SFS\QAL\AIRSYTKFVMGIAVS MLTYPFLLVGDLM AVNNCGAA SWGSPPYSPVFKSW\IHCWKYL SVQGGQLFRGSS\CFSAGC\HQDH GFALGVN*NHLKNT\VSTWPPW VRPDHLGTPARRLQPNNNQMC SSPAG\FQFHICHVSV\QMWG |
| 22007 | 52375 | A | 22135 | 2 | 425 | |
| 22008 | 52376 | A | 22136 | 2 | 430 | |
| 22009 | 52377 | A | 22137 | 2 | 406 | |
| 22010 | 52378 | A | 22138 | 1 | 297 | |
| 22011 | 52379 | A | 22139 | 1 | 111 | |
| 22012 | 52380 | A | 22140 | 1 | 398 | |
| 22013 | 52381 | A | 22141 | 1 | 409 | |
| 22014 | 52382 | A | 22142 | 500 | 1234 | GPNCRPPSCSAVEGAWPRPQGA GARA AIALSQKLELGGVGLVQ VQCPSLAPSTSSILFLCLLPHPP PHRCLQENTTCLLGV EGVLLLQ SPFPLLKTDHSSLPALAPTQSQA ALWGFADFGFMFESSPGGNLG WEPDIKLTDEMVMIMGGKMEA TPFKWFMEMCVRGYLA VRPY MDVVVSLVTIMLDTGLPCFRG/ QIKFLKHRFSPNMTEREA*NFIM KVIQSCFLSNRSRTYNMIQYYQ NDIPY |
| 22015 | 52383 | A | 22143 | 2 | 6378 | SAGPAGPLQVQKLLCMCPVDF HGIFQLDERRRDAVIALGIFLIES DLQHKDCVGPYLLRLLKGLPK VYWVEESTARKGRGALPVAES FSFCLVTLLSDVAYRDP SLRDEI LEVLLQVLHVLLGMCQALEIQ DKEYLCKYAIPCLIGISRAFGRY SNMEESLLSKLFPKIPPHSLRVL EELEGVRRRSFNDRSILPSNLL TVCQEGTLKRKTSSVSSISQVSP ERGMPPSPSGGS AFHYFEASC LPDGTALEPE |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22016 | 52384 | A | 22144 | 3 | 398 | IHKAASGVPPQPDAGCPGTGEQ QGGQRCGQ*AGP/AQAPC*SRA GTR/PTCFFVLTSLSWYRVDS NKL MNPLVAGFFG/CHCGSGQC LRKCSSARDRAPDARPLDLAQ GRCCHCNKACLHASETGVGTT SVL |
| 22017 | 52385 | A | 22145 | 344 | 498 | |
| 22018 | 52386 | A | 22146 | 344 | 406 | FLADQEDPLDPRAGCR*ETTAP RIPSKGPSSTEPLHASTAVPPCQ GELGCSRASPASEKI/DLAGRLIS PCNSDTVSPGLGGFMTCAQSLI SRRPGGPPIPPGWLQGPPLHG |
| 22019 | 52387 | A | 22147 | 3 | 2058 | LSGSGAPPGVGGAQAAAAAEE EEREVVRVRVKVRLAVSRPSRR GKFRSFAVDPQITSLDVLQHILI RAFDLSG*VGRCWGLLGRDRL GQEVYLSLLSDWDLSTAFATAS KPYLQLRVDIRPSEDSEYSVPPG AISP KDVIGSDVLLAEKRSSLTT AALPFTQSILTQVFSGTLGTQQ VLSWSYGEDVKPFKPPLSDAEF HTYLNHEGQLSRPEELRLRIYH GGVEPSLRKVSILSHLLVYPDG LTGRERMDYMKRKSREYEQLK SEWAQRANPEDLEFIRSTVLKD VLRTDRAHPYYAGPEDGPHLR ALHDLLTTYAVTHPQVSYCQG MSDLASPILAVMDHEGHAFVC FCGIMKRLAANFHPDGRAMAT KFAHLKLLLRHA\DPDFYQYLQ EAGADDLFFCYRWLLLELKREF AFDDALRMLEV TWSSLPDPPE HEVELVGPPSQVADTGFGDHR G\WPVRQRHMLRPAGGGGSTF EDAVDHLATASQGPGGGGRLL RQASLDGLQQLRDNMGSRDDP LVQLPHPAALISSKIGLSEPLLN YPDPLSSFSHPDSPSSSSPSTQ EASPTGDMAVGSPLMQEVGSP KDPGKSLPPVPPMGLPPPQEF RGNPFMLFLCLAILLEHRDHIM RNGLDYNELAMHFDRLVRKHH LGRVLRARALFADYLQSEVW |
| 22020 | 52388 | A | 22148 | 130 | 387 | |
| 22021 | 52389 | A | 22149 | 1 | 279 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22022 | 52390 | A | 22150 | 105 | 499 | DMSDTSESGAGLTRFQAEASEK DSSMMQTLT\TV\TPEAREAPA TQASSTTQ\LTDTQVLA\ENKSL AADTKKQNADPQAVTMPATET KKVSHVADTKVNTKAQETEEA PSQAPADEPEPESAAAQSQENQ DTR |
| 22023 | 52391 | A | 22151 | 285 | 984 | TSLSCYFSRTKDSPKLGLLMVL LSHFMNGNRSSEAVIWEVLRK\L GLRPGYDWALSALAVRVVLW QERTVLGLHQSGGLVERVGCW TG*RAQGS\DLGG*WVNGPELS APSLSVSWASMELPSCAGNLFS ILEMPLPTSGKCHSLE*IYLFYF SFSSLRIHHS\LF\GDVKKLITDEF VKQKYLDYARVPNSNPPEYEFF WGLRSYYETSKMKVLKFGCKV QK\KDPKEWAAQYRE |
| 22024 | 52392 | A | 22152 | 259 | 578 | |
| 22025 | 52393 | A | 22153 | 296 | 2242 | NMSDTSESGVAGLTRFQA\EAASE KDSSMMQTLT\TV\TQNVEVPE TPKASKAL\EVSEDVKVSKASG VSKATEVSKTPEAREAPATQAS SYLLSLTD\TQVLA\ENKSLAA *HQQNRMVDPQAC*QLPAT\ET KKVSHVADYGRFNYKGFRRLR LAPS\QAPADEPEPESAAAQFSG RFRVFGPKVKAKKARKVKHLD GEKDGSSDQSQASGTTGG\RRV SKALMASMARRASRGPIAFWA RRASRTRLAA\WARRAFALPLEI TLKPRRAKGLRR\RVAKFQ\SSQ EPEAPPPRG\LALLQGRAN\DLV KYLLAKDQTKIPIKRS\MDLKDII KEYTDVYPEI\NERAGYSLE\KVF GIQLKEIDKNDHLYILLSTLEPT DAGILGTTKDSPKLGLLMVLLS IIF\MNNGNRS\SEAVIWEVLRKL\ GLRPGIHHSL\LLGDVK\KLITDE F\VKQKYLG\LCQKVPNSNPPEY EFLLGACALY**EPAKMKSPQS FACK/VYQKEGSPRNWGSSVPP REGKGRMEADFEGCKLRLTLE AKAKGPRLEAPNGPLGLGSGE MLAGP\CNWDEA\DIGNPWAK ARIPRREQKLKAKAPKRS\GSA\S TGA\STST\NNSAS\ASA\STSGGF \SAAASL\TATLHIWGSSAGLWL ELGCQHQSARS\GAC\GVSYK |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22026 | 52394 | A | 22154 | 1 | 487 | EFRQPSFRRSIWP/YFLLTQA/VR TGNPAKFNQVLDQFGEKFQAD GTYTLIIRLRHNVIKTGVRMISL SYSRISLADIAQKLQLDSPEDAE FIVAKAIRDGVIEASINHEKGYV QSKEMIDIYSTREPQLAFHQEG KDSSVYSFREWGTRTGMSWL V CFLKLRL |
| 22027 | 52395 | A | 22155 | 2 | 429 | |
| 22028 | 52396 | A | 22156 | 1 | 328 | GTRFQADGTYTLIIRLRHNVIKT GV/RSGSEGLLEEKPGQGKPS GYPWASEGSVSTLPTPSLLPLPG VRMISLSYSRISLADIAQKLQLD SPEDADFIVAKVGLVQEPQ |
| 22029 | 52397 | A | 22157 | 138 | 2206 | AVTPGAMKQEGSARRRGADK AKPPPGGGEQEP\PAPAPQDVE MKEEAATGGGSTGEADG\KTA AAAA*SNFPAKSWDYSHLWKD IKEHRETS*RKAVSGKEPRFVLR ALRMLPSTSRRLNHYVLYKAV/ QGAFFTSNNAT\RDFLLPFLERA HGTQEADLLFRPRTGKAAGTP LLPEVEAYLQLLVIFMMNSKR YKEAQKISDDLMMQKISTQNRRA LADLVAAKCYYYHARVYEFLAD KLADVVRLSLHG\RLRTATLRHD ADGQATLLNLLLRNYLHYKL VPTSLRSLVSKSVFP/EEQAQQP NEWGQVTSYLHQGRIKAIQ\LE YSEARRTMTNALRKAP\QHTAV GFKQTVHKLLIVVELLLGEIPDR LQFRQPSLKRSLMPYFLLTQAV RTGN\LPRTQVLDQFGEKFQA DGYTLIIRLRHNVIKTGVRMIS LSYSRISLADIAQKLQLDSPED AEFIVAKAIRDGVIEASIN\HEK AYVQ\SKEMIDIYST\RDPLAL H\QRISFCLDIHNMVWSRPMRV PSPKSYKQGSWSLQRNGRERR NKQDLE\FPKEMA\EDDDDSFPL KLGGWGGVRGKWGTRQLCPP WGYPLPQGTCPPFSPTAHML AFRGRGWGCWEPATPDLPPGL LPSRVTLVQPGRRVGRQPPRG RVLASSVADRRGRISLCTPFRE WGTRTWDVYGLLCFLKLRL |
| 22030 | 52398 | A | 22158 | 86 | 348 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22031 | 52399 | A | 22159 | 3 | 356 | LPLSMDVRAPPVMAAVDQAL KEFGRIDILINCSSSSCGLPFCR\ AAGNFLCPAGALSFNAFKTVM DIDTSGTFNVSRLYEKFFRDH GGVIINITATLGNRGQALQVHA G\SAKAAVD |
| 22032 | 52400 | A | 22160 | 3 | 255 | GPWSCHAGA*GPGATQVSEDQ GLREPHGSRDLCSLG*KH*GAPI CAWPMSWDGPPAAHKVRPSVS APPVCINTLCYNLASAFS |
| 22033 | 52401 | A | 22161 | 3 | 360 | |
| 22034 | 52402 | A | 22162 | 240 | 1356 | AGNPSGIPGTRVHRGQRGGFAS TWSGRGAGSTPLQNSPPRQPHR EKEFLRQVLEGGSHTGVRPSA ARLVPNPHSLVSPDLL*LVSRA T\PHIFLAARKLAGATGRRCLPL SMDVRAPPVMAAVDQALKEF GRIDILINCESVLSEVGGFSQAP AAPAVSHSAGAAGNFLCPAGA LSFNAFKTVMDIDTSGTFNVS RLYEKFFRDHGGVIVNITATLG NRGQALQVHAGSAKAAVDAM TRHLAVEWGPQNIRVNSLAPGP ISGTEGLRRLDASQGMSWGRG EGAGSWGSRGLSLLLPS\GGPQ ASLSTKVTASPLQRLGNKTEIA HSVLYLASPLASYVTGAVLVA DGGAWLTFPNGVKGLPDFASF |
| 22035 | 52403 | B | 22163 | 214 | 1647 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22036 | 52404 | A | 22164 | 1765 | 1910 | LSHPHSRTPPNRTPRRTRIPQRP AVMYSPLCLTQDEFHPFIEALLP HVRAFAYTWFNLRARKRKYFK KHEKRMSKEEERAVKDELLSE KPEVKQKWASRLAKLRKDIR PEYREDFVLTVTGKKPPCCVLS NPDQKGKMRRIDCLRQADKV WRLDLVMVILFKGIPLESTDGE RLVKSPQCSNPGLCVQPHHIGV SVKELDLYLAAYFVHAGRISSQS ESP\SQ\PSDADIKDQPENGTFGA SRDSFVT\SGVF\SVT*A*LRVSQ TP\AAGVTGPNFSLSDLESSYY SMSPGAMRRSLPSTSSTSKRL KSVEDEMDSPG\EEPFTGQAR SPGKWTVSPSGLSVSWSQGMPS PTTLKKSEKSGFQQPLPFHRPPS LGNGFHTAFTDLFIYQGPQSKF HIATPSIL\HFPRHSPFFQQPGPY FSHPAIRYHPQETLKEFVQLVCP DAGQQAGQPNGSSQGVHNPF LPTPMLPPPPPPMARPVPLPVP DTKPPTTSTEGGAASPTSPTTRS /PGRTRPQQPFL/SYGPP*PHFLR AGIHHL |
| 22037 | 52405 | A | 22165 | 63 | 250 | |
| 22038 | 52406 | A | 22166 | 1 | 817 | SRLGHPRKMDDDTKATLISY MSLSFRHGYCFSEDPCVHTELG IQSGRGGRGDPDPGNALE*LA HLGP/SSHLGP*AQDGLVDAAG RASPLAGTEGAGRFSHLQPI/GP RGPPE*GAAGERFPSGVAG/GPR GAHGLPCPEQLQLQPPPPS*MP KTGSTFVAHFPSPLAQGHSPPG GGAGWCSGCSPDRPPLLGVGS HGELLNPNSPAYEVGAG/RPAT GSSGTRAGPPSPSHSAPGRTPSV SLCD/RHQCLRASPTGSIGSLPA HWREGLAGPLMD |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22039 | 52407 | A | 22167 | 240 | 1790 | TAKNSYLESCPLHMENSIHQWP RQFPFPVRRQGADAACGAGSQ ALVPSHSDTDGVLPGAEWLGD GGPARVP/GAAGGRGPAPTS*A GP*LSL*APLCFASGLSGNGKQL LGAAGRSSSHAQMHELHPAQ* HE*ATDHTGGQGPP/G*KQQNG PP/GPDNDLPAPESTPPTWNEDF LPDAIPLAHPVPRQRRPTGPAGP PGQTGPPGPAGPPGSKGDRGQT GEKGPAGPPGLLGPGRGLPG EMGRPGPPGPAGNPGPSPN SPQGALYSLQPPTDKDNG/TQG WPLPSWTQCW/SGVPGRGPPG PPGPPGRGPPGPGTPGSQGLA GERGTVPSG/AGGAAAERGPE DPGRASPHPGAHDWDPRSPGLP RGRFWPGCCPESQPQDEEGWH PTRWGPCCPAWARPWTEERG/S RPAAGS/RGVSDIETPGRPIYPD DKSQA VSVLCARSRLRAQLRP GAEQMNDCKGITGRQDIHAV SFASEHNIQNWVSKHLQLSPPV TPATQAPLKVRVPQASTLVL |
| 22040 | 52408 | A | 22168 | 104 | 271 | PSCTNPYGGGRRCDSSVVPNQCF TKHMQSRLLG*GEKALEGGGG RGVKS LVTKRDF |
| 22041 | 52409 | A | 22169 | 494 | 1074 | KGTTLCQKHWGGGYLHWGHHF EMMRLTINRSMDPKNMF AIWR VPSPFQPITRKSVGHRM\GGGK\ GAI*HYLTP/VKAGRLV VEMG GRCEFARSAKVSLTQVALRSCP FASKRL*ACGTPREGCEQDQEE RERQQPRTPTWTI*AE*PTAQHG WAYGKVPEPHMTLTPQGEILG ARFYMPKTCVVSVGDILYIGY |
| 22042 | 52410 | A | 22170 | 61 | 329 | NQRSGKKSQPW*STITPPSLIWL SNSSTTLSSSKMGQSYSSS*PSY NCSVSRMFGSNMVPAATASGA SLTCPLLWLSMTHFRKVG GW A |
| 22043 | 52411 | A | 22171 | 21 | 444 | STAQSI RSDLHYFLALLVYYW AADARFLPGRIPWLIHKELEKS HTEYCLVGSSQYTPLVQVFRSN TLVSVLSTKTI*NQRSGKKSQP W*STITPPSLIWL SNSSTTLSSSK MGQSYSSS*PSYNCSSRAKSPTL TVFQS |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22044 | 52412 | A | 22172 | 163 | 1056 | LEKSDHRISWSPGKTA\SPKSMP ERWHR*WAQILKD\MGITEYEP R\VIN\QMLEFAF\RYVTIL\DD AKIYSSHAK\KATVD\ADDVPIG QSRC\RAGSSLFTSPPPKRF/LLL RYLARQKKSNPFCPLIKPY\SGP RLPPDRYC\LTAP\NYRLKSFTE KGHSTSAGKELTVP\RLSVGFRLL LSRTKVLPTLGAHPTPQ\TMSVF NLK*GTPHVPSPGQRFSTRCPT S\QS\PAVKSFQFPGNLSQFQNV L\NPIH*IGSQKHSYYPLNMMS S\QNTA\NESSNALKRKREDDDDG\DDDDDDDYDNL |
| 22045 | 52413 | A | 22173 | 215 | 344 | |
| 22046 | 52414 | A | 22174 | 302 | 1330 | ACEQKRGGEGGNKNRERRKGE KAGRRQGTRQPCSRMRRTKQ VEKNDDDDQKIEQDGIKPEDKA HKAATKIQASFRGHITRKKLKG EKKDDVQA\AEAEA\NKKDEAP /VFADGVEKKGEG\TTTARSSPQ PLAPKP\DEPGKAGETS\SEEKM GEG*LLATEQGSPPRLLAS\SEE KAGSAETESATKASTDNSPSSK AEDAPAK\EEPQADVPA/AFG VFPNPLGALLLAATTPAAEDAA AKATAQPPTETGESSQAEENIE AVDE\TKPKESARQDEGKEEEP EA\DQEHA WNSGEMGFPHPHPP GCLACLSLPSSQLHSEVPSCPAH VCESVLSHPLALFLSVWANI |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22047 | 52415 | A | 22175 | 2 | 1577 | HGFRLPHPQPALRRLLDQRRPK TEDRCGHWDQILDLSIIKHLFS MSFIPVAEDSDFPIHNLPYGVFS TRGDPRPRIGVAIGDQILDLSIIK HLFTGPVLSKHQDVFNQPTLNS FMS\LGHAAWKEARVFLQNLL/ SL*SQARLRDDTELKRCAFISQA SATMHLPATIGDYTDFYSSRQH ATNVGIMFRDKENALMPNWLH LPVG\YHGRASSVVVSGTPIRRP MGQMKPDDSKPPVYGACKLLD MELEMAFFVVGPNRLGEPISK AHEHIFGMVLMNDWSARDIQK WEYVPLGPFLGEEFWGPLSLP WGGCPWDALMPFAVPNPKAV PQAPCRYLCHDEPYTFDINLSV NLKG\EGM\SQAAT\ICKVQILK YMYWT\MLQQAHSPTLSNGC\N LRPGGPPGLSGTHQAGPEP/EKN FGSMVE\LSWKGTKPI\DLG\NG Q\TRKFLLD\GDEVIITAMATRD FKWYC\QGDG\YRIGFGQ\CAGK VLPALLPIMRFSLLFWKQRAQS TPFQPCDWGSSPRAVGLVPPFQ |
| 22048 | 52416 | A | 22176 | 3 | 623 | DSRNSSILPRRGALLKVNQELA GYTGGDVFSFIKEDFELQNLKQL IFDSVFSASFVGGMLVPIGDKP SSIADRFYLGGPTSIRGFSMHSI GPQSEG DYLGGEAYWAGGLHL YTPLPFRPGQGFGELFRTHFFL NAGNLCNLNYGEGPKAHYIVK LAECIRWSYGAGIVLRLGNIAR L\ELNYCVPMGVQTDGRICDGV QFGAGIRFL |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22049 | 52417 | A | 22177 | 352 | 2397 | GPMSEGIASQGARRRRGIMGLR GLWASRADGRRGETEPEAKQEI LENKDVSFLKVLIELLVETFTS IHH*GDDVFKAKNLIEVGVVST WCAFPVSSEELVNVPM*NIDTC QGTTCGVVSL*FPFCPSEKSCFY GQNNTMVGNNEGSMVCYRLF TFLYWNLELGTFTL*LHSETS YGLSFFKPRPGNFERK*EAQQII EYTGLIEKLK*VAYL*KSAEYS VS\AFQSFPLGLGENRVAFLIP KGSYLIQ*VSNGCWHLHCQPLL WGSYHRILAEELRVLIESTWPFE G*LCNGTSQAFSCGPCTPSRSSA RHGHSVCGQLLVADVPGVKG MLGENNHLFLKY*SMNG*FA/L YFPLDLFSCFL*ESFPLTAPSLEG SRLTLETMYLLCQGGFGELFRT HFFLNAGNLCNLNYGKTCAIQE TIVVQLFSLCKAQYTKIRLGNI RLELNYCVPMPGVQTDYVVLG IIFHNHPLSSNFILFWTFASGD TAGAARLLRLPTDDRAFRDGG GCSHNRQLPFPSTPLLFSTQSPS WKGCSHAGCMHVCLGAQLPG LGAQLGHGSESQVERLLACGG RWGARRQGCCWHDLPKAPHA GCFLAGEKKVGDDQEPCTKTA AVREGESVGCTAEGGCLGLSG GCQGWLAPGLVELRSAAARQE GSRRRRKRRRHLLRVHPQKV |
| 22050 | 52418 | A | 22178 | 1 | 1017 | |
| 22051 | 52419 | A | 22179 | 1 | 435 | |
| 22052 | 52420 | A | 22180 | 1 | 1353 | |
| 22053 | 52421 | A | 22181 | 1 | 834 | |
| 22054 | 52422 | A | 22182 | 2 | 2675 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22055 | 52423 | A | 22183 | 72 | 1339 | AMRGANAWAPLCLLLAATQ LSRQQSPERPVFCTCGGILTGESG FIGSEGFPGV\WPPESKCTWKIT VPEGKV\VLNFRFIDLESDNLC RYDFVDVYNHANGQRIGRFC GTFRPGALVSSGNKMMVQMIS DANTAGNGFMAMFSAAEPNER GDQYCGGLLDRPSGSFKTPN\W PDR\DYAGVTCVWHIVAPKNQ LIELKFEKFDVERDNYCRYDYV AVFNGGEVNDARRIGKYCGDS PPAPIVSERNELLIQFLSDLTA DGFIGHYIFRPKKL\PTTTEQPV\ TTTFPVTGLKPTVALCQQKCR RTGTLEGNYCSSDFVLAGTVIT TITRDGSLHATVSIINIYKEGNL AIQQAGKNMSARLTVVCKQCP LLR\RGLNYIIMGPSRVKDGAR QNSWPNSFIMMFQT\RNQKLLG CP*KISQC |
| 22056 | 52424 | A | 22184 | 49 | 170 | HTVGDGRLLRRP*REFGASFL* CFLEARFGLKNWGHCHWRH |
| 22057 | 52425 | B | 22185 | 597 | 651 | |
| 22058 | 52426 | A | 22186 | 1 | 791 | |
| 22059 | 52427 | A | 22187 | 2 | 943 | TGACAEPRVGLLFRLLKGRCRG GRNMELGSCL\YGFREAEEEG EPEVKKRRLLCVEFASVASCDA AVVAQCFLAENDWEMERALNS YFEPPEAES\ALERRPETISEPKT YVDLTNEETDSTTSKISPSED QQENG\SMFSL\ITWEYLMGL\D LKQSVQRRARGVCSYLAL*VLS LLFNSNVSYVYTERMNQLKMV LKKMQEAPESATVIFAGDTNLR DREVSDKVSLMFEDRLLLRLLI *VPFCQYTWDTQMNSNLGITA ACKLRFDRIFFRAAAEEGHIPR SLDLLGLEKLDGCRFPSDHWGL LCNLDIIL |
| 22060 | 52428 | A | 22188 | 277 | 534 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22061 | 52429 | A | 22189 | 29 | 1305 | VGVLRLVECPLCPGPAPMSVPA FID\SEEDQAAELRAYLKSKGA\ EISEENSEGGLHVDLAQIIEACD VCLKEDDKD\VESVMNSVGIPY SWIL\EPDKQ\EAFDLKALCEKA GSKFPRR*TAPSLETCSFLSNLF H\GMG*GILPVKIHSVICSL\IKV\ AASCGAIQYHPQLEPGIKFRK WDFLNWN\LTGKKSTPLLKTT FMKALVE\CKKSDAASKGM\VE LLGSYP\EGNASQ\ARVDAHR\C IV\RALKDPN\AFLFD\HLLTLKP VKFFGKASLFHCSFLT\K\VSA* MGHHMSRFYPD*LRTFH*IPLG PVTMDPGIWPKMRLLF/TFMGN GQ*KNKEISF*PQCQEPSRLGA DDVESHVIDA\VRN*KWVYC QNWSRPRRKVVVSHSTHR\TFG K\QQWQTTVLTHLNAW\KQNL NK\VKNSLLSLF |
| 22062 | 52430 | A | 22190 | 194 | 413 | |
| 22063 | 52431 | A | 22191 | 3 | 160 | EVKFQWVLSLG*SFSLPKSSFQ RCGAGGAVHWSTALFLLGAAS ASSYHQRPG |
| 22064 | 52432 | A | 22192 | 268 | 473 | |
| 22065 | 52433 | C | 22193 | 93 | 500 | |
| 22066 | 52434 | A | 22194 | 2 | 398 | FFLRRSLALSPRPDCGLQWRNL GSLQAPLPGFTPFSCSLPSSWD YRRPPRPANFLYF**RRGFTLL ARMVIS*PHDPPASASQSAGIT GVSHRARPETYNFCSFIHSSLPV EPEARMTKNSDIGEIW |
| 22067 | 52435 | A | 22195 | 972 | 2180 | PRHCCASASSAPASRPASSSSP PAACPW*GSLGPAATPATWR R |
| 22068 | 52436 | A | 22196 | 2271 | 3074 | RDPSTPTVVRSLGVPLLSRRRFK MAPSVAATKLAERNETMVQTC WTETQSSSDGSTPRRVRISLAL WRPSLFFSMADTSLVLNFPVRS SSGVIRPSNKRPSLAILTRISRTS SPKYMPLTIFSNSCFPGLRDPRSI SLSNSVRMSSNDPSSPKAPHS/G IDTHPPLVSFHQINVQPFLHVAS IGASADDQADFTVLVVIATGHH GAHCVIHHSYDVGIIVPSLFDGF VKQFDHICSFHSARFKSLCPGD QDGLIYFGLLARKRKRESHR |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22069 | 52437 | A | 22197 | 1956 | 2747 | FAFSPK*HSCLRCPCI*FSSGLLH EVL*LLPLCWP*THGWDPGSRE ANKSPKLHAIRCWWLEEENL WLSSNSQSLQTVKN*ESHIN*SC RSNLI/HH*FWNQVK*K*LLNIS GNCFFFLRWSL/DSVAQAGVY WRDLGSLQPPPPGFKRFSCSLP SSWDYWHLPCLAKFCIFSRDG /GFTIWARLVLS*SCDLPASGS QSAGITGVSHHTWLQVTYFLK EMRSCYFSQVGWPQTPGLKQC SHLKLSSWDYRHMSPHLAISG |
| 22070 | 52438 | C | 22198 | 85 | 228 | |
| 22071 | 52439 | A | 22199 | 2 | 434 | |
| 22072 | 52440 | A | 22200 | 1 | 1356 | |
| 22073 | 52441 | A | 22201 | 146 | 1909 | ILHSLEISALLSLMMLTIGDVIK QLIEAHEQGKDIDLNKVTKTA AKYGLSAQPRLVIIA\SVPPQY RKVLMPKLKAEPK\TA\SGIVV VAVMCKPHRCPHISFTGNICVY CP/GVGPDSDFEYSTQSYTG\YE PTSMRS/IFRARYDPFLQTKDRI EQ*RQLGHSVDKVEFIVMGGTF MALPEEYRDYFIRNLHDALSGH TSNNIYEAVKYSERSLTKCIGITI ETRPDYCMKRHLSMDLTYGCT RLEIGVQSVYEDVARDTNRGH TVKAVCESFHLAKDSGFKVVA HMMPDLPNVGLERDIEQ\FTEFF ENPAF\RPDGLK\IYPTLVIRGTG LYELWKS\GRYKSYFS**PGLN WVARFLALVPPWTRVYRVQRD IPMPLVSSGVEHGNLRELALAR NEDLRIQCRDVRTREVGIEIH HKVRPYQVELVRRDYVANGG WETFLSYEDPDQDIL\IGLLR\LR KCSEETFRFELGGGVSVIRELH VYGSVVPVSSRDPTKFQHGGFG MLL\MEEAERIS*RRNMGLGKI AVISGVGTR\NY\GKIGYRLPR PRTMVKMLEIMGHTQSHSFC LPWHEHRRIRISLNTQQRGL |
| 22074 | 52442 | A | 22202 | 1 | 457 | |
| 22075 | 52443 | A | 22203 | 2 | 297 | CVMYRDYPLELFMAQCY/GNIS DLGKGRQMPVHYG/CKERHFV TISSPLATQ/IPQAARGPGYGIM/ SIRVDGNDVFAVYNATK/EARR RAVAENQPFLIEARPT |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22076 | 52444 | A | 22204 | 3 | 1446 | DWLLAKMAEAIAAAR\WRLN RGLSHAALLLLRQLGGSGD*AR SHPPRQQQCSALDDKP\QFPG ASAGVIDKLEFIQ\PNVISGIPIYR VM\DPQGQIHQPQARDPHLAEG ERWLKL\YKS\MTLL*HPWDRIL **VFSGQGRILLLT*TNYWLRR GTHVG\SARRLGQTRTLVFGQY REAGVLMYRDYPLELFMAQC YGNISDLGKGROMPVNYG\CKE RHFVTISSPL\ATQDPSGRWGAA YAATGGANANRVR\VICYFRAR GAAS*GGDAHA\GFNFRCHNL SCPIIFFCRNNGYAISTPTSEQYR GDGIAARGPG\YGIMSIRVDGN DVFAVYNATKEARRRAVAENQ PFSHQAHDRVQAPSP\SDAS*T YRSVDEVN\YWENKGPPILPGF GHYLF\SQ\GWWDEEQQKAWR KQSRRKDPGPVQPS\VMEAFEQ AERK\PKPNP\NLL\FSDVYQNM PAPVRQPPES\LARHFKTYGNH YPWDHFDK |
| 22077 | 52445 | A | 22205 | 2 | 292 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22078 | 52446 | A | 22206 | 1 | 1894 | QSLADLLQSQPSITLTSQIWSPSP A*GFWSWGNLSVTTSPSK\PATP TRTIAATPIQTL PQSQ TAPKRID TPSLEEPSDLEEELEQFAKTFKQR RIILGFT\QGDAGLAMVKLYGN DFSPTTIFRFEALNLSFKNMCKL KPLLEKWLND AENLSSDSSLSS PSALNSPGIEGLSRRRKRTSIE TNIRVALEKS FLENQKPTSEEIT MIADQLNMEKEVIRVWFCNRR QKEKRINPPSSGGTSSSPIKAIFP SPTSLVATTPSLVTSSAATTLTV SPVLPLTSAAVTNLSVTASTSEA SSASETSTTQTTSTPLSSPLGTSQ VMVTASGLQTAAAAALQGAA QLPANASLAAMAAAAGLNPSL MAPSQFAAGGALLSLNPGTSLG ALSPALMSNSTLATIQALASGG SLPITSLDATGNLVFANAGGAP NIVTAPLFLNPQNLSLLTSNPPG GFTIEISNNNSTMVMTGMRIQIG TQAIERAPSYIEIFGR TMQLNLS RSRWFDFPFTREEALQADKKLN LFTVRKFQNI RHTLFK CENKNT FQQCLLLEQDSSCGTGFCSM TT YPVMLLSSEQPVQSLSVRQCVI LLDAAA VISGGMGAVCLLLTH LCPLCYAGLLSEITDPESFVKDL LYSVP |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22079 | 52447 | A | 22207 | 1 | 2417 | MRVRTSSLPSTMLRVQNYARA KAGPEYAFVDSTECSPQWMVS PLKRGQTQTNGLDFQKQPVVVG GAISTAQAQAFGLHGHVQVLA GTSLQAAAQSLNVQSKSNEESG DSQQPSQPSQQPSVQAAIPQTQ LMLAGGQITGLTLTPAQQQLLL QQAQAQAQLLAAAVQQHSAS QQHSAAGATISASAATPMTQIP LSQPIQIAQDLQQLQQLQQQNL NLQQFVLVHPTTNLQPA\QFIIS QTPQGGQQGLLQA\QNLLTQLPR QSQANLLQSQPRINTLTSQPATP TCTIAATPIQTLPQSQSTPKRIDT PSLEEP\SDLEELEQFAKTFKQR RIKLGFTQGDVGLAMGKLYGN DFSQTTISRFEALNLSFKNMCK LKPLLEKWLND\AENLSSDSSL SPSALNSPGIEGLSRRRKRTSI EA\NIRVALEKSFLEN\QKPTSEE ITMIADQLNMEKGVIRVWFCN RRQKEKRINPPSSGGTSSSPIKA IFPSPTSLVATTPSPVTSSATTTL TVSPVLPLTSA\VTNLSVTGTS DTTSNNTATVISTAPPASSAVTS PSLSPSPSASASTSEASSASE\TS TTQ\TTSTPLSSPLGTSQVMVTA SGLQTA\AQLLPFKGAAQLPAN\ ASLA\AMAAAAGLNPSLMAPS QFAAGGALLSLNPGTL\SGALSP ALMSK\STLA\TIQTLASGGSL K*TSLECKLGTLVICPMREEPPD |
| 22080 | 52448 | A | 22208 | 3 | 114 | |
| 22081 | 52449 | A | 22209 | 1 | 505 | NLGVDLLPGYQDPYSGRTLTK GEVGCFLSHYSIWEEVVARGLA RVLVFEDDVRFESNFRGLRL MEDVEAEKLSWYSYWTLAYA LRLAGARKLLASQPLRRMLPV DEFLPIMFDQHPNEQYKAHFWP RDLVAFSAQPLLAAPTHYAGD AEWLSDTETSSPWDDDSGR |
| 22082 | 52450 | A | 22210 | 3 | 626 | RAARAAPLLHLLLLGPWLEA AGVAESPLPAEVLAILARNAEH SLPHYLGALERLDYPRARMAL WCATDHNVDNTTEMLQEWA AEGDDYAAV\WRPEGEPRFYP DEEGPKHWT\KERHQFLMELKQ EALT\FARNWGADYI\LGATLGL WQDHSVNSLGGCSPGRAGACD VPSSKFADTDN\ILTNNQTLRLL MGQGLPVVAPMLDSQTNV |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22083 | 52451 | A | 22211 | 1 | 2004 | MRAARAAPLLQLLLLLGPWLE AAGVAESPLPAVVLAAILARNAE HSLPHYLGALERLDYPRARMA LCLQGPAQPQWDLWLAGFEEE QTGTSEVHWGPTWQGSTTLEA SGHRCATDHNVDNTTEMLQE WLAAVGDDYAAAVWRPEGEP RFYPDEEGPKHWTKERHQFLM ELKQEALTFARNWGADYILFA DTDNILTNNQTLRLLMGQGLPE VAPMLDSQTYYSNFWCGITPQ GYRRTAEYFPTKNRQRRGCL RVPMVHSTFLASLR\AEGADQL AFYPPHPNYTWPFDDIIVFAYA CQAAGVSVHVCNEHRYGYMN VPVKSHQ\LEDERNFIHLILE ALVDGPRMQASAHVTRPS\KRP SKIGF\DEVFVISLG\RRPDRRER MLASLWEMEISGRVVDVAVDG WMLQQQVPFRNLRP*DLLPGL/ YKDPYFGPHS*PRAEVGLLSSD HYSIWEEVVSQGAWPR\VLVV *RNDVAPLRTNFQGGGLERL\M E\DVEGKRNLSEWKPPFRILPLG R\KQVEPLRRETAVEGLPG\LV VAG*LPNWTLA\YALRLAGGP ASLLALQPFAPHCCPVERISLPI HCFDQ\HPNEASTKAHFWRPD\ LVAFSAQ\PLLAAPTHYAG\DAE WILLSRRHHSPWDDDSGRLISW SGSQKTLRSPRLDLTGSSGHSL |
| 22084 | 52452 | A | 22212 | 1 | 468 | ELSHNAKAKVMVASHNEDT/V LFALRRMEELGLHPADHQVYF GQLGMCDQ\SFPLGQAGYPIL TQIHLFSPHTCRAAGGEVRCLP ALPRVWALRCGPNLIPAWDSH WKLLGTLELCAQGPHLCDPH VLGPRGLSTFCQGQPTQPEPLG EQWPGWG |
| 22085 | 52453 | A | 22213 | 1 | 1893 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22086 | 52454 | A | 22214 | 390 | 2005 | INRDVETACTYILRNTEdVMLE FVMREWKKSRKLLGQRLFNKL MKMTFYGHFVAGEDQESIQL LRHYRAFGVSAILDYGVEEDLS PEEAHEKEMESCSSAAERDGGSG TNKRDQYQAHRAFGDRRNG VISARTYFYANEAKCDSHMETF LRCIEASGRVSDDGFIAIKLTAL GRPQFLLQFSEVLAKWRCFFHQ MAVEQQQAGLAAMDTKLEVA VLQESVAKLGIASRAEIEDWFT AETLGVSGTMDLLDWSSLIDSR TKLSKHF/V*VPNAQTGQLEPLL SRFTEEEELQMTRMLQRMdVL AKKATEMGVRLMVD AEQTYF QPAISRLTLEMQRKFNV EKPLIF NTYQCYLKDAHDNV\TLD\VDL SPREGWCFGAKPVRGAYLAQE RACAAEIGYEDPINPMYEATNT MYHRCLDYVLEELKHNAKAK VMVASHNEDTVRFALRRMEEL GLHPADHQVYFGQLLGMCDQI SFPLG\QAGYPVYKYVPYGPVM EVL PYLS\RRALE\NSSL MKGTH \RER\QLLWLELLRRLRTGNLFH |
| 22087 | 52455 | A | 22215 | 3 | 303 | |
| 22088 | 52456 | A | 22216 | 798 | 2250 | VPRAPQGML*GPRKDAGTPER RAGPPGGRGTADGGGCGALAG SGS/DDPRLCIWTF LVTdQLLL TGPGRPRGSVAAAATGPGVGA LRAPARAQPRGAVDGRPLLQ VLPHRRLEVSLGKSPKECVLW/ RHLLSESEKRPFVEEAERLRVQ HKKDHPDYKYQPRRRKSAKAG HSDSDSGAELGPHPGGGAVYK AEAGLGDGHHHGDHTGQTHGP PTPLTPKTELQQAGAKPELKL EGRRPVDSGRQNIDFSNVDISEL SSEVMGTMDAFDVHEFDQYLP LGGPAPPEPGQAYGGAYFHAG ASPVWAHKSAPSASASPTETGP PRPHIKTEQSPGHYGDQPRGSP DYGSCSGQSSATPAAPAGPFAG SQGDYGD LQASSYYGAYPGYA PGLYQYPCFHSPRRPYASPLL GLALPPAHSPTSHWDQPRRNGS TAQGPKEGVAGALQGAVRSKA GLGAEKPLHSRPHSLDNGCTGC PGSGVSVRRLG |

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|------------|--------------------------------|---------|-------------------------------|---|---|---|
| 22089 | 52457 | A | 22217 | 299 | 1631 | LLEPHCGGKCFKRHWFPSCSEA SC\PSAAPQRW*HTG/SPEVPAA PGAQGREPSM/RDGEHAVRGGS CMEAGPMGLQCVDKHHQGVH N/RGEARVFLQSQVGAILPRPW PNPAPSEP/VQSPLASSTGP*VFP SRPGQQASGPA/RRHPGAEPGQ RGDAVQLLPRPQTSPHGPQDA ALSSAPHPWRQL/MASPLQEA PLHPFCGHRSPCPVPWQLSPTD PIQSRPPARGWAPANQGRPSHP RCRGGGGAFCGHGF/SYTQPLT FRLASMVL SIHPKPPKETLRF NMVVAAEPGVPAMSQRRPRGC TRFSHTDKAPLDTCTDMNAYT CARRHSSTYS DHITLQGAFACT HTWAQSCTCQPPPTPAACKLDR GQSSGMLHAGCVGWGGGTHV RVDLSSQLNRRVRPHLCMLRC WSSCHRASVSCTHPSLHTTGPV LISARTGADHTWYTAGTY |
| 22090 | 52458 | A | 22218 | 383 | 762 | RHQGNQKRKELSLK/CQKSRQE SPRAEENPKWREGKKTSESSV QKAGRAAAAQAGAAASRVPG LSGSNLAPCNKGRLSAREDVSN SKLKILSSGRKHTEHVIMLKAW GLGRQSLRCRLFDLIPSHKV |
| 22091 | 52459 | A | 22219 | 325 | 945 | QPSPLAPKADLSAREGRFQLKV RCRLQQYQQQR\RKFAAAFLA FHFSLLGSCGILAEAG\KKEKPE KK\VKKSDCGRIGSWVCVAPP SGDCGLGHHGRATRT*\AECKQ \TMKTQRCKIPCNWEGRQFGRG SAKLPSFQAWGECDLDTALKT\ KTGSLKRALHKSPNAQKTVTIS/ KSPCGKLTQPQLQAES\KKKK KEGKKPEGRLRD |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22092 | 52460 | A | 22220 | 1 | 1908 | MKYIQDFQREKQEFERNLARFR EDHPDLIQNAKKSDIPEKPKTPQ QLWYTHEKKVYLKVRPDATTK EVKDSLQKQWSQLSDKKRLK WIHKALEQRKEYEIMRDYIQK HPELNISEEGITKSTLTKAERQL KDKFDGRPTKPPPNYSYLYCAE LMANMKDVPSTERMVLCSQQ WKLKLSQKEKDAYHKKCDQKK KDYEVELLRFLFESLPEEEQQRV LGEEKMLNINKKQATSPASKKP AQEGGKGGSEKPKRPVSAMFIF SEEKRRQLQEERPELSESELTRL LARMWNDLSEKKKAKYKARE AALKAQSERKPGGEREERGKLP ESPKRAEEIWQQSVIGDYLARF KNDRVKALKAMEMTWNNME KKEKLMWIKKAAEDQKRYERE LSEMRAPPAATNSSKKMKFQG EPKKPPMNGYQKFSQELLSNGE LNHLPLKERMVEIGSRWQRISQ SQKEHYKKLAEEQQKQYKVHL DLWVKSLSPQDRAAYKEYISN KRKSMTKLGRPNPKSSRTTLQS KSESEEDDEDEDEDEDEDEEEEE DDENGDSSEDGGDSSESSSEDE SEDGD/EGGADRAQWEGRGVL PGGPPGDSTSFLTQNEEDDED EDDDEDDDEDEDNESEGSSSSS SSSGDSSDSDSN |
| 22093 | 52461 | A | 22221 | 129 | 2365 | |
| 22094 | 52462 | A | 22222 | 5 | 2730 | PSLRFAISGFVWRLAAPASAAA ELRLDCSARRAPRCPRPALPSTR SAEGAVLCAFRREEQQAATA AAAAAAATAAAAAAPAPPPRP EEEPLPPREGAAVPGRAGEGA ATQSQGGSRWSGKPGGRAAPA RPRRWLDSWRMNGEADCPDLD EMAAPKGGQDRWSQEDMLTLLE CMKNNLPSNDSSSKFKTTESHM DWEKVAFKDFSGDMCKLKWV EISNEVRKFRTLTELILDAQ*HF KNPYKG\KKLKKHPDFPK |
| 22095 | 52463 | A | 22223 | 1 | 446 | RPSPTSSM/PGLWGYSRPCSSG VPASALQA*SPAFSPASQRPPTT SWWEVP*EEGRA\PVWEGRIRA VGPAPAS*PSDLPAWSCRWRE TRG\SPAEDAMLLRAVEPLEGC QRPLLDSEPP/SPARTSAPAASA SPPAPGGPPCLARPLPR |

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|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 22096 | 52464 | A | 22224 | 582 | 1175 | THTHVPAGTHPHTQTTSLSHLI GRALTVPESPKCPCLLPSAC*PR PGRAQPAGPAWSKKEASNPGS E/PPQHSL*RRMAPPE\VPARA VHTCRCLSSAPPGARLPLDPER RAPQSPRSPPPSAQPPPPPPPP PPPGRRGPSQQSWRPSPPPPRTR SRSPRRSRVRGPRAPALAAPPP GARPGPCAAACGSPTGCS |
| 22097 | 52465 | A | 22225 | 609 | 5241 | GPQTTWCGRPTMCQHCGPAVS SWKQPSHDPCCRGGENRRQPG TPARATQGRLLRRRPEGARVPSA RRGRPRARWRDKERNNTCVA ML*QVTNSTANAPQNNPEVDS IMAEKVEAPASVDWQKRCLT LETQLFRFRLQASKIRELLADK GHGTYISPFSLAKQMQELEQRL LEAEQRAENAETQVGVMEEKV KLSNLKNVDSEGLHRKYQELL KAIKGKDELISQLEAQLEKQKQ MRAEEAKTVQEKA AKIKEW |
| 22098 | 52466 | A | 22226 | 2 | 205 | |
| 22099 | 52467 | A | 22227 | 1 | 6186 | |
| 22100 | 52468 | A | 22228 | 96 | 1584 | DLGSGITASPPRPEPEHPVFPPA PHTPSKMGKEKTHINIVVIGHV \DSGKSTTTGHLIYKCGGIDKRT IEKFEKEAAEMGKGSFYAWV LDKLKAEREPG\TIDISLW\KFE\ TTKYIYI\ID\APGHRDFIKNMIT G\TSQADCAVLIVAAGVGEFEA GISKNGQTREHALLAYTLGVK QLIVGVNKM DSTEPAYSEKRY DEIVKEVSAYIKKIGYNPATVPF VPISGWHGANMLEPSNMPWF KGWKVERKEGNASGVSLLEA\ LDTILPPTRPTDKPLRLPLQD\ YK\GGIGTVPVGRVETGILRPG MVVTFAPVNITTEVKS VEMHH EALSEALPGDNVGFNVKNVSV KDIRRGNVCGDSKSDPPQEAAQ FTSQVILNHPGQISAGYSPVIDC HTAHIAKFAELKEKIDRRSTK KLEDNPKSLKSGDAAIVEMVPG KPMCVEFS\Q*PVIG/RTPV RD MRQTAA\GVVIKNVQKKS VGA GKVTKSAQKAQKAGK |
| 22101 | 52469 | A | 22229 | 1 | 1023 | |
| 22102 | 52470 | A | 22230 | 1 | 396 | |
| 22103 | 52471 | A | 22231 | 2 | 1259 | |
| 22104 | 52472 | A | 22232 | 1 | 2514 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22105 | 52473 | A | 22233 | 3 | 2027 | EESDCLTEYEEDAGPDCSRDEG GSPEGASPSTASEMDVSLHFVL WGCLHVVYQRMIDKAEDVCLFV AQPGEVLGQLAVLTGEPLIFTL RAQRDCTFLRISKSDFYEYDSP KLECGWHEDPNPWTSPSTGL NPLFLELCRHMVFQRLGQGDY VFRPGQPDASIYVVQDGLLELC LPGPDGKECVVKEVVPGDSVN SLLSILDVITGHQHPQRTVSARA ARDSTVLRLPVEAFSAVFTKSA RTITGCVWRYVRASASYCPYLP PLCDPKDGHLLVDGCVNNVP GSLWRYVRASMTRRATCPRCA TPRTGTYSWMAATSTICQASGR PHHPHTQAPPAPHTRTRRTSPA AWVPKRSSPLTWGARMRTSA PTGTACPAGGCCGSG*IPGLTR* RFQTLWKSSPAWPTCPVCGS*R LSSPAPTASTCARPSTASRPWTL GSSTRSILRTTRRMSTAVTTTAT PAPIITPST*GTNGTGCAQIRPA EPSPGARTSWNPSLSATFAPEEF VASP*LDVPICRMGQCCSLPGG ATLP*GPCGPQCMPGNVVPPER TAARYRQTTAYQTPACPTPPRG QRPT/CVPTVSSLQAGLQGGPRS DFDMAYERGRISVSLQEEASGG SLAAPAREPREQPAGACEYSYC EDESATGGCPFGPYQGRQTSSIF EAAKQELAKLMRIE |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22106 | 52474 | A | 22234 | 281 | 1832 | NDSGLPDRPSSWNQPM EAPLQ TGMVLGVMIGAGVAVVVTAV LILLVVRRLRVPKTPAPDGPRY RFRKRDKVLFYGRKIMRKVSQS TSSLVDTSVSATS RPRMRKKLK MLNIAKKILRIQKETPTLQRKEP PPAVLEADLTEGDLANSHLPSE VLYMLKNVRVLGHFEKPLFLE LCRHMVFQRLG/QGDYVFRPG QPDASIYVVQDGLLELCLPGPD GKECVVKEVVP GDSVNSLLSIL DVITGHQHPQRTVSARAARDST VLRLPVEAFSAVFTKYPESLVR VVQPGPPSGPAPYPAPSYGHAP RALQIIMVRLQRVTFLALHNYL GLTNELFSHEIQPLRLFPSPGLPT RTSPVRGSKRMVSTSATDEPRE TPGRPPDPTGAPLP GPTGLQGG PRSDFDMAYERGRISVSLQEEA SGGSLAAPAREPREQAGACEY SYCEDESATGGCPFGPYQGRQT SSIFEAAKQELAKLMRIEDPSLL NSRVLLHHAKAGTHIARQGDQ MEEVKVPAFAVIVD |
| 22107 | 52475 | A | 22235 | 50 | 4287 | PGRKSPGAEDRALWGPACRLL TDSGLPDRPSSWNQPM EAPLQT GMVLGVMIGAGVAVVVTAVLI LLVVRRLRVPKTPAPDGPRYRF RKRDKVLFYGRKIMRKVSQSTS SLVDTSVSATS RPRMRKKLKM LNIAKKILRIQKETPTLQRKEPP PAVLEADLTEGDLANSHLPSEV LYMLKNVRVLGHFEKPLFLELC RHMVFQRLGQGDYVFRPGQPD A\SIYVVQDGLLELCLPGPDGKE CVVKEVVP GD\SVNS |
| 22108 | 52476 | A | 22236 | 283 | 403 | TCLSLVSGCGHCEKMNSEENW *IPIQWASSNPGRRRNIR |
| 22109 | 52477 | A | 22237 | 33 | 222 | NGPM\CFVKQLEIPQYGYRNNV PTTTPRSNLAKELEKYSKTSFEY TINDNHTYGGGLGCMRPLV |
| 22110 | 52478 | B | 22238 | 1 | 1860 | |
| 22111 | 52479 | A | 22239 | 303 | 672 | GITACVFFSMAEGRTRAERSCD SK*AIGAPAE*GGASPGKSP WQGAGYSPLGACGHKARLWIP WRRSWSGEKGARGCRGTGKK LGHQGWRWETPGRPGGAGPA GFPDPVVMGCEKEASRV |
| 22112 | 52480 | A | 22240 | 1 | 1377 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22113 | 52481 | A | 22241 | 1 | 2232 | MQDTEKDDNNNDEYDNYDEL VAKSLLNLGKIAEDAAYRARTE SEMNSNTSNSLEDDSDKNENLG RKSELSLDLSDVVRVETVDSLK LLAQGHGVVLSNMNDNRNYA DSMSQQDSRNMNYVMLGKPM NNGLMMEKMVEESDEEVCLSSL ECLRNQCFDLARKLSETNPQER NPQQNMNIRQHVVRPEEDFPGR PDRNYSMDMLNLMRLEEQLSPRS RVFASCAKEDGCHERDDDTTS VNSDRSEEVDMTKGNLTLL KAIALETERAKAMREKMAMEA GRRDNMRSYEDQSPRQLPGED RKPKSSDSHVKKPYYGKDPST EKESKCPGCDGTGHVTGL YPHHRSLSGCPHKDRVPPEILA MHESVLKCPGCTGRGHVNS NRNSHRRDIQVFNLQKQEMIDR LESLSGCPAAAAEKLAKAQEKH QSCDVSKSSQASDRVLRPMCFV KQLEIPQYGYRNNVPTTTPRSN LAKELEKYSKTSFEYNSYDNHT YGKRAIAPKVQTRDISPKGYDD ANGYCKDPSPSSSTSSYAPSSS SNLSCGGGSSASSTCSKSSFDYT HDMEAAHMAATAILNLSTRCR EMPQNLSTKPQDLCA TRNPDM EVDENGTLDSL MNKQRPRDSC CPILTPLEPMSPQQQAVMNNRC FQLGEGDCWDL PVDYTKMKPR \\RIDEDESKDITPEDLDPFQEAL |
| 22114 | 52482 | A | 22242 | 727 | 4372 | LWACVLPGVTLPPFLGEKTSCK MEVDTEEKRRHRTSRKGVVRPV EPAIQELFSCPTPGCDGSGHVSG KYARHRSVYGCPLAKKRKTQD KQPQEPAPKRKPFVKADSSSV DECDDSDGTEDMDEKEEDEGE EYSEDNDEPGDEDEEDEEGDRE EEEEIEEDEDDEDEDGEDVEDE EEEEEEEEEEEEENEDHQM CHNTRIMQD TD LDDNNNDEY DNYDEL VAKSLLNLGKIAEDA AYRARTESEMNSNTSNS |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22115 | 52483 | A | 22243 | 34 | 1558 | PASEEFNSLHGRTPRRDLECRN QQSTTEERRRHDCVQQASEHN EGKWDFAFSAQSQPKP*KPFDV PC*DSRPACP*EHTAGTSGSTSS ETCFFQSSEWPYGELGAYNIFT GPKSTLSSSLVTGVSNSSSL*LP SPKNTITNWFHTRDHSSYSEIHS KACANP*APSQPSR*ASW\IATG SFRRAGLAT*PCCTGSKLLPAW VLANHRWDRTRDGIQKQGNSE *PSSPGTRAFEGNSSSPAPAASIT SMLSPSFTPTSVIRKMYESKEKS KEEPASGKAALGDSKEDTQKA SEENLLSSSSVPSADRDYFSHY KFQTVRHYRGSSCS\PHLSQGQP FTPKEQDYSDLKGNWGRKNTH FGHSPVSLQHFFFRPVPPSSPLSP MVPNG*GLLTKLHPGFGTEDA GPGSTSTASSKFAPNWCASSWD GLESFTGNIWPHPGSALLPFN*S LVHPLLNPRPGNTSASGNGATA ANSAQ\SCILQALVSHGSSCSAF QDNPSETCPAGQACPHALP |
| 22116 | 52484 | A | 22244 | 1502 | 2657 | EGKVPLAFIVLTSLNNAVMSPSF FSCRLLVTALKVSSRCSAMKGV EFFTCWSTFKPFRPASTSSTEST TPECELSLSFSLFAERLERRGFK STLAFCSISKISTLFSAWSSNGIG AK*FPEFCPGDRMACSRPASLSS SSCG/S*PKTAGSAS*SARVREPP TEPTGRD*PFSQ\TSSIIIEAKHGT LSRLKNSLKSKSPGDCSGKTAS LGTS*SAAGSCARMTSTSSSSAT PPLHSTIPSFTEAVRRLVLFPL* SSSSILSSKPVSSMVSD*LVGPA ENHSGSSSV*ESFLLRSPKTRLL SPNSLLKRLSLKSLSRSLSLKSR RSLSL\SGDPSQRSGQRLSSHQC SYVHQADEAHHYLSLMDFLSA GS*QRLSRGSPLQSSVSEG |
| 22117 | 52485 | A | 22245 | 324 | 391 | |
| 22118 | 52486 | A | 22246 | 42 | 274 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22119 | 52487 | A | 22247 | 1 | 835 | MCAGNLCWEERWAVDEKEA TDKKPHVGGFGQGAPAPA AAMSGRSVRAVTRSRF*DDIKK VMAAIEKVRKWEKKWVTVGD TSLRIFKWVPVTDSEKEKSKS NSSAAREPNGFSDASANSSLL LEFQDENS\NQS\SVSDVYQLKV DSSTNSSPKPPKQSESLSPAHTS DFRTD\DSQPPTLGQGDPRSP LPASSEVADEPPTLTGRTSFHL ETQVVVEE\EDSGAPPLKRFCV\ DQPTVPQTGSEKLAPSRPSAFW ALPLFIAFWFWPRRVCWG |
| 22120 | 52488 | A | 22248 | 3 | 244 | |
| 22121 | 52489 | B | 22249 | 271 | 711 | |
| 22122 | 52490 | B | 22250 | 73 | 200 | |
| 22123 | 52491 | A | 22251 | 885 | 975 | GSTWWPAD*AQL*LHLPTRCM AECWEIPA |
| 22124 | 52492 | A | 22252 | 102 | 909 | PGGRHGRQNDFAAPGGRLEARI HGTVSAPLYHRVLCRLGSRPA SAAGPAARGGDLAPGEHSFCE DGN YARVESVDRSAINRAMQN PRKSTASVCWTFTASDLPAQGV \PRTSSTRTLREDPFPPSAEKWL RAVLHHFVNEKLQQIFIETLKP SRRSMSGRHPLDSNPVLQQQGR CDLIENKLSPPGIMSVLDDVCP CTPRAGEQTRHCCRTAGGCGD PRAFQQLERRFVIHHYAGKTHR PLPGLTPTGNSTNARNIVMDTQ QRTGNN |
| 22125 | 52493 | A | 22253 | 48 | 112 | |
| 22126 | 52494 | A | 22254 | 1243 | 1615 | YSPSSWFSNLYQPSTGALSSSET PKDMAPMKSLREVRSQSHTSTL SRRSTSPGFRNLTKVSFHTGFSV AFTVRVFCFVRFRGSGMSFSFT* GSERPLGSIGIRLRASPTVTWISS AVGARISSC |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22127 | 52495 | A | 22255 | 468 | 1431 | SVSTTRSFSVDSSAKTAAMPVT VTRTTHHNHPDVIFGAWGPP*S WGPLWALTQPLGLLRLLQLV STCVAFSLVASVGAWTGSMGN WSMFTWCFCFSVTLHILVELCG APGPFPPWSWR\NFPNTFACYA ALFCLSASIYPTTYVQFLSHGR\ SRDHAI AATFFSCIACGCYATE VAWTRARPGEITGYMATVPGL LKVLET FVACIIFAFISDPNLYQ H\QPALEWCVA VYAICFILAAIA ILLNLGECTNVLPPIPFPSFLSALA \FCLSSSMPPPLFSGPSTSSMRSM AASLGAREM*AAAAGMPTTW VPGTADWLRPS |
| 22128 | 52496 | A | 22256 | 98 | 414 | CTRVSAEKT SVCLFGLYWESL SISSSCSSAKWPFSTIRSASSTT RHLSRRFLK**CFSLINSHSRP GVATTISGRRFSILCCFCVDIPPT KIAVLIPVNLAT |
| 22129 | 52497 | A | 22257 | 2 | 224 | |
| 22130 | 52498 | A | 22258 | 2 | 115 | |
| 22131 | 52499 | A | 22259 | 2 | 118 | |
| 22132 | 52500 | A | 22260 | 472 | 648 | GPGGRSFTVWWNW*RRMAQC P\PAEGVQRPECLGPHRAVPAP AHVGLHQEPSRLLPALH |
| 22133 | 52501 | A | 22261 | 540 | 1893 | GRCATPRPRWRGHQCDPPPGD VCVAWREMQLRNKRRR\DLG NLIK\RFLTAPNSLPD/AVVLTTE EAVIFWCNVLAQQIFGL/PLEM MNEQPLEGAVREKALHTMREQ TQRMGLVKQL/LTLSKIEAAPT HLLNEKVDVPM/MLRVVEREA QTLVYNVNHTEPGTHITVRW QRVPHGAEFVVEE*SEGWPVPV PKPHRAVVGANAHISFCPPQEL SKRFTAIRKTKGDGNCFYRALG YSYLESLLPDAFQPLLPQAWV SPGESQGAGIRDPLWPVPVPKP HRAVVGANAHISFCPPQELSKR FTAIRKTKGDGNCFYRALGYSY LESLLPDAFQPLLPQAWVSPG ESQGAGTRDPLWLWLFRLWLL RLLCLLLLLLGETAQSRLALTW GRHKQGRRLARLSGILGFLALRK QWLGQQAQQLLQNLHLLLLR WAGLGVIVFQVSNQPAWERTG |
| 22134 | 52502 | A | 22262 | 1 | 1772 | |
| 22135 | 52503 | A | 22263 | 107 | 294 | LHLLSFGYLTHQLLCLHLKWDS HTLHHSHTIAR*AGCSEATWS PPRRLRAPRSRALCSGFR |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22136 | 52504 | A | 22264 | 1 | 474 | |
| 22137 | 52505 | A | 22265 | 1 | 148 | VKYHEFTCSFKKQITVPEDARL LK*DVRGRPSRLFLADPPPPHT VNREY |
| 22138 | 52506 | A | 22266 | 509 | 2755 | YQSQSFEDEMNQVTDWVDPS FDDFLECSGVSTITATSLGVNN SSHRRKNGPSTLÆSSRFARK\R GNLSSLEQIYGLENSKEYLSENE PWVDKYKPÆTQHELAVHKKKI EÆVETWLKAQVLGRQPKQGG SILLITGPPGCGKTTTLKILSKEH GIQVQEWINPVLPDFQKDDFKG MFNTESFHMFPYQSQIAVFKE FLLRATKYNKLQMLGDDLRTD KKIILVEDLPNQFYRDSHTLHE VLRKYVRIGRCPLIFIISDSLSGD NNQRLLVPKEIQEWSISNIRFN PWAPTMMKFLNRIVTIEANKN GGKITVPDKTSLELLCQGCSDI RSAINSLQFSSSKGENNLRPRKK GMSLKSDAVLSKSKRRKKPDR VFENQEVQAIGGKDVSLFLFRA LGKILYCKRASLTELDSPRLPSH LSEYERDTLLVEPEEVVEMSHM PGDLFNLYLHQNYIDFFMEIDDI VRASEFLSFADILSGDWNTRSL LREYSTSIATRGMHSNKARGY AHCQGGGSSFRPLHKPQWFLIN KKYRENCLAALKALFPDFCLPAL CRQTQLLPYLALLTIPMRKSSFR FSFYSKDIGEGLPSGRRTLWGRI GKWEGLDRGTWDD*TPDSG DEA\QLNG\GHSAEESLGEPTQA TVPETWSLPLSQNSASELPASQP QPFSAQGDMEENIIEEDYESDG DIEASLLIRLLLHSFHFCFHSGT |
| 22139 | 52507 | A | 22267 | 2 | 161 | |
| 22140 | 52508 | A | 22268 | 1 | 599 | VTRLFFQPGYGTLQPQRLLMPK KNR\IAIYE\LLFK\EGVMVPKK\ DVPIPKHPELA\DRNVPNLHVM KPMQ\SLKS\RGYVK\EQFAWR HFYWYLTG*GYQGVSISSRDYL \HLPPÆIIVPCHPYGRSPSRLAR PSG*KVLEG*ANLRGLHKNGEA DKRLPTRRECLCHPGA\DKKAE AG\ALGSSNPNFQFRGGFGRGR GQ\PPQ |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22141 | 52509 | A | 22269 | 1 | 345 | KHPELADKNVPNLHVMKAMQ SLKSRGYVKE\DY\HLPPPEIVPA TLRRSRPETG/RPRPKGLEGERP ARLTRGEADRDTYRRSAVPPG ADKKAEAGAGSATEFQFRGGF GRGRGQPPQ |
| 22142 | 52510 | A | 22270 | 2 | 161 | |
| 22143 | 52511 | A | 22271 | 2 | 641 | RRPQHRACSSFFSPGTGPCSRRR CLMPKKNR\IAIYE\LLFKEG\VM VAKKDVHMP\KHPE\LAD\KNG APTFHVMKGHAGLSKSPRATV KGTSAWGDIFYW\YL\TN*GY QGVSISSRDYLS\SCPREICCLAT ATARSPSKRLGKAFGLKRSWE GLRRPGEDFTRGGKFDRGYLT GRIAVATLVADKKAEAG/ALGS SNPNFQFRGGFGRGRGQPPQ |
| 22144 | 52512 | A | 22272 | 1 | 1693 | MFNSVPVQNE\DG\SFNFEGVKA EFRPGTQTQEYIKGMEDSASEV TVNREVTTDN\PYTISVTNKTLS AIRIKMFMPR\AYELKVTVIKM AFELSTRCSKRLM/DGSFETVLT DVIEGKTMSGYDRSRRVNLPNF NNQVIFRVVRKTPDSNDSNVV DAIQVRSYAEVIDAKFRYPLTG LLFVEFDSKMFPNQLPTISIRKR WKIVNVPSNYDPESRTYNGNW DGTFKKAWTNNPAWVLYDLM INQRYGLDQKELGISVDKWAL YEAAQYCDQM\VLTA\KAARNL ATFVT/CIIQSQTDAPREPAYIFT NDNVVNGDFS\YT\SQARRACTR RAT*CLMMSKTCINRTLSQYSI/ V/EGHSTVR\NNVTSITAIG\AHV EA/KANRRGRWILKTNL\RSTTV NFATGLEGM\IPTIGDVVAISDNF WSSNLTMNLSGR\LLVSGSQIF LPFRVDARAGDFIIVNKP\DGKP VKRTISSVSADGKTIEINIGFGFP VKPNTVFAIDRTDLALQ\QYVVT KIDKGDDDEEFT\SKSRRWSTIL ISTMKLITGLTSTTD\RQASLSQI R/CPKPENVK\CPQSRESSRG |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22145 | 52513 | A | 22273 | 1 | 1843 | MEDNLSINKIKILLSVSDGEIDE TFSLKQLMFNSVPVQNEGDSFN FEGVKAEFRPGTQTQEYIKGME DSSSEVTVNREVTTDNPYTISVT NKTLSAIRIKMFMPR\AYELKVT VIKMAFELSTRCSKRLM/DGSFE TVLTDVIEGKTMSGYDRSRRV NLPNFNNQVIFRVVRKTPDSND SNVVDAIQVRSYAEVIDAKFRY PLTVLLFVEFDSKMFPNQLPTIS IRKRWKIVNVPSNYDPESRTYN GNWDGTFKKAWTNNPAWVLY DLMINQRYGLDQKELGISVDK WALYEAQAQYCDQMV\LTAKA ARNLATFVT/CIHQSQTDAYKVV RDICSIFRGMSFWNGPREPAYIF TNDNVVNGDFS\TSQARRACT RRAT*CLMMSKTCINRTLSQYS I/V/EGHSTVR\NNVTSITAIG\AH VEA/KANRRGRWILKTNLRSTT VNFATGLEGMPTIGDVVAISD NFWSSNLTMNLSGRLLLEVSGSQ IFLPFRVDARAGDFIIVNKPDKG PVKRTISSVSADGKTIEINIGFGF PVKPNTVFAIDRTDLALQQYVV TKIDKGDDDEEFT\SKSRRWSTI LISTMKLITGLTSTTDRQASLSQ IR/CPKPENVK\CPQSRESSRG |
| 22146 | 52514 | B | 22274 | 1 | 1452 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22147 | 52515 | A | 22275 | 1 | 1902 | MIQKVISGSKGGSQKPHNPVEM EDNLISFNKIKILLAVSDGEIDET FSLKQLMFNSVPVQNEGDSFNF EGVKAEFRPGTQTQEYIKGME DSSSEVTVNREVTTDNPYTISVT NKTLAISIRIKMFMPRIAYELKVT VIKMAFELSTRCSKRLM/DGSFE TVLTDVIEGKTMSGYDRSRRV NLPNFNNQVIFRVVRKTPDSND SNVVDIAIQVRSYAEVIDAKFRY PLTGLLFVEFDSKMFPNQLPTIS IRKRWKNVNAPSNDPESRTY NGNWDGTFKKAWTNNPAWVL YDLMINQRYGLDQKELGFSVD KWALYEAQYCDQMVLTA AARNLATFVT/CHQSQTDA PREPAYIFTNDNVNGDFSYSQA RRACTRRAT*CLMMSKTCINRT LSQYSI/V/EGHSTVR\NNVTSIT AIG\AHVEA/KANRRGRWILKT NLRSTTVNFATGLEGMPTIGD VVAISDNFWSSNLTMNLGRLL EVSGSQIFLPFRVDARAGDFIIV NKPDKGPKVRTISSVSADGKTI EINIGFGFPVKPNTVFAIDRTDL ALQQYVVTKIDKGDDDEEFTS KSRRWSTILISTMKLITGLTSTT DRQASEVKPVNFTSSRHQAQPE VGLIPPLWPQKGIIAQTSKSS |
| 22148 | 52516 | A | 22276 | 1 | 675 | |
| 22149 | 52517 | A | 22277 | 155 | 700 | SGVLVGHALTARQPSSGRRLV VDHSANRRGRWILKTNLCSTT VNFATGLEGMPTIGD/GDFIIVN KPDGKPKVRTISSVSADGKTIEI NIGFGFPVKPNTVFAIDRTDLAL QQYVVTKIDKGDDDEEFT\SKS RRWSTILISTMKLITGLTSTTDR QASLSQIR/CPKPENVK\CPQSRE SSRG |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22150 | 52518 | A | 22278 | 1 | 1871 | MEDNLSINKIKILLAVSDGEIDE TFSLKQLMFNSVPVQNEGDSFN FEGVKAEFRPGTQTQEYIKGME DSSSEVTVNREVTDDNPYTISVT NKTLSAIRIKMFMPR\AYELKVT VIKMAFELSTRCSKRLM/DGSFE TVLTDVIEGKTMSGYDRSRV NLPNFNNQVIFRVVRKTPDSND SNVVDAIQVRSYAEVIDAKFRY PLTGLLFVEFDSKMFPNQLPTIS\ IRKRWKIVNVPSNYDPESRTYN GNWDGTFKKAWTNNPAWVLY DLMINQRYGLDQKELGISVDK WALYEAQAQYCDQMVLTA ARNLATFVT/CIQSQTDAYKVV RDICSIFRGMSFWNGESISVIID RPREPAYIFTNDNVVNGDFSYT\ SQARRACTRRAT*CLMMSKTCI NRTLSQYSI/V/EGHSTVR\NNVT SITAIG\AHVEARPTDCGRWILK TNLRSTTVNFATGLEGMPTIGD VVAISDNFWSSNLTMLNSGRLQ EVSGSQIFLPFRVDARAGDFNIV NKPDAKPVKRTISSVSADGKTI EINIGFGFPVKPNTVFAIDRTDL ALQQYVVTKIDKGDDDEEFTS KSRRWSTILISTMKLITGLTSTT DRQASLSQIR/CPKPEENVK/CPQS RESSRG |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22151 | 52519 | A | 22279 | 3307 | 5305 | CRSSQNTQETSPDRALLVNLRP SQGPLLALWVPAEGVGGKGHC LPPRSFFRMDNQLVPAVSDGEI DETFSLKQLMFNSVPVQNEDGS FNFEGVKAEFRPGTQTQEYIKG MEDSSSEVTVNREVTNDNPTYI SVTNKTLAISIRIKMFMPRAAYEL KVTVIKMAFELSTRCSKRLM/D GSFETVLTDVIEGKTMSGYDRS RRVNLPNFNQVIFRVVRKTPD SNDSNVVDIAQVRSYAEVIDAK FRYPLTGLLFVEFDSKMFPNQL PTISIRKRWKIVNVPSNYDPESR TYNGNWDGTFKKAWTNNPAW VLYDLMINQRYGLDQKELGISV DKWALYEAQYCDQMVLTA KAARNLATFVT/CHQSQTDAYK VVRDICSIFRGMSFWNGESISVII DRPREPAYIFTNDNVVNGDFS T\SQARRACTRRAT*CLMMSKT CINRTLSQYSI/V/EGHSTVR\NN VTSITAIG/AHVEA/KANRRGRW ILKTNLRSTTVNFATGLEGMIPT IGDVVAISDNFWSSNLTMLNSG RLLEVSGSQIFLPFRVDARAGD FIIVNKPDGKPVKRTISSVSADG KTIEINIGFGFPVKPNTVFAIDRT DLALQQYVVTKIDKGDDDEEF T\SKSRRWSTILISTMKLITGLTS TTDRQASLSQIR/CPKPENVK\CP QSRESSRG |
| 22152 | 52520 | A | 22280 | 3 | 412 | PAAVA*VKTEPETPGPSCLSQE GQTA\VKTEESSELGNVVIKIDH LETIQQLLTAVVKKIPLITAK\W QRAMTMRKVLQEILEKNPRFH HLTPLKTKHIAHWCRCHGYTPP DPESLRNDGDSIEDVLTQIDSEP |
| 22153 | 52521 | A | 22281 | 2 | 513 | IFACWGGKQAWPACCNSLRGQA VKGNNQLLPVSLVKKRTTLAPNT QTASPRALADSLMQLARQVSR LE/QRAKREPENEEVDILSLSE PVKINIKKEQEEKQEEVKFYLP TPGSEFIGDVTQKRLEEV DSTFG DDL VQGFSGGISRRYGEKPGVQ DLEVEPDSVTEMLQFYD |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22154 | 52522 | A | 22282 | 1 | 1197 | MAWPCISRLCCLARRWNQLDR SDVAVPLTLHGYSDDLSEEPGT GGAASRRGQPPAGARDSGRDV PLTQYQRDFGLWTPAGPKDPP PGRGPGAGGRRGKSSAQSSAPP APGARGVYVLPIDADAAAAV TTSYRYGLGRDRNESPPCGGRT RRPGARGMGWAAERRRLEPGS HATSELPAASEVTPVWSVGTA GGAFAAPCPETVLEHPRAGSAP LPSQPPSWGQPSWPAFSRVGT GLPLTPTAGPSRARGARRPCPP ALPGHCLLDRTYTGLQTLGAET LLAVVNSAAMNVGVQVVDVE LHRHSLGEDCIYPQSSESDISDA PPSLPLTIPAPVKASSPIKQSHEP VPDTSVEKGS\PGSCPFHL*GPL SHLGSSPGFLLWRPPGLLSSVA |
| 22155 | 52523 | A | 22283 | 131 | 677 | PSSLS/CDIFLRSPISTPSPSPLPRT PTSTPVHVKQGTAGSVINNPYV IMDKQPGQVIGATTPSTGSPTN KISTASQISQGTGSPVPKIHGSSF VTSTVKVIKQEPGEAPHVPAT GAASQSPLQYVTVKGGHMIA VSPQKQVITPGEGIAQSAKVQP SKVL/GQIG*CLPTLARADLLYS |
| 22156 | 52524 | A | 22284 | 3 | 5128 | LLKIHSSQSSPQQA VLTIPSQLK PLSVNTSGGVQTILMPVNKVVQ SFSTSKPPAILPVAAPTPVVPSS APAAVAKGEDASCFSAKSVEQ YYGWNIGKRRAAEWQRAMTM RKVLQEILEKNPRFHHLTPLKT KHIAHWCRCHGYTPDPESLRN DGDSIEDVLTQIDSEPDHGS LG DGKSSSVGPTAVVTLLACHLEC PSSFSSADNLCKLEDLQQFQK REPENEEVDILSLSEPVKINIKK EQEEKQEEVKFY |
| 22157 | 52525 | A | 22285 | 112 | 651 | GGLCTMARTKADWPANRTGG KAP\RKQLAYKKPASQECGPLT GGVKKPHRYR\PGTVGGSVKFR R\YQKST\ELLIRKLPFQ/RRLVR EIAQGL*NKILRFQSAAGALQE GKWRPNLVWPFLKDTNLVC*S MAKRVTIIAKKTFQLAPPHTVE NRALRIHSMGKHFISQKKKK NFSSSCYW |
| 22158 | 52526 | A | 22286 | 1 | 339 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22159 | 52527 | A | 22287 | 2 | 1369 | EPAPPARRSLSAAAAASGTTVD TASHSLVFSQQ\LNMQREIGFRV NCTVAM*DVYFKAHRAVLA AF SNYFKMIFIHQ TSECIKIQPTDIQ PDIFS YLLHIMYTGKGPKQIVD HSRLEEGIRFLHADYLSHIATE MNQVFSPETVQSSNLYGIQISTT QKTVVKQGLEVKEAPSSNSGN RAAVQGDLPQLQLSLAIGLDDG TADQQRACPATQALEEHQKPP VSIKQERC DPESVISQSHPSPSSE VTGPTFTENS VKIHLCHYCGER FDSRSNLRQHLH THVSGSLPFG VPASILESN DLGEVHPLNENSE ALECRRLLSSFIVKENEQQPDHT NRGTTEPLQISQVSLISKDTEPV ELNCNFSFSRKRKMSCTICGHK FPRKSQ LLEHMYTHKGKSYRY NRCQRFGNALAQRFQPYCDSW SDVSLKSSRLSQEHLDLPCALES ELTQENVDTILVE |
| 22160 | 52528 | A | 22288 | 363 | 947 | STARRGKSR SRPAVALQRQPSA ASRSPSSSRRRRGVSKEVSVPLA RTKQTARKSTN\GK\APRKQLA YKKPARKSA\ PSTGGVKKPHRY RPGYCGRSVKFRR\YQKSH*DF* FRKL PFQAVVWRENLLKDF*K QILRF\QSRSYRVALQGGQVEA LSGVGLF*KTTNLLC*SMPKRV NNYCQKDIPAKHARIPWRTVL |
| 22161 | 52529 | A | 22289 | 1 | 92 | |
| 22162 | 52530 | C | 22290 | 10 | 198 | |
| 22163 | 52531 | B | 22291 | 74 | 205 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22164 | 52532 | A | 22292 | 2 | 1914 | RGHCEPSRAAPSRADRH PASAL ARDPGRRRGPAGQAAPQPMEP ENIVANTVLLKAREGGGGRK GKSKKWRQMLQFPHISQCEEL RLSLERDYHSLCERQPIGR\LF* EFCATRPELSRCIAFQDGM AEY EATPDEKRRKACGRRLMQNFL\ S HTGPD LIPEVP\ RQLVTNCTQRL EQGPCKELSQELTRVTHEYLSV APFADYLD SIYFNRF\ QGKGLE REA\TKNTLRQYRVLGKGGFG EVCACQVRATGKMYACKKLE KKRIKKRKGEA\MSLNEKQILE KVNSRFVVS LA YG\YETKD\AL CLVLTLMNGGDLKFHIYHMGQ AGFPEARAVFYAAEICCGL\EDL HRERIVYRDLKPENILLDDHGH I RISDLG\LA VHVPEGQTIKGRVG \TVGYMAPECLKNERYTFSPDW WALGCLLYEMIAGQSPFQQRK KKIKRE\EVERLVKEVPEEYSER FSPQARSLCSQLLCKDPAERLG CRGGSAREVKEHPLFKKLNFKR LGAGMLEPPF\KPDPQAIYCKD VLDIEQFSTVKGVELEPTDQTF YQKFATGSVPIPGKNEQMVET ECFQELNVFGLDGSVPPDLDW KGQPPAPPKKGLLQRLFSSPKD CCGN\CS DSEELPYPLAPSPRP |
| 22165 | 52533 | A | 22293 | 102 | 403 | |
| 22166 | 52534 | A | 22294 | 1086 | 1436 | |
| 22167 | 52535 | A | 22295 | 965 | 1231 | |
| 22168 | 52536 | A | 22296 | 1434 | 2215 | TPSFSLRTGVNKEHWVLLGFST EDGRW\MFTRGGE\ DCTARIWD LRSRNLQCQRIFQVNAPINCVC LHPN\QAEIIVGDQSGAIHIWDL KTDHNEQLIPEPEVSITSAHIDP DASLHGQLFNSTGNCYVWD\LT GG\IGDEV TQFIPKTKIPAHTRY ALQCRFSPDSTLLATCSA*LRR/ CKIWRTSNFSLMTEL\SIKSGNP GE\SSRG\WMWGCALIGGTSPNI VTASSNNLARLWCVKTGEIKRE YGGHQKAVVCLPFND SVLG |
| 22169 | 52537 | B | 22297 | 158 | 385 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22170 | 52538 | A | 22298 | 145 | 1232 | LPVRAEPTRAAAMSGDEMIFDP TMSK/NMKKKKKKPFMLDEEG DTQTEETQPSETKEVEPEPTED KDLEADEEDTRKKDASDDLDD LNFFNQKKKKKK\TKKIFDIDEA \EKGVKDL\KI*SDVQEPTEPED DLDIMLGHHKKKKKNVKFPDE DEILEKDEALEDEDNKKDDGIS FSNQTGPAWAG\SERDYTYEEL LNR\VFNIMREK\NPGYWLPGG RKRKFGPWKPPQ\VRVGTKKT FFCPLLQDICKLLHRSASISFA FLLG*IGVPSGSIDG**PNL*SKG RF\QQKQIENVLRRY\KEYVTC\ HTC\RSPDTIL\QKDTRLLPYS AETC\HSRCFCWPVFKTGLPQA VHGQSRGTAPVPA |
| 22171 | 52539 | B | 22299 | 50 | 319 | |
| 22172 | 52540 | A | 22300 | 3 | 235 | LLLYPLRSLPENPLRLVQQIYSF LKGSSEK*NDLPRVPLLELGVG LLPPNQYSCSRAKPLTCGLTM SLDGAQQGF |
| 22173 | 52541 | A | 22301 | 3 | 2849 | WAKPVARASPAAPVGRQCQIR GAWSWGEGRGQGPAPSPAGS PATSEESLAPMAWRCPRMGRV PLAWCLALCGWACMAPKGTQ\ AEESPFVGNP\GNITGARGLTGT LRCQLQVQGEPPVHWLRDGG ILELADSTQTQVPLGEDEQDDW IVVSQRLRITSLQLSDTGQYQCLV FLGHQTFVSQPGYVGLEGLPYF LEEPEDRTVAANTPFNLSCQAQ GPPEPVDLLWLQDAVPLATAP GHGPQRSLHVPGLNKTS |
| 22174 | 52542 | A | 22302 | 3364 | 3899 | LVFLFDDLIGIVELVLPGNIVHGI MSVRPRVAAGLRVRLQPGRRW LRGPLQLGAPLGLDLLVDVPGS PRFVVGVPLVVEAPRPPTPP AAAQQARS*GLECPGRGAAAP REV\LHLQTAHIHGPGPRGGPR ARPGLPGLCPP*T\FSCQEAKGE RGGAHNSGGSGSKWPPPPPPPS |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22175 | 52543 | A | 22303 | 1660 | 4652 | PNPNTCLCNHVESGPCCPSTHT YTLTDLQPLFGVRVPTRPSSGRG TQAEESPFVGNPGNITGARGLT GTLRCQLQVQGEPEVHWLRD GQILELADSTQTQVPLGEDEQD DWIVVSQLRITSLQLSDTGQYQ CLVFLGHQTFVSQPGYVGLEGL PYFLEEPEDRTVAANTPFNLSC QAQGPPEPVDLLWLQDAVPLA TAPGHGPQRS LHPGAAVGAW EGGSRLWLRAP EAGKRWGG E VPPVTHAGAGMLR SERD |
| 22176 | 52544 | A | 22304 | 54 | 288 | SEAGQAQPA AAVGVFWTGRRA WETGEGYYSNLSLMELQL*RQ CI*DCFFSSSWRCSVPVYFKEEK YKGNLVCLLFFK |
| 22177 | 52545 | B | 22305 | 243 | 2641 | |
| 22178 | 52546 | A | 22306 | 35 | 204 | |
| 22179 | 52547 | A | 22307 | 244 | 424 | PSLFKNIMTFYPNLHFLWCRGR LYLDVWRQ/VR*FVRNTNYQLP LVLHNLLSRFNTFDEL V |
| 22180 | 52548 | A | 22308 | 1 | 477 | |
| 22181 | 52549 | A | 22309 | 2 | 418 | WYQHLLLMRASGSFQSWWKV KGEPAYHMANRP**SLISLRTK AKTGA*LFDYFVPHFIRKN*SLF TIAKAWNHPKCTSVTDWIKKM WYIYTM EYYAVTRRNKIVSFA ET*MELEVIIVSKLTQE QKTKHC MFSLTSGS |
| 22182 | 52550 | A | 22310 | 30 | 199 | |
| 22183 | 52551 | A | 22311 | 547 | 682 | LVFLTNQRLVSTHQGTWWE*K *CQPVIPSL*FYFLRKFSVIVIW* *LLILP*HPMALKI/C/CCQAACS GHFTAGTGEITRPCSIS SKVLKR LSRL*STSGS**LVFLTNQRLVS THQGTWMKLEA ILSKVTQE QK TKHHMLSLRSGS |
| 22184 | 52552 | A | 22312 | 2 | 194 | CPSMIDWLKKMWHRYTMEYY AA\IKKNEIMS\FAGTWMKLEAI ILSKLTQE QKN\KHCMFSLITGS |
| 22185 | 52553 | C | 22313 | 1 | 1845 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22186 | 52554 | A | 22314 | 1 | 1384 | MRFDRTWQVPYPSQCSWGSS RQGYVPQARGIVLDSQEAYPSP GGTTLCDHDPDKQAPG/PVRRP APGN\PNRLVVSVALQFLTFHES GITSALRVRPLPQSV\SFQGGPGC TEA*RRASICRRRV*S*HSTKLDL GAVAAQQQAWVAG\PRSPQRR CHQYS*AGPAWLGLQRGRGSH RPDTSPWHFWALAGREEQVL PPESLL/RARTPGTHLAPGPGA* TRVQSGPGSWLTWAG*GTPQVI SS/PGAGAVGAPETTAVPTVIA PRRSVEMWPETKEHLVAVARR KWVSAQEKRLSLRGCGSEKMG VSPGETRVYFPALTSRCRRRCG RVSEPSPTASWAPAPSLGWAYQ LAGGRLVLRVGLSAGWRAACP QGGPISWLEGLSSGVLSAG WRAACPQGGPISWLEGLSSST MRQPRAPQSSLPAPAPWGAPDP LAMLAAWIEARPGVWPTQPGP WQVSWVCV |
| 22187 | 52555 | A | 22315 | 11 | 431 | RHLLAAPPAPPAAAAAALSH CLRSSGRLAPHTSRRLPRVVKR RVNALKNLQVKCAQIEAKFYE EVHDLERKYAVLYQPLFDKRF EIINAIYEPTEEECEWKPDEEDEI SEELKEKAKIVDEKK\DEEKEDP KGIPEFW |
| 22188 | 52556 | A | 22316 | 64 | 467 | PAAWLPILVAARQLTVQMMQN PQILAALQERLDGLVETPTGYIE SLPRVVKRRVNALKNLQVKCA QIEAKFY\EEVHDLQRKYAVLY QPLFDKRFEIINAIYEPTEEECE WKPDEEDEISEELKEKAKIEDE |
| 22189 | 52557 | A | 22317 | 2 | 177 | |
| 22190 | 52558 | B | 22318 | 228 | 377 | |
| 22191 | 52559 | A | 22319 | 630 | 767 | WRVKFKNTVKIQANF*KSRFIH LTVVPVTILSQVTLQLTMSPKT |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22192 | 52560 | A | 22320 | 80 | 1362 | VTACAAPAAWLPILVADIWSSY NMADIDNKEQSELDQDLDDVE EVEEETGEETKLKARSA*LFR MM\QNPQILA\ALQERLDG/LW VETPT\GYIESLP\RVVKRR\VNA LKNLQVKCAQKETQ\FYE\EVH DLERKYAVLYQPLFDKRFEIIN AIYEPTEEECWKPDEEDEISEE LK\EKGQIEDEKKDEEKEDPKGI P*IWLTVFK\NVDLLSDMVQEH DEPILKHLKDIKVKFSDAGQPM SFLVLEFHFEPNE\YFTN\EVLTKT YRMRLEPEPDDSDHFSFDGQEI MGCTGCQIDWKKGKNVTLKTI RK*/RRNHKGRGT\VRTGH*NQ FPNDSFSNFFCPLLKSPESGDLD ED\AEAILAADFEIG\HFL\RERI PRSVLYFTGEAIEDDDDDYDEE GEEADEEGEEEGDEENDPDY\N PKK\DNPAECKQQ |
| 22193 | 52561 | A | 22321 | 3 | 425 | GCGCGGAAARGSPAPGRPAAS PPDCPLWLQGCYPPPSCDALSA TEADGCD*IYPPDTSRDGPHQA SLPGESSFPGQPND SYLPERGS ERSRQASYATPAAETQDPDEGL PQPGPEALPGGLQVPKSAAPFC GAQHAAGQ |
| 22194 | 52562 | A | 22322 | 2 | 285 | SRFEPRVRPTGGDRPHQASPPG DSSSFPGQPND SRLPECGSECRG QASYATPAAETQDPE*RSSPTRS *SP\PGGFQVPKSAAPFCGAQHA AGQ |
| 22195 | 52563 | A | 22323 | 85 | 473 | FTMPAVALVPKELYLSSSLKDL NKKTEVKPEKISTK/QDYVHSIL GTANIKKAIEEAERLSESLKRLRY KEAEVRK*LEEKDRQKEAQQ LQQRQETGRE\DGGLAKVSLE NVL DYQDKTQKSNGEKSEKM |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22196 | 52564 | A | 22324 | 1 | 1449 | MMRAHMFVYKELKQIYKKKT HPHQKVGKGYKQTLRGRHLR GQETYEKKLTHVYETDFFKQQ QYYFHSILGPANIKKATGETER LSESLKLRYYEEVEIWKKLEEKD RQGEAQWLQQKRQETGREDGS MLAKGSLEIVLDSKDKTQKSN GEKNEKCETKEKGAITAKELYT MMMDKNISLIIMDAQRMQDYQ DSCILHSLSVPEKAISPGVTASW IEAHLPPDSIDTWKKRGNVEY MVLLDWFSSAKDLQIGTTLWH LKDALFKWEKGGYKNWFLCY SQYTTNAKVTPPPQHQNEELIS LDFTYPSLEESIPSKPAAEMPPP PIKVDEIDIELISDQISDNDQNER TGPLNISIPVESVAASKSDVSPH QPVPSIKNVPQIDHTKKLAVKL PEEHIKSESTNHEQQSPQNEKV IPDCSTKPVVSSPTLMLTDEEKA HIHAETALLMEKNKQEKELQE RQQGKQ/K/EKLREEHEQKAK |
| 22197 | 52565 | A | 22325 | 185 | 2983 | FIMPAVASVPKELYLSSSLKDL NKKTEVKPEKISTKSYVHSALK IFKTAEECRLDRDEERAYVLYM KYVTVYNLIKKRPDFKQQQAD CAYFLGQTVHILFQHRALLEKK YRAVGAITAKELYTMMTDKNI SLIIMDARRMQDYQDSCILHSL SVPEEAISPGVTASWIEAHLPPD SKDTWKKRGNVEYVVLLDWF SSAKDLQIGTTLRSLKDALFKW ESKTVLRNEPLVLEGGYENWL LCYPQYTTNAKVTPPPR |
| 22198 | 52566 | A | 22326 | 313 | 3720 | FIMPAVASVPKELYLSSSLKDL NKK\TEVKPEKISTKSYVHS/AP RKIFKTAEECRLDRDEERAYVL YMKYVTVYNLIKKRPDFKQQQ DYFHSILGPGNIKKAVEEAERLS ESLKLRYEEAEVRKKLEEKDRQ EEAQLRQKQETGREDGGTL AKGSLENVLDSKDKTQKSNGE KNEKCETKEKGAITAKELYTM MTDKNISLIIMDARRMQDYQDS CILHSLSVPEEAISPGVTASWIE AHLPPDSKDTWKKR |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22199 | 52567 | A | 22327 | 46 | 562 | LLQGPFGCGDSMPVEARPSAA WRGGRAPGWTPFSPPDRETWK PQ/RASQGESGQRRFGPCPRSGG RPPGPGSAAHSSRSQRWRKASR AWPAAPRKGLLPQAQAWPPTP AAGL*GFLAACKR/PPVGGRRGP APAPCRPASSRCFLICDSGPPCL CSASRAAWMGSAASSRVLFIEG |
| 22200 | 52568 | B | 22328 | 51 | 445 | |
| 22201 | 52569 | A | 22329 | 51 | 366 | CQWNTQTQVCYKQDVQSITAL GSAAQCTCLSSPR*SGKFKLLFS PGLPGTLVPSTIPATSAPRA/SHR AGEAWVGEPGRALAALQNSS\PD WAGYQGLPCKPSIRAA |
| 22202 | 52570 | A | 22330 | 257 | 916 | SPSGSNLETHLRAPDLGGPCPP GPRWWA*TPQPGHPQTRPSAA QPCPFPPQCQQLIHCP/SPAPGT VAAPPAP/PTPASQCLLCPWTS PVCSPAPTFPCMAPVMAFMLP SYSFP/PGTPNLPQAFFPSQPQFP SHPTLTSEMASASQ/GSPAGPR SPDSHVLVQPPGPPHHRPWVGP PHRSFSPAAARPCSSTCCSWRK PLRVALEPWGPQGPQRQQL |
| 22203 | 52571 | A | 22331 | 151 | 1232 | GRLGDARGPQGPEAPGGEEAA RADSTRACRSCGLLLGRRGCR PSLKNAELLELTVRRVQCVLRG RAREREQLQAEARRALRCRLHP VACTKVHTFVSTCQAIDATVA AELLNHLLSMPPLREGSSFQDL LGDALAGPPRAPGRSGWPAGG APGSPSPPPGPGDDLCSDEEA PEAELSQA/PC*GARLGARSPGQ PDHSPNCPGVSGGLGDQCQPES CRGGARPSLGSPPLLPGVQMW WG*GPGSLPGSSLPLMDGLQG QPLVTSPAQRPSVS*KNF*GPC SSGSWREGATGRRKNFVELP ALSQVSPSPAFNPRLCGLWGQR WQKLVLGTSPVPGSPGLNKSLN LPLQRGDERQVH |
| 22204 | 52572 | A | 22332 | 1 | 1524 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22205 | 52573 | A | 22333 | 3 | 8875 | EDGSLLQEVGIIICLARGPGCGPE TPLYSPATGLALQLQGPAAMG ALWSWILWAGATLLWGKSG EDWISGPTTVFSQPGLTQEASV DLKNTGREEFLTAFLQNYQLA YSKAYPRLLISSLSESPASVSILS QADNTSKKVTVRPGESVMVNI SAKAEMIGSKIFQHAVVIHSDY AISVQALNAKPDTAELTLRPIQ ALGTEYFVLTPPGTSARNVKEF AVVAGAAGASVSVTLKGSVTF NGKFYPAGDVLRV |
| 22206 | 52574 | A | 22334 | 2 | 2214 | ISATDGPLAPCHGLVPPAQYFQ GCLLDACQVQGHPPGLCPAVA TYVAACQAAGAQLGEWRRPDF CPLQCPAHSHYELCGDSCPVSC PSLSAPEGCEACREGCVCDAG FVLSGDTCPVPGQCGCLHDGR YYPLGEVFYPGPECERRCECGP GGHVTCQEGAACGPHEECRL DGVQACHATGCGRCLANGGIH YITLDGRVYDLHGSCSYVLAQ VCHPKPGDEDFSIKNAAGD LQRLLVTVAGQVVS LAQGQV TVDGEAVALPVAVGRVRVTAE GRNMVLQTTKGLRLLFDGDAH LLMSIPSPFRGLCLCGNFNG NWSDDFVLPNGSAASSVETFG AAWRAPGSSKGCGECCGPQGC PVCLAEETAPYESNEACGQLRN PQGPATCQAVLSPSEYFRQCV YDLCAQKGDKAFLCRSLAAYT AACQAAGVAVKPVWRTDSFCPL HCPAHSHYSICTRTCQGSAAAL SGLTGCTTRCFEGCECDDRFL SQGVCIPVQDCGCTHNGRYLPV NSSLLTSDCSESCSCSSSSGLTC QAAAGCPGVRVCEVKAERIN CWATRGLCVLSVGANLTTF DGARGATTSPGVYELSSRCPL QNTIPWYRVVAEVQICHGKTE AVGQVHIFFQDGMVTLTPNKG VWVNGLRVDLPAEKLASVSVS RTPDGSLLVRQKAGVQVWLGA |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22207 | 52575 | A | 22335 | 3 | 7639 | ITCPENSHYEVCGPSPASCSPSP APLTTPAVCEGPCVEGCQCD GFVLSADRCVPLNNGCGCWAN GTYHEAGSEFWADGTCSQWCR CGPGGGSLVCTPASCGLGEVCG LLPSGQHGCQPVSTAECQAWG DPHYVTLDGHRFDFQGTCEYL LSAPCHGPPLGAENFTVTVANE HRGSQAVSYTRSVTLQIYNHSL TLSARWPRKLQVDGVFVTLPF QLDSLHHAHLGADVVTTS GLSLAFDGD SFVRLRPAA |
| 22208 | 52576 | A | 22336 | 2 | 224 | HCYMVVQLWKPRSLRRKSDQL WSSWNQLNTSELSSFISAEMQT EAFDCGSMAGRM*QGGRYLLA ALWDSSVPLS*PQAPWSGVGP AHLTE/LLSPSRFVSISDLLAPKD LGTESQVSMEV*KDMGRFHWE DIPP*A*VFVIFVFQIFISRTY\DA TTHFETTCDDIKNLL*R*QGRYL LAALWDSSVPLS |
| 22209 | 52577 | A | 22337 | 2 | 206 | LSSSYLDQPCYETINRIKLYSES LARYGKSPYLYPLYGLGELPQG FAR*EPVFKTSVIQNLIFNIMCI |
| 22210 | 52578 | A | 22338 | 2 | 457 | |
| 22211 | 52579 | A | 22339 | 2 | 1556 | FVFPSEVAVGLALSPASIFLSFSS PFLRAQERLPSSLWWARSPCAF SLLGSCVRACPAMNEEYDVIV\ LGTG\LTECILSGIMSVNGKKVL HMDRNPYYGGESASITALEDL YKRFKIPGSPPRVKWGEERDW NVDL\IPKFLKANG\QLVKMLL YTEVTRYLDFKVTEGSFVYKG GKIYKVPSTEAEALASSLMGLF EK\RRFKEFLVYVANFD\EKDPR TFEGIDPKKTTMRDVYKKFDL GQDVIDFTGHALA\LYRTDDYL\ DQPCYETINRIKLYSESLARYG KSPYLYPLYGLGELPQGFARLR CYLWEGTYMLNKPIEIIVQE WGKVIGCKI*REEIARCMQLIC DPSYVKDRVEKVGQVITVICIP QPPPSKNTNDANSC\QIIPQNQ\ VNRKSDIYVCMISFA\HNVAQ GKSIAIVSTTVET\KEPEKEIRPA L\ELL\EPIGTEILVSISDLL\VPKD LGTESQIFISRTYDATTHFETTS D\DIKNIYKRMTGSEFD FEEMK |
| 22212 | 52580 | A | 22340 | 66 | 420 | |
| 22213 | 52581 | A | 22341 | 64 | 140 | |
| 22214 | 52582 | A | 22342 | 2 | 254 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22215 | 52583 | A | 22343 | 82 | 3530 | HLIVAMPEPTKKEENEVPAPAP PPEEPSKEKEAGTTPAKDWTLV ETPPGEEQAKQNANSQLSILFIE KPQGGTVKVGEDITFIAKVKA DLSEKPTI/KWF/K/GK WMDLAS KAGKHLQLKETFERHSRVYTFE MQIIKAKDNFAGNYRCEVYK DKFDSCSFDLEVHESTGTPNID IRSAFKRSGEGQEDAGELDFSG LLKRREVKQQEEEPQVDVWEL LKNTKPSEYEKIAFQY/GITDLR GMLKRLKRSI |
| 22216 | 52584 | A | 22344 | 66 | 358 | TWVRGNPKPKITWMKNKVAIV DDPRYRMFSNQGCVCTLEIRKPS PYDGGTYCCKAVNDLGTVEIE CKLAEVKVIYQGVNTPGQPVFL EGQQQSLHNKDF |
| 22217 | 52585 | A | 22345 | 67 | 3515 | HLIVAMPEPTKKEENEVPAPAP PPEEPSKEKEAGTTPAKDWTLV ETPPGEEQAKQNANSQLSILFIE KPQGGTVKVGEDITFIAKVKA DLLRKPTIKWFKGKWMDLASK AGKHLQLKETFERHSRVYTFE MQIIKAKDNFAGNYRCEVYK DKFDSCSFDLEVHESTGTPNID IRSAFKRSGEGQEDAGELDFSG LLKRREVKQQEEEPQVDVWEL LKNAPSEYEKIAFQYGITDLR GMLKRLKRMREEK |
| 22218 | 52586 | A | 22346 | 2 | 39 | FQFCVSLFVYIQLNSDVLPE*PR HKKKPPTLSHWFLK*NLHL*N* NTKALKYRKL*V*LTQKH*QM TYPFCNYLKTN*VTTNTKVK*T EGY*TAKTQKLYPDKVVMATN KPLKTRSPK\PAKYGSPHDTAT WTGSGLGLEAS*HSA |
| 22219 | 52587 | A | 22347 | 1 | 113 | |
| 22220 | 52588 | C | 22348 | 47 | 337 | |
| 22221 | 52589 | A | 22349 | 1 | 2292 | |
| 22222 | 52590 | A | 22350 | 2 | 441 | LRHAKWFQARANGLKSCVIVIR VLRDL\VTRVPTWGPLRGWPLE LLCEKSIGTANRPMGAGEALRR VLECLASGIVMP/QHALRLAAF GQLHKVLGMDPLPSKMPKKPK NENPVDYTVQIPPSTTYAITPM KRPMEEDGEEKSPSKKK |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22223 | 52591 | A | 22351 | 45 | 402 | HALAALEKLFDPDTPLALDANK KKRAPVPVRGGPKFAAKPHNP GFGMGGPMHNEVPPPNLRGR GRGGSIRGRGRGRGFGGANHG GYMNAGAGYGSYGYGGNSAT QGYK*LFHKTAYGYS |
| 22224 | 52592 | A | 22352 | 243 | 3113 | FPDTTEEVKMRPMRIFVNDDRH VMAKHSSVYPTQEELEAVQNM VSHTERALKAVSDWIDEQEK SSEQAESDNMDVPPEDDSKEG AGEQKTEHMTRTLGRVVMR\VG LVAK\CLLLKGD\DL\ELVLLC\ KEKPTTALL\DKVADNLAI\QL AAVTEDKFEILQSVDDAAIVIK\ NTKEPPLS\LTIHLSPPVREE\M EKVLGETLS\VNGPPGNVLD SRIAAAFRGSLPETQRWFQAR ANGLKSCV |
| 22225 | 52593 | A | 22353 | 139 | 245 | |
| 22226 | 52594 | A | 22354 | 875 | 2019 | NPNSQMPKMTSTKQLTNKSG QIDGCPGCRVVPTWCRLGHL YWAVWASILRFWEVWKYWL NMGRKSSEFPILKLNGRTMGD *VLPFHMYV\QPVV\HPQLY PHSVTELTGDYFKPWWDGQPS LQQVL\ERVDEWM\AKEGLLDP NVQVQFLFTLWEDWGLKKS VLPGL\QCQ*LGAWPVGGFTS KQWD*S*KKAYSFAMGCWPK NGLLDMNKGLSLQHIGRPHS GIDDCKNIANIMKTLAYGGF IFKQTSKPVLIGRGQDGAGQ GSLVGPPQNPPLPHQRGKRE SGHKLCCPKVVPSASLWGS MPLGRGLCCPLQGALATW PFLERHFCAPPSPTQSQPS ISPSHCGPGLRGTPGTHRL LPWYNRLWGHQDPRCAPSHP |
| 22227 | 52595 | A | 22355 | 507 | 916 | RKKNEKEGTKPPRNMGICEKT KPTFDWCT*K*RGWNVQVGKY TSGYYTGELPQSSKTGQHSNSG NTENTTKILLEKSNPKTHNW*I HQQ*NEGKTVKGSQREK*GYP QREAHQTNSRSLCRNPTRQKR VGVNIKHS |
| 22228 | 52596 | B | 22356 | 72 | 359 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22229 | 52597 | A | 22357 | 1236 | 1987 | GNSSPPGLPCKSSSSPPPPPSLTG APARRAAAAPPRPASRPRPLA\ GGGVQQLFATRPP/PGPTRARRP TWR*GPRGSPEETPRRRREWTR RPEPGCRAQGSRRPARPPSGSS AVRSASPASSPAPAASAPLGPRS RWS*RPPSRPRR/SPPPPPGRRS SDRER/GRRKEASPLTLAEAPA Y/RQDQAPPPGSPHLGFQSAAG PSRTASSAP/RSGIGGRGANTPA PAAIFPPSLRPPRAGPVGDRLAS GVDAAA |
| 22230 | 52598 | A | 22358 | 287 | 2082 | LKTETSEEKARRYKDRPSQLNA VFQEQQKMIQAQESITLEDVAV DFTWEEWQLLGAAQKDLYRD VMLENYSNLVAVGYQASKPDA LFKLEQGEQLWTIEDGIHSGAC SDIWKVDHVLRLQSESLVNRR KPCHEHDAFENIVHCSKSQFLL GQNHDFDLRGKSLKSNLTLVN QSKGYEIKNSVEFTGNGDSFLH ANHERLHTAIKFPASQKLISTKS QFISPKHQKTRKLEKHHVCSEC GKAFIKKSFLTQVMHTGEK PHRCSLCEKAFSRKFMLTEHQR THTGEKPYECPECGKAFLKKS LNIHQKTHTEKPYICSECGKG FIQKGNLIVHQRHTGEKPYICN ECGKGFIQKTCLIAHQRFHTGK TPFVCSECGKSCSQSGLIKHQ RIHTGEKPFECSECGKAFSTKQ KLIVHQRTHTERPYGCNECGK AFAYMSCLVKHKRIHTREKQE/ CSQGGKSSCREAQLITHQ*CHA GEKLC*RGDYTSAFCGPSDIKH QRP/HSQNRN/CSPCGTASGQM CSLRR*QWICTGQKPCECSECG CAFRDQLCLILCYRKPIGRK\PD LCGKGLSKNL*FIMWPKSIHCE |
| 22231 | 52599 | C | 22359 | 90 | 344 | |
| 22232 | 52600 | A | 22360 | 2 | 543 | |
| 22233 | 52601 | A | 22361 | 373 | 490 | |
| 22234 | 52602 | A | 22362 | 111 | 396 | GAPPGIWCLSLWACRALSPLSS AAQHRKRPSALSPATPAGSRPL RRCAPGFAATKTQRVQRRPPRR *GAAAGAGGS*RPLCGVVIHSV LHNTPE |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22235 | 52603 | A | 22363 | 1902 | 3474 | VPQRSTGSGRARSARRPLRAPD PCAAAPRVSPQPRPSECSGGRR GGSKTWAKRNAGKELTDRNW DQEDEAEVGTFSMASEEVLK NRAIKKAKR\RNVGFSDTGGA FKGFKRFGGYPSEERFSGFGVS GAGGKPLEGL\SNGNNT\SAPP FASAKAAADP\KVAFGK*LPSPS RLLVDKNVSNPKTNGDSQQPSS SGLASSKACVGNAYHKQLAAL DCSVRDWMVKHANTNSLCDL TPIFK\DYEK\YLANIETANTGN\ SGRNSESESNKVA AETQSPSLF GSTKLQQUESTFLFHGNKTEDTP DKKMEVASEKKTDPSSLGATS ASFNFGKKVDSSVLGSLSSVPL TGFSFSPGNSSLFGKDTTQSKPV SSPFPKPLEGQAEGDSGECKG GDEEENDEPPKVVVTEVKEED AFYSKKCKLFYKKNDFKEKGI GTLHLKPTANQKTQLLVRADT\ NLGNILLNVLIPP\NMPCTRTGK NNVLIVCVPNPPIDEKNA\TMP\ VTML\RVKTSDEADELHKILLE |
| 22236 | 52604 | C | 22364 | 65 | 283 | |
| 22237 | 52605 | A | 22365 | 3 | 419 | |
| 22238 | 52606 | A | 22366 | 1 | 512 | CGRPPWKTGQRSQPSCPPGSSG SGRGIPPAAWHEGEGPEAVLQ GHRAGRGPACRGLCCLPSQL GGPTSPTSASRACGSRGAATL VVKVKWFYHP/CRRPSWARGS ATARMRCTSPATRMRTTCRPSP TSARSWRASSMSRWPGAASAR TGRTSTTGHLRPHHRAPGDG |
| 22239 | 52607 | A | 22367 | 1 | 2940 | MRRRRKVAAIHAGPRPRSA SSEQRGRGPGAARRAGGA ASGVTGGGGGGAGQHAGGLG FSAGGRAPSQRPLCGSMPARLF SKQEVGYCGLPAPPASSLRSG HRQRIYSLNQLLQALRTGRAR PGEGPGWLVTDKGGLGWSSH SQAQGPDSQAAWGRAPAHGS SPAFLQVLDVRPQSSRYLPPGT RVCAIYWSQKSRCLYPGNVRA PPPCFGRLLGVPAASSGVPSTG ASGDEDEDLDSVVVEFDDGD |
| 22240 | 52608 | B | 22368 | 215 | 356 | |
| 22241 | 52609 | A | 22369 | 282 | 499 | YLLHCLPSDPPSFTNSPDGRGR RRRQRRRRSDPPGRGRTKSSTR VPGSNRFV*FHQR*GRLKEWM ANQDTN |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22242 | 52610 | A | 22370 | 105 | 619 | ACQASSHSGPVWGPGERITPG A*ASARREPSRNQHPNLWVTE Q/I*IASPRTVANPLVPARTPTGP RTNKP KHLIKQGRGQPRQPLSG STGGAGESPASGCAGGQPAHR VWIAPAARGCGQHTPWKAPAG NGQSPRPASATRMIGPSPSLSP APPAVVGVAALGSRNRCIL |
| 22243 | 52611 | A | 22371 | 1 | 441 | |
| 22244 | 52612 | A | 22372 | 10 | 621 | LRQLERGLAKGQPSTPVDRPLG PDPSAPGTLAGAALPPLEPPAPC LCQDPQEDSVEDEEPPGSLGLP PPQAGVQPA AAAVSGTTQPLG TGPRVSLSPHSPLLSPKVASMD AKDLALQILPPCQVPPPSGPQSP AGPQGLSAPEQQEDEDSEEDS PRALGSGQHSDSHGESSAELDE QDILAPQTVQCPAQAPAGGSEE T*LRQLERGLAKGQPSTPVDRP LGPDPAPGTLAGAALPPLEPP APCLCQDPQEDSVEDEEPPGSL GLPPPQAGVQPA AAAVSGTTQP LGTGPRVSLSPHSPLLSPKVAS MDAKDLALQILPPCQVPPPSGP QSPAGPQGLSAPEQQEDEDSE EDSPRALGSGQHSDSHGESSAE LDEQDILAPQTVQCPAQAPAGG SEETIAKA |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22245 | 52613 | A | 22373 | 1 | 2271 | MPGELLAPSCCCRGGPTRDRTD LSCDAAAATTILGGDRREPCAL TPGPSHLALTFLPSKPGARPQPE GASWDAGPGLSTEAPLPATLE PRIVMGEETCQALLSPRAARTA LRDQEGWGL/SPQGSMDEREL HPAGTPEPPSSESSLADSSSSW GQEGHFFDLDFLANDPMIPAAL LPFQGS LIFQVEAVEVTPLSPEE EEEEAVADPDPSASYAEADDE RLYSGEPHAQATLLQDSVQKTE EESGGLRYDTASAPTRHRSLSVS PKACSCSHDCAP\AG*RGPHLTP GLRYDTASAPTRHRSLSIPKAC GCSHDCVPAG*RGPHLTPGLRY DTASAPTRHRSLSVSPKACSCSH ACVPAG*RGPHLTPGLRYDSTS ASARHRPHLRSRASGCGHPSNL AGRSRLCPRDRACGHHSAGS/ SAWTGSMMSGSA\RHR*WG*A*L TPKGDPPG*EPAGRPEGTGT GTWTQPQGGLHGCQRPGLADL AALPSASSLWAPESWPS/SALS PRAARG*GQPGGRLASGPGLGP AFG*PRGVISRAGRAGHLGSSD RAVSSPGAQSREEGPSRRQ*GD HRQSAESQ*EEGPKGNVKAG LAADSGSHQDHHPEVQEHPLC HRQA*CLQGDPASAHLCG\FWR GQ\T*GPCPASAQSRS*EV*GAL R\DL SLGP*VST\QGP*G*A*VQG KGKG\GGGKGGPGGAGTA*HL |
| 22246 | 52614 | A | 22374 | 2 | 211 | |
| 22247 | 52615 | A | 22375 | 43 | 241 | |
| 22248 | 52616 | A | 22376 | 184 | 332 | |
| 22249 | 52617 | A | 22377 | 1292 | 1923 | KAGARGNQEGTMASSSG\TQK VLTIPRGCYQ*K*SKETLP*CSG WPNDAR\EAVVNC\CTEF\HLIS SEANEICNKSEKKTISPEHVIQA LESLGFGSYISEVKEVLQECKT VALK\RRKASSRFGKPLGIPEEE\ LFGDQANKELFGKSLDQQQAE\ LAQQ\EW\LQMQQAA\HQA\QL AAASAKCI*SRRGSFSGMEEDG GWISEIPPAEFLFLL |
| 22250 | 52618 | B | 22378 | 1 | 1701 | |
| 22251 | 52619 | A | 22379 | 1 | 147 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22252 | 52620 | A | 22380 | 1 | 484 | IRHEGRGQRGKMELVQ\VLKRG LQQITGHGG/LFRGYLRVFF\RT NDAKVGTLVGEDKYGNKYEE DNKQFFGRHRWVVYTTEMNG KNTFWVDVDSMVPEWHRWL HSMTDDPPTTKPLTA\RKFH LG RNH*ISTWTGAPQEQYVPYSTT RK\KIQEWIPPSTPYK |
| 22253 | 52621 | A | 22381 | 3 | 258 | DMAAQIAEGMAFIEERNYIHRD LRAANILVSDTLSCKIADFGLA RLIED\FTIKSDVWSFG\ILLTEIV THGRIPYPGMNPEVIQN |
| 22254 | 52622 | A | 22382 | 1 | 738 | |
| 22255 | 52623 | A | 22383 | 233 | 1898 | GAGPTGYLRRLPGWAGTMGC GCSSHPEDDWMENIDVCENCH YPIVPLDGKGTLLIRNGSEVRDP LVTYEGSNPPASPLQDNLVIAL HSYEPSHDGDLGFEKGEQLRIL EQSV\EWKQSLTTGQEGFIP FNFVAKANSLEPEPWFFKNLSR KDAERQLLAPGNTHGSFLIRES ESTAGSFSLSVRDFDQNQGEVV KHYKIRNLDNGGFYISPRITFP LHELASAITPIASDGLCTR\LSRP CQTQKPQKPQKPWWEDWEV PRETLKLVERLGAGQFG\RCGW GTTTGTTKVAVKSLKQGSMSA GRLP\AEANLMKQLQ\HQRL\VR LYAVVTQEPYIITEYMENGSL VDFLKTPSGIKLTINKLLDMAA QIAEGMAFIEERNYIHRDLRAA NILVSDTLSCKIADFGLARLIED NEYTAREGAKFPIKWTAPAI*S RGNSPPRSDVWSF\GDLLPEIFT\ HGRIP/YPQGIPNPELIQKLERGY RMVRP\SNCPKLYQL\MRLCW KERPED\RPTFDYLRVLEDFFK RHRRASNQPQALREPLRKPLCF |
| 22256 | 52624 | A | 22384 | 3 | 203 | |
| 22257 | 52625 | A | 22385 | 2 | 467 | |
| 22258 | 52626 | A | 22386 | 1 | 468 | |
| 22259 | 52627 | A | 22387 | 1 | 645 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22260 | 52628 | A | 22388 | 821 | 2637 | AAASAWRATHSTTAAGRRTAL FRSPEPGNTRDTRRRRRATAPD CCRPATSPRALDWTSLHTRRHP VQNYLQWSYWQVLVSRWIAF AGLAMADYLISGGTGYVPEDG LTAQQLFASADDLTYNDFLILP GFIDFIADVDLTSAITRKITLK TPLISSPMDTVTEADMAIAMAL MGGIGFIHHNCTPEFQANEVRK VKNFEQGFITDPVVLSPSHTVG\ DVLEGKMRHGFSG\IPITETGTM GSKLVGIVTSRDIDFLAEKDHT TLLSEVMTPRIELVAPAGVTL KEANEILQRSKKGKLPVND CD ELVAIIARTDLKKS RDYPLASK DSQPQLLCGAAVD TREEDKYR LDLLTQAGVDVIVLDSSQGN SV YQY\ARVLYFKQKYPHLQV\LG GNVVTAQA KNLIDAGVDGLR VGMGCGSICITQEV MACGRPQ GTCCVTR*AEYARRFGVPIIAD GGIQT VGHVVKALALGASTVM MGSLLAATTEAPGEYFFSDGVR LKKYRGMGSLDAMEKSSSSQK RYFSEGDKVKIAQGVSGSIQDK GSIQKFVPYLIAGIQHGCQDIGA RSLSVLRSM MYSGELKF EKRT MSPQIEGGVHGLHSYEKRL Y |
| 22261 | 52629 | A | 22389 | 2 | 332 | |
| 22262 | 52630 | A | 22390 | 3 | 608 | MTAVHAGHLNLKWDPKSLEIR TLAAERLVTQVTTLVNTNSKGP SDKKRGHSSKKVHVLAASVEQA AENFLEKEDKIVKESQFL*E*LL AAVEYVRKQ/GKECLRPSLEE H LEGIISGAALMGDSSCKHDDHR ERIAAECNTVLQACRTCF/SEY MGNAGCKERSNSLNSAIDKMT KKTRDLRRQLHKAVMDHVSDS FLETNVPLL |
| 22263 | 52631 | A | 22391 | 2 | 2864 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22264 | 52632 | A | 22392 | 14 | 2897 | PDWRETKQRPSASGLWNLALA QLAAEMTAVHAGHLNLKWDP KSLEIRTLAVERLLEPLVTQVT TLVNTNSKGPSDKKRGHSKKV HVLAASVEQAAENFLEKEDKIV KESQFL*E*LLAAVEDVRKQG DLMKAAARRRSHDDPCSSVEQ GNMVQAA*TLLSAVTCLLILA\ DMGNVYKLLVQLKVVEDGILK LRNAGNEQDLGIQYKALKPEV DKLNIMAAKRQQELKDVGHRD QMAAARGILQKNVPILYAS |
| 22265 | 52633 | A | 22393 | 1 | 1584 | |
| 22266 | 52634 | A | 22394 | 1 | 3519 | |
| 22267 | 52635 | A | 22395 | 3 | 673 | |
| 22268 | 52636 | A | 22396 | 1 | 1574 | DVPRDLEVVAATPTSLISWDA PAVTVRYRITYGETGGNSPVQ EFTVPGSKSTATISGLKPGVDYT ITVYAVTGRGDSPASSKPISINY RTEIDKPSQMQVTDVQDNSISV KWLPS SSPVTGYRVTTTPKNGP GPTKTKTAGPDQTEMTIEGLQP TVEYVVS VYAQ\NPSGESQPLV Q\VAVPTIPAPTDLKFTQVTPTS LSAQWALPNVQLTGYRVRVTP KERTGPMKEINLAPDSSSVVVS GLMVATKYEVS VYALKDTLTS GPAQGVVTTLENVSPRRARVT DATETTITISWRTKTETITGFQV DAVPANGQTPIQRTIKPDVRSY TITGLQPGTDYKIYLYTLNDNA RSSPVVIDASTAIDAPSNLRFLA TTPNSLLVSWQPPRARITGYIHK YEKPGSPPREVVPRPRPGVTEA TITGLEPGTEYTIYVIALKNNQK SEPLIGRKKTVQKTPFVTHPGY DTGNGIQLPGTSGQQPSVGQQ MIFEEHGFRRTTPPTTATPIRHR PRPYPPNVGQEALS |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22269 | 52637 | A | 22397 | 3 | 2382 | QTEMTIEGLQPTVEYVVSVYAAQ NPSGESQPLVQTAVTNIDRPKG LAFTDQDVDSIKIAWESPOGQV SRYRVITYSSPEDGIHELFPAPDG EEDTAELQGLRPGSEYTVSVVA LHDDMESQPLIGTQSTAIPAPTD LKFTQVTPTSLSAQWTPPNVQL TGYRVRVTPKEKTGPMKEINLA PDSSSVVVSGLMVATKYEVS YALKDTLTSRPAQGVVTTLEN VSPRRARVTDATETTITISWRT KTETITGFQVDAVPANGQTPIQ RTIKPDVRSYITITGLQPGTDYKI YLYTLNDNARSSPVVIDASTAI DAPSNLRFATTNLSLLVSWQP PRARITGYIHKYEKPGSPPREVV PRPRGVTEATITGLEPGTEYTI YVIALKNNQKSEPLIGRKKTDE LPQLVTLPHPNLHGPEILDVPST VQKTPFVTHPGYDTGNGIQLPG TSGQQPSVGQQMIFEEHGFRT TPPTTATPIRHRPRYPNVGEEI QIGHIPREDVDYHLYPHGPGLN PNASTGQEALSQTTISWAPFQD TSEYIISCHPVGTDDEPLQFRVP GTSVTSATLTGLTRGATYNIIVE ALKDQQRHKVREEVVTGNSV NEGLNQPTDDSCFDPYTVSHYA VGDEWERMSESGFKLLCQCLG FGSGHFRCDSRWCHDNGVNY KIGEKWDRQGENGQMMMSCTCL GNGKGFEKCDPHEATCYDDGK |
| 22270 | 52638 | A | 22398 | 48 | 7500 | GATMACCAAQGEERVTPCASG KRGPAATTSLVLWIPVPPVPPF PTLWPPSWRRQPPGGIRRD RRLRREANLVATCLPVRASLPH RLNMLKGGPGLLLAVLCLG TAVPSTGASKSKRQAQGMVQP QSPVAVSQSKPGCYDNGKHYQ INQQWERTYLG NVLVCTCYGG SRGFNCESKPEAEETCFDKYTG NTYRVGDTYERPKDSMIWDCT CIGAGRGRISCTIANRCHEGGQS YKIGDTWRRPHETGGYM |
| 22271 | 52639 | A | 22399 | 1 | 403 | NSTNKRGRFCFITFKE\EMEKKY HNVGLSKCEIKVAMSKEQYQQ QQQWGSRGGFAGRARGGGG PSQWNWQGYSNYWNQGYGNY GYNSQGYGGYGGYDYGYN YYGYGDYSNQSGYGVSRRG GHQNSYKPY |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22272 | 52640 | C | 22400 | 36 | 214 | |
| 22273 | 52641 | A | 22401 | 3 | 182 | |
| 22274 | 52642 | A | 22402 | 223 | 452 | LESMTIFPYSDDKRAQYIFIQKD LLKKPVRHYYIMTLSHWAFNT RLALQYWGKGHKQTQIDSEA*Q LRNKTMKANFF |
| 22275 | 52643 | A | 22403 | 1 | 1037 | MSEEQFGDGA AAAAATAA VG GSAGEQEGAMVAATQGAAAA AGSGAGTGGGTASGGTEGGS ESEGAKIDASKNEEDEGHSS PRHSEAATAQREEWKMFIGGLS WDTTKDLKD YFSKFGEVVD TLKLD PITGRSRGFGVLFKESE SVDKVM DQKEHKLNGKVIDPK RAKAMKTKEPVKKIFVGG LSP DTPEEKIREYFGGFGEVESIELP MDNKTNRGRGFCFITFKEEPPV KKIMEKKYHNVGLSKCELK\VA \MSKEQYQQ\Q\QQWDSRGGCA GRA\RGRGGDQAE\GYGKGIQA RWA IKN SYKPYLNYSICQPYPP TAGTSLQALCRADFRFSQARSM |
| 22276 | 52644 | A | 22404 | 299 | 1508 | HYVGGSSSGDGA AARAT\AR AVGGSAGEQ\EGA\MVAATHG ARGGVWEADAATGGGTASGG T\EGGSAE\SEG\AKIYASKNEED EGHSNSSPRHSEAATAQRGRM\ KMVIGGLSWDT\TKKDLKD YFS KFGEVVDCTLKLD PITG\QSRGF GFVLFKESESVDKVM DQKEH K\LVNGKVNDPKRAKAMKTKE PVKKIFVGG LSPDTPEEKIREYF GGFGE\VESIELPMD\NKTN*RG RGFCF\ITFKEEPPVKKI\MEKK YHNVGLSKCEIKV VLLNEQYQ QQQQW*SIGGFAGIALVIGGGP SQNWNQGYSNYWNQGYGNYG YSS\QGYG\GYGGYDYTG YNN YYGYGDYSNQSGYGKVS\RR GGHQ\NSYKPHTKFIPICNLF PN RWLKQYFPNLKIQFERG SCHLL |
| 22277 | 52645 | A | 22405 | 3 | 189 | EESEPERKRARTDEV L\PEEAAP RRKMRTTRTTCPVSRYAAP\QL LLQKLLQRRRKGSCSRG |
| 22278 | 52646 | B | 22406 | 1 | 1356 | |
| 22279 | 52647 | C | 22407 | 135 | 260 | |
| 22280 | 52648 | A | 22408 | 1 | 1740 | |
| 22281 | 52649 | B | 22409 | 80 | 371 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22282 | 52650 | A | 22410 | 257 | 1200 | ISWCCMEQKKRLP\FSKREG\PY EFHICPSEDSSPLLRC AFCIGGMS VKEQMETIRHPLQTTRGPGPGP LFTDGPDP\PIEAFLHGLLSIREM VSTEKVKPVGQSESEPRVKPLEL DDSASGGVHMMVATPGRLMD LLQKKMVSLNICRYLALDEAD RMIDMGFEGDIRTIFSYFKHTSA AAIGLQLALDGGTGSQKQKGC EEFPSSMSAVSTGLEASACCLS VTMDPLETLSRMASSTSSMSSL ARAWLSPEPGDSPGMVGGGLPR ELPGMAPLECGEFQRPESLCAD RNELGSQSPEFPGQEEDEDED DEEDEDE |
| 22283 | 52651 | A | 22411 | 107 | 2069 | GGVSPWRACVQQRMESEPER KRARTDEVLP\EEAAPRRKMRT TRTTCPMCRYGSAGSLLLQKLL QR\RRKGAAEEEQQDSGSEPRG DEDDIPLGPQ\SNVSLLDQHQL \KEKAESA AKESCQGRKQLEGK KEKILGRIVCRAELDVK*KAD WLKGITVLIDPIKTQLGLPPR/Y MFLSMSEERHERVRKKYHILVE GDGIPPIKSFKEMKFPAAILRG LKKKGIHHPTPIQIQGIPTILSCR DMIGIAFTGSGKTLVFTLPVIMF CLEQEKRLPFSKREGPYGLIICP SRELARQTHGILEYYCRLQED SSPLLRC\ALCIGGMSVK\EQ\ME TIRQGVHMMVATPG/RALMDL LQKKMVSLDICRYLALDEADR MIDMGFEGDIRTIFSYFKGQRQ TLLFSATMPKKIQNFA\KSALVK PVTINVGRAGAASLDV\IQEVEY VKEEAKMVYLLECLQKTPPPV LIFAEKKADVD\AIHEYLLKGV EAVAIHGGKDQEERTKA\IEAFR EGKKDVLVAT\DVASKGLVFPA IQHVINYDMPEEIENYVHRIGRT GR\SGNTGIATTFINKACDESFLI D\LKALLVRKPKQKVPPVL\QV L\HCGGWSPMLDIGRSSRGCAF CGG\LGH\RTDCPKL\EA\MQTK QVSNIGRKDYLAHSSMDF |
| 22284 | 52652 | A | 22412 | 435 | 1428 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22285 | 52653 | A | 22413 | 3 | 597 | HKMAPYSPLVTRLQKALGVRQ YHVASVLCQRAKMAMSHFEPN EYIHYDLLEKNINIVCKRLNWP LTLEKIVYGHLD DPASQEIEQ GK/S/YLWLWPDHVAMLQFISKI GATTSVFPYNHRMRRYLSK/TG RTDIANLADEFQDHLVPDPGCH YDQLIEINLSELKPHINGPFTPD QAHPVAEVGKVAEKEGWPLDI RVGLT |
| 22286 | 52654 | A | 22414 | 29 | 512 | |
| 22287 | 52655 | A | 22415 | 1 | 543 | |
| 22288 | 52656 | B | 22416 | 271 | 719 | |
| 22289 | 52657 | A | 22417 | 1 | 2438 | SVHKMAPYSLLVTRL*KALGV RQYHVGSVLCQRAR\AMSHF EPNEYIHYDLLEKSINIVRKRLN RPLTLSEKIVYGHLD DPASQEIE RGKSYLRLRPDRVAMQDA\TA QMAMLQFISSGLSKVAVPSTIH CDHLIEAQVGGE\DL\RAKDI NQEVYNFLATAGAKYGVGF KPGSGIIHQIILENYCVPWLSF*L GPDFHTPNGGG\LGGI\IGSCG WPNAWEWNLGIPWELKCPK VIGVKLTGSLSGWSPKDVILK VAGILTVKGGTGAIVEYQGPV DSISCTGMATICNMGAIEGATT SVFPYNHRMCKYLSKTGREIDIA NLADEFKDHLVPDPGCHYDQLI EINLSELKPHINGPFTPDLAHPV AEVGKVAEKEGWPLDIR\VGLI GSCTNFKLWKIWGRSAAVAKQ ALAHG\LKCKSQF\TITPGFPRQI RATFE\RDGYAQILRDLGG\IVL ANACGPCIGQWDRKDIKKGEK NTIVTSYNRNFTGARNDANPET HAFVTSPEIVTALAIAAGTLKFN PETDYLTGHGWARSFRLGGSRI AD*VFPKGEF*PRGRDTYQHPP K\DSSGAACWDLSPQSRLQLL EPFDKWDGKDLEDLQILIKVKG KCTTDHISAAGPWLFKRGHLD NISNNLLIGAINIENGKANSVG\ NPVTQEFGPAPD\LARYYKKHG I\RWVVGIDENYGE\SSREHAA |
| 22290 | 52658 | A | 22418 | 14 | 260 | RLCIGDAGVSPVCGP/CSAGGGP R*LNLEGGESSSVPRGG/CCSP VTATTAPGPCFPK*SDGSGCAE APDSGE/CS*ALGPHCGD |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22291 | 52659 | A | 22419 | 160 | 460 | RLCIGDAGVSPVCGPLSAGGGP R*LNL*GGESSSVPRGG/CCSP VTATTAPGPCFPK*SDGSGCAE APDSGNCGAFCALRSPHRHPGP KPARERLLLTGL |
| 22292 | 52660 | A | 22420 | 43 | 418 | SLGCAEQN/FPAIAIQPGMAQEE RLSRYQQFKDFQRRILVATNLF GRGMDIERVNIVFNYPEDS DTYLHRVARAGRFGTKGLAITF VSDENDAKILNDVQDRFEVNV AELPEEIDISTYIEQSR |
| 22293 | 52661 | A | 22421 | 1 | 592 | RFSKYMPSVKVSFSGLSIKK DEEVLKKNCPHVVRTRARILA LVRNRSFSLQNVKHFVLDECD KMLEQLDMRRDVQEIFRLTPHE KQCMMF/ERLSRYQQFKDFQRR ILVATNLFGRGMDIERVNIVFN YDMPEDSDTYLHRVARAGRFG TKGLAITFVSDENDAKILNDVQ DRFEVNV AELPEEIDISTYIEQS |
| 22294 | 52662 | A | 22422 | 2 | 575 | |
| 22295 | 52663 | B | 22423 | 100 | 412 | |
| 22296 | 52664 | A | 22424 | 2 | 441 | |
| 22297 | 52665 | A | 22425 | 682 | 1032 | |
| 22298 | 52666 | A | 22426 | 1 | 1324 | MAEQDVENDLLDYDEEEEPQA PQESTPAPPKKDIKGSYVSIHSS GFRDFLKPELLRAIVDCGFEHP SEVQHECIPQAILGMDVLCQAK SGMGKTAVFVLATLQQIEPVN GQSGQVHIFGLHIGARALVISEH ILKDEGAVEGCGVVQCLMARV TVLVMCHTRELAFQISKEYERF SKYMPSVKVSFFGGLSIKKDE EVLKKNCPHVVGTPGRILALV RNRSFSLKNVKHFVLDECDKM LEQLDMRRDVQEIFRLDTTPR KQCMMFSATL\SKDI\RPV\CRK FMQDPMEVFVDDTKLTLHG\ LQQYYVKLKTSEKNRSLFDLL\ DV\LEFNQV\IIFVKSQRCMAL AQLL\VEQNFPAA\AIHRGMAQE ERLSRYQQFKDFQRRILVATNL FGRGMDIERVNIVFNYPEDS DTYLHRVARAGRFGTKGLAITF |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22299 | 52667 | A | 22427 | 9 | 1535 | EAQQLVSRPAENRSWKCLLA ARGEERGASIMAEQDVENDLL DYDEEEEPQAPQESTPAPP\KKD IKGSY\VSIHSSGFRDF/LCLKPE LLRAIGGLVAFEHPSEVQHE\CI PQGHPGA WDVLLPGQSPGMGK TAVFRCWPPLQQI\EPVNGQVT VLVM\CHTRELAFQISKEYERFS KYMPSVKVSVFFGGLSIKKD\E EVMKKNCPHVVVGTPGRILAL VRNRSFSLKNVKHFVLDEC DK MLEQLDMRRDVQEIFRLTPHEK QCMMF SATLSKDIRPVCRKFM QDPMEVFVDDETCLTLHGLQQ YYVKLKDSE\KTRKVF DLWD\V LEFNQVDILRQGQCKRCMAL\A QLL\VEQNFP AQWPI\HRGN GPQ KERPVNAYQASSKDFPSGRDPL VATQILFG\RGMDIEAKSNI\VFN Y\DM P*GLGTPYL\HRV\ARRGR FGTKRP*PFTFVSDG\NDA\KILN DV\QDRF*S*MWAE L\PEEIDIST YIEQSRLNHQLARAGPPGAAPH AASPPLSRRHC |
| 22300 | 52668 | A | 22428 | 3 | 290 | |
| 22301 | 52669 | A | 22429 | 1 | 690 | MNQTSEKEIISKEQGNVKAAGA SDVVLYKIDVPANRYDLLCLEG LVRGLQVFKERNFFLTVLEVEK SKTKVEQIQCLCSQEDIADKLG VDISATKAVHISNPKTAEFQVA RTTLLPGLLKTIAANRKMPLPL KLFEISDIVIKDSNTDVGAKNYR HLCVYYNKNPGEIHHGLLDRI MQLLDVPPGEDKGGYV/IQSVG KLGVLHPDVITKFELTMPCSSL EINIGPFL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22302 | 52670 | A | 22430 | 2 | 1834 | GTRPTVSVKRDLLFQALGRITYT DEEFDEALCFEFGLELDEITSEKE IISKEQGNVKAAGASDVVLYKI DVLATRYDLLCLEGLVRGLQV FKERIKAPVYKRVMPDGKIQKL IITEETAKIRPFAGAAVLRNIKFT KD\RYDSFIELQEKLHQNICRKR ALVAIGTHDLDTLSGPFTYTAK RPSDIKFKPLNKTKEYTACELM NIYKTDNHLKHYLHIIENKPLYP VIYDSNG\VVLSMPPIINGDHSRI TVNTRNIFIECTGTDFTKAKIVL DIIVTMFSEYCENQFTVEAAEV VFPNGKSHTFPELAYRKEMVR ADLINKKVGIRETPENLAKLLT RMYLKSEVIGDGNQIEIIPPTR ADIIHACDIV\EDAAIAYG\YNNI \QMHSPEFTP*ANQFPLNK\LT ELLRHDMA\AAGFH*STLPLAL CSQGRYWLDKLGVGYLWQQR AVHISN\PKTAEFQVARTTLLPG PP*RP*AANRKV\PLPL\KLFEIS\ DIVIK\DSNT\DVGAKKTTRQSL VAGLLPTKNPG\FEINSWGCWD RIMAVCSDV\PPGGRQGGDM*F KASEGPAFFPGAMCRDSFARGQ SL\GKLG\VLHPDVIHQIWS*PLP CSSLE\NIGPFL |
| 22303 | 52671 | A | 22431 | 1 | 304 | |
| 22304 | 52672 | A | 22432 | 1 | 642 | |
| 22305 | 52673 | B | 22433 | 1 | 423 | |
| 22306 | 52674 | A | 22434 | 1 | 525 | LHEHPVTESPMNCSVTLQLSLY MKSVA/GIGQTGKIEPVVLP WFAESGAMEGETLHTFYTQLV LMPKVMHYAQYVLLALGCVL LLVPVICQIRSQ/DRCWPEGSPG *QPFAFPPA*TDIILWTEPATLM AEVSACCAPELPPPHRV PQIIG AQAEVNEPGGPAFRALLDPGA |
| 22307 | 52675 | A | 22435 | 3 | 483 | VRGSGNSHGEVSKGRMCLAGA LPLPGACAALVLLLVILPEPLRC PLHTLYGGRDPVDSIRLWRQA GEFRHKSNTFNNDTVSFLEY RTFQFQPSKSHGESDYIVMPN ILVLNKPRSTWISVCFVHGCIPA SRTGPRTESMHSKSLWKAWLA APGLPLL |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22308 | 52676 | A | 22436 | 1 | 1623 | RRRPRLPGAEPCEPRVGPARRA DMGCSAKARWAAGALGVAGL LCAVLGAVMIVMVPSLIKQV LKNVRIDPSSLSFNMWKEIPIF YLSVYFFDVMNPSEILKGEKPQ VRERGPYVYK/ESSRHKSNITFN NNDTVSFLEYRTFQFQPSKSHG SESDYIVMPNILVLGVAVMMME NKPMTLKLIMTL\AFTTLG\ERA FHGTALWGEV\MWGYKDPLVN LINKYFPGMFPPKGGFGVFAEL NNSDSGLFTVFTGVQNISRIHLV DKWNGLSKVDFWHSQDCNMI NGTSGQMWPFFMTPESSLEFYS PEACRSMKLMYKIESGVFEGIP TYRFVAPKTLFANGSIYPPNEGF CPCLESGIQNVSTCRFSAPLFLS HPHFLNADPVLAEAVTGLHPN QEAHSLFLDIHPVTIIPMNC SVK LQLSLYMKSVAGIGQTGKIEPV VLPLLWFAESGAMEGETLHTF\ YTQLVL\MPKVMHYAQYVPS WALGCVLLLVPV/LSCQIRSQE KCYLFWSSSKKGSKDKEAIQA GSE*SLMTSAPKGS\VLQEAKL |
| 22309 | 52677 | A | 22437 | 198 | 1062 | STCVEMPRNLLYSLLSSHLSPHF STSVTS AKVAVNGVQLHYQH GEGDHAVLLLPGMLGSGETDF GPQLKNLNKKLFTVVAWDP\R GYGHSRPPDRDFPADFFERDAK DAVDLMKALKFKKVSLLGWS DGGITALIAAAKYPSYIHKM\VI WG\ANAYVT\DERPAG*YEGHP RMVSQMGVEGKKESL*EALYG YDYFARTCEKWVDGIR\QFKHL PDGNICRHLLP\RVQ\CPPPLIVH G\EKDPLVPRFHADFIHKHVKG SRLHLMPEGKHNLHLRFADFE NKLA\EDFLQ |
| 22310 | 52678 | A | 22438 | 223 | 393 | AQASPPLLPP**ERSNVPCPIS |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22311 | 52679 | A | 22439 | 524 | 1516 | FILEDITGYVMAPIDGLLCREPR RGLYLEGTPMTLFIQFLNSV GDLLDIPSLSPKNGSLKVFKR WDMGHCSALIKVLPGFENILFA HSSWYTYAAMLRIYKHWDFNII DKDTSSSRLSFSSYPGFLESLDD FYILSSGLILLQTTNSVFNKTL KQVIPETLLSWQVRVANMMA DSGKRWADIFSKYNSGTNNQ YMLVGPEESKAEPQSLTKGT/P VTLWEQIPTV/VRNISGTNLMFL RGKGFWA\SYNVPFHEKIYNWS GLSHC*FRKLGLGPTPYDFRPH EPKIFRRDPR/DK*LIRHPMKYI MRYN\NYKE\DPYSRGDPPVNT |
| 22312 | 52680 | A | 22440 | 1 | 306 | |
| 22313 | 52681 | A | 22441 | 698 | 1613 | FQFFQIFPEYKNNDFYVTGESY AGKYVPAIAHLIHLNPNVREVKI NLNGIAIGDGYSDPESIIGGYAE FLYQIGLLDEKQKK\YFQKQCH ECIEHIRKQNWFEAFEILADKLL\ DGDLTSDPFLTSQNVTCGSNY YNFLRCTEPEDQLYYVKFLSLP EVRPAHPTLGN\QTFN\DGPIV* KVPCGEDTSTSPVKPWALTE\MM NNYRVLIY\NG\QLGHPSVAAAP DQSAPLMG\MDWKGSP\EYKK AEKK\VKIFKS\DSEVA\GY\NR QVGDF\HQVIIRGGGHILPYDQP LRAFDM\NRFIYGKGWDPPYVG |
| 22314 | 52682 | A | 22442 | 1 | 258 | |
| 22315 | 52683 | A | 22443 | 366 | 848 | |
| 22316 | 52684 | A | 22444 | 1 | 585 | ECLCVSTAVRIRHELKTMLTEL LRGGSFEFKDMRVPSALVTLH MLLCSIPLSGRLDSDEQKIQNDI IDILLTFTQGVNEKLTISEETLA NNTWSLMLKEVLSSILKVPEGF FSGLILLSELLPLPLPMQTTQVS LPYNMHLINDCSNTF*KASDSV KKQKPSSPFLPKRHKITG*GGD KTETSWSLRKYGGKNFK |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22317 | 52685 | A | 22445 | 625 | 2700 | YIRGHSTPRKLWSMHLHVQAK LLQEIVRSFSGTTCQPIQHMLRR ICVQLCDLASPTALLIMRTVLD LIVEDLQSTSEDKEKQYTSQTT RLLALLDALASHKACKLAILHL INGTIKGDERYAEIFQDLLALVR SPGDSVIRQQCVEYVTSILQSLC DQDIALILPSSSEGSISELEQLSN SLPNKELMTSICDCLLATLANS ESSYNCLLTCVRTMMFLAEHD YGLFHLKSSLRKNSSALHKLLK RVVSTFSKDTGELASSFLEFMR QILNSDTIG\CCG\DDNG\LMGSR RGAHTSRTMSINAAELNQLLQS TEESPEDLFLELEKLDLEHSD DDNLYSLD**RGLKQMLESSG DPLPLSDQDVEPVLSAPESLQN LFNNRTAYVLADVMDLQKLS MWFTPFQAE\EIGTDLVLKVD LIELSEKCCSDFDLHSEVLESL SEPSSPGRTKTTKGFKLGKHKH ETFITSSGKSEYIEPAKKEFMLC PPPRGRGRGGFGQGIRPHDIFR\ QRKQNTSRPP\SMHVDDF\VA E\SKVVPQDGI\PSHPNRPLKVS QRISRVGFSGNRGGRGAFHSQ NRFFTPASKGNYSRREGTRGS SWSAQNTPRGNYNESRGGQSN FNRGPLPQLRPLKFPTG*PAPK SLGTRAS*MVRGG\LGTFPGLS AKLAASGGSRGKFVSGG\SGRG |
| 22318 | 52686 | A | 22446 | 2487 | 3161 | TWWLHISIIIPGGKKSYSRLGR GKR FATFVLLVGGELCLTSYAP PSIHPILRSEAELNYSIFSFLA PAGEFALPRSFDCNCPVRLRAL RLALLILLTFILCWTPYYLLGM WYWFSPH\MLTEVPPLSHILFL LGLLNAPLDPSPSYGAFTLGCR RGHQELSIDSSKEGSGRMLQEEI HAFRQLEVQKTVTSRRAGETK GISITSI*S*QSM*EQNSKSLVP |
| 22319 | 52687 | A | 22447 | 232 | 337 | |
| 22320 | 52688 | A | 22448 | 1 | 1449 | |
| 22321 | 52689 | A | 22449 | 1 | 2004 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22322 | 52690 | A | 22450 | 3 | 1558 | APARDRAGGGRRALPRLPAAS ARARGLTRALSRAMACRQEPQ PQGPPPAAGAVASYDYLVI SGGLASARRAAELGARA SHKLGGTVCNVGCVPKKVMW NTAVHSEFMHDHADYGFP GKFNWRVIKEKRDAYVSRL IYQNNLTKSHIEIRGHAF PKPTIEVSGKKYTAPHIL MVPSTPH*EPRSRGASL*ITSDG FFQLEEIVPAAASLVGARLPLSV EMAGILSALGSKTSLMIRHD\K VLRSFDSMISTNCTEEL EVLKFSQVKEVKKAL\SGLEAS MVTAVPGRLPVMPMIPD LWAIGGVPNTKDLNKLGIQT DDKGHIIVDEFQNTNVKGIYAV GDVCGKALLTPVAIAAGR HRLFYKEDSKLDYNNIPTV SHPPIGTVGLTEDEAIHKY VKTYSTSFTPMYHAVTKR CVMKMVCANKEEKVVG GLGCDEMLQGFVAVKMGAT KADFDNTVAIHPTSSEELVTLR |
| 22323 | 52691 | A | 22451 | 51 | 464 | |
| 22324 | 52692 | B | 22452 | 103 | 1184 | |
| 22325 | 52693 | A | 22453 | 52 | 148 | |
| 22326 | 52694 | A | 22454 | 1 | 3282 | |
| 22327 | 52695 | A | 22455 | 145 | 436 | |
| 22328 | 52696 | A | 22456 | 1 | 3622 | MPGYRAGPFEEAFDRE CQGRGVDRKITGEHTTF PDHELTLDSGKGCTRS ASEDRRLPIIVEDEGG CSSPARGSRPPPSAIG SDSAAGPARRTALQSL QIDRHSVPVYVFKSPL KHKSSDAGNLDPRKRS SEKVKVLDLIRKDKKSY KIYGKNESSIREIVKKE AVSPPTAKVTATVRDK EQALHLWVEE |
| 22329 | 52697 | A | 22457 | 3 | 422 | VVELRCQDKEGNPAPEY DGIRLLENPRLGSQSTN NTKTGTLQFNTVSKLDT EARNVSGY/PQVPGKRMQ LNISGIIAAVCGLGVCY YFSKETSFQKSNSSSKA NDFKHTKSFII |
| 22330 | 52698 | A | 22458 | 1 | 208 | |
| 22331 | 52699 | A | 22459 | 122 | 321 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22332 | 52700 | A | 22460 | 2 | 1169 | HTPKTEQTPIPGLEDPPPLGSQLR RRPGEGETDIPSRAVPPLPPLPT LCSFPAPEVQGPAPSCAPAAGT LDLLRAAGCRPGKMARRSRHR LLLLLLRYLVVALGYHKAYGF SAPKDQQVVTAVEYQEAILAC KTPKKTVSSRLEWKKLGRSVSF VYYQQTLQGDFKNRAEMIDFNI RIKNVTRSDAGKYRCEVSAPSE QGQKPGVEDTVTLEVLGDVHVL APAVPSCEVPSSALSGTVVELR CQDKEGNPAPEYTWFKDGIRLL ENPRLGSQSTNSSYTMNTKTGT LQFNTVSKLDTGEYSCEA\RNS VG*SEGPCETNASR*SQHKVGII GSR*S*LWALVDFFVGLVYSYG SEGKATFSKETSFQKSNSSSKAT TMSENDFKHTKSFI |
| 22333 | 52701 | B | 22461 | 57 | 168 | |
| 22334 | 52702 | A | 22462 | 1 | 682 | |
| 22335 | 52703 | A | 22463 | 398 | 1465 | GTFPPSGLITGKKRKALLGACD CTQIVKPSGVHLKLVLRFSDFG KAMFKPMRQQRDEETPVDFFY FIDFQRHNAEIAAFHLDRILDFR RVPPTVGRIVNVTKEILEVTKN EILQSVFFVSPASNVCFKCPY MCKTEYAVCGKPHLLEGSLSA FLPSLNLA PRLSVNPWIRSYTL AGKEEWEVNPLYCDTVKQIYP YNNRQLLNVIDMAIFDFLIGN MDRHHYEMFTKFGDDGFLIHL DNA\RGFGRHSH\DEIPILSLLSQ CGMIKNTLLHLQLLAQADYR LS\DV MRSLLEDQL\SPVLTEP HLLAL\DRRLQTILRTV\EGCIV\ AHG\QQSVH*FDGPSGNSSGPR |
| 22336 | 52704 | A | 22464 | 2 | 424 | GRVGVS AVIVRAWITHKYSGR DWNVKWEENLLHAVAKNYTL LQTIPPFERPFKDHQVCLEWNM GYIWNLRANRIPQCLEN/DFRE DFHYNDTAGYFIIGGSRYVAGI EGFFGPLKYYRLRSLHPAQIFNP LLEKQLAEQIS |
| 22337 | 52705 | A | 22465 | 23 | 323 | |
| 22338 | 52706 | A | 22466 | 3 | 287 | LSVQMYAQAALDGDSQGFFNL ALLIEGT YERCWSHSNEESFS PCSLAWLYLHLRLLWGAILHSA LIYFLGTFLLSILIAWTVQYFQS VSGKDL |
| 22339 | 52707 | A | 22467 | 1 | 348 | |
| 22340 | 52708 | A | 22468 | 1 | 738 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22341 | 52709 | A | 22469 | 1 | 507 | |
| 22342 | 52710 | A | 22470 | 187 | 3682 | SILCLLSPCVVQFGKPVVSILSS RSRHSPCTKKGWEGMRKHLHT RQGHK*VHVVKFP/SIMGLQGM DYFHPDISIFCNLA VIVRA WITH KYRGRDWNV KWEENLLHAVA K\NYTLLQTIPPFERPFDHQVC LEWNMGYIWNLRANRIPQCPL ENDV VALLGFPYASSGENTGIV KKFPRFRNRELEATRRQRM DYP VFTVSLWLYLLHYCKANLCGIL YFVDSNEMYGTPSVFLTEEGYL HIQMHLVKGEDLA |
| 22343 | 52711 | A | 22471 | 3 | 153 | |
| 22344 | 52712 | A | 22472 | 1 | 408 | TEPEFPGRFRPRMAVMA PRT LVLLLSGALALTQTWAGSHSM RYFSTSVSRPGRGEPRFIAVG YV DDTQFVRFDSDAASQRM EPRA PWIEQEGPEYWDEETGKVKAH SQTDRNLRIALRYYNQSEAGS HTLFPR |
| 22345 | 52713 | A | 22473 | 1 | 823 | MAVVAPRTL L L L L LSGALALTQT WAGSHSMRYFSTSVSRPGSGEP RFSAVGYVDDTQFVRFDSDAA SQRM EPRAPWMEQE EPEYWRD QTEISK TNAQIDLESLRIALRY Y NQSED/GPPPKTHMTHHPISDHE ATLRCWALSFP AEITLTWQRD GEDQTQDTEL VETRPAGDGT F QKWASVVVPSGQE QRYTCHVQ HEGLPKPLTLR WEPSSQPTIPIV GILAGLVLF GAVIAGAVVA AV MWR RKSSDRKGGSY SQAASSD SAQGS DVSLTACKV |

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|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 22346 | 52714 | A | 22474 | 1 | 1162 | NSRVDDFVAVMAPRTL\LLLLS GALALTQTWAGSHSMRD\FFTS VSRPG\R*EPRFIAVGYVDDTQF VRF\SDAASQRM EPRAPWIEQ EGPEYWDQETRNMK A\HSQTD RENLRIALPLTYNQSEAGS\HTL QMMFGCERGGSDGALSFRGLP PVTAY\DGKGFTFALNE\DLRS WT\AADMAAQITQRKWETPPM WRS/EQEEAYLEG\QCV\DG LRR YL\ENGKEDAAAQRTPPKTHMT HHPIS*P*RPL*RCW\A\AFYPC GDHT*PWQRDG\EDQTQ\DTL V\ETRPAGDGT F\HKWAAVVVP SGEESEITPANVQQ*RVL PKPLT LKM\WEPSSPAHPSPIVGHLLA LVL\LLGAFDHLKLWVAAVML KEGTAQVGKG*KIEKGGSYSSR LPSQ |
| 22347 | 52715 | A | 22475 | 9 | 316 | IPAMGLETEKADVQLFMD DDS YSHHSGLEYADPEKFADSDQD RDPHRLNSHLK\ILMPFVK TCL MVLPSVQTIWKS VTDVIIAPLCT SVGRCFSSVSLQLSQD |
| 22348 | 52716 | A | 22476 | 3 | 606 | RPRTKAAMGLETEKADVQLFM DDDSYSHHSGLEYADPEKFADS DQDRDPHRLNSHLKLGFE\ DVI AEPVTT\HSFDKV\W\CSHALFEI \SKYRM\YRSLT\VFLGHSPWAFI CGEFSFATL\SCLAHLGF*WPFV \KTCLM\VFLPSVQTIWEEC*QM V\ISLAPLC\TSVG\RCFLFLFLA TEPRNGILGPQVWRLGYCNTSF VIIT |
| 22349 | 52717 | A | 22477 | 101 | 432 | ATRDQLKAKPENLLGSISRDSG RTQEGIPARVPYPPPP/PTREPPQ ST*PGRNLLGCLGGGAPRPG WLDSEAGGAPAFHCPG*CPRRH RRGGTRLKQLPPPTTVHDQPL |
| 22350 | 52718 | A | 22478 | 794 | 1209 | VKVDEVTVKHLGCQRCQWSRC PPSCSGTCLCCGAEAPCAAQPA WPPPPAAPPPTPPAPPSD\NSSCT Q*PTPRCGT*DKDKGIFTLPKGH P*V*SLEHGFLKLGSCP\PPPPHA LVRPPQVRFNTPHGAEPQRDQL PQST |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22351 | 52719 | A | 22479 | 3 | 1041 | GSNCPLRQADPGPPRHTLFMDF VAGAIGGVCGVAVGYPLDTVK VRIQTEPKYTGIVHCVRDITYHR ERVWGFYRGLSLPVCTVSLVSS VSFGTYRHCLAHCRLRYGNPD AKPTKADITLLGCGLRTRPRVP DVAH*GGQSPLADADTGFLSSS GGFRLSALLAAPPMPVPPACP EPKYRGPLHCLATVAQ\EEGLC GLYKGSALVLRDGHFSFATYFL SYAVLCEWLSFAGHFRPDVPG VLVAGGCAGVLAWAVATPM\D GIKSRLEANGQGG\NGYRGLLH CMVTSVREEGPRVLFKGLVLN CCRAFPVNMVVFVAYEAVLRL RPGSAHHSRSPTRGATHQQLV |
| 22352 | 52720 | A | 22480 | 38 | 453 | |
| 22353 | 52721 | A | 22481 | 287 | 413 | DMDYRRGGWTVIHRKIGGRID FQRVR*DYLHGYADLLREFWL |
| 22354 | 52722 | A | 22482 | 1 | 393 | MPKLLKWNIEGGACWGNLW KLPNVERLCFSEATVFRSAAQC LVVGLGLLLVSRACSHEDAIEW RGDSSVNVNVEDGSSNAKDESKS NDTVCKEDCEESCDVKTKITRE EKHFMCIFHNVQSLGTVCGEK GIDVN*NYTRRKTFHVYLPQCS VTGNSLRGERH |
| 22355 | 52723 | A | 22483 | 505 | 854 | |
| 22356 | 52724 | A | 22484 | 584 | 1009 | FTQKDLFIPFEVMCDMDYRGG GWTVIQKRIDGIIDFQRLWCDY LDGFGDLLGDAFL\FL*KEDNQ NAMPFSTSDVDNDGCRPACL NGQSVKSCSHLHNKTGWFFN KCGLANLNGIHHFSGKLLATGI QWGTGNQKQLTWQE |
| 22357 | 52725 | A | 22485 | 1 | 3123 | MSHRARPCPAPFLFWMLGVKT EPAGQDRRKKARSRCIFRVHA SGLWGLRFPSVEWGKPSRDKA QLSESPQSVYLFAETALSAIVP GDGVAGGGGTGDGGPGAPYPG AVADMEELTIWEQHTATLSKD PRRGFGIAISGGRDRPGGSMVV SDVVPGGPAEGRLOTGDHIVM VNGVSMENATSAFAIQILKTCT KMANITVKRPRRIHLPATKASP SSPGRQDSDEDDGPQRVEEVD QGRGYDGDSSSGSGRSWD |
| 22358 | 52726 | A | 22486 | 191 | 267 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22359 | 52727 | A | 22487 | 2 | 609 | PPRSEDPAKMAEVEHEEGSG PFRKFTLPAAVDL\DQ\RLDISY DQLEQPMQAVPVARPAAGGLN PGACGRKQ\HSPA*KRLLQGGS KGGAAPCHKPEAGEDATLRD\ MI\NPEMWGS\MVGVYH\GKTF \NQVEDQGVCGRPCRLGWAGV A*CRRDQLTPSFALGLPQPEMI GHYLGFEFSITYKPVKHGRPGIG ATHSSRFIPLK |
| 22360 | 52728 | A | 22488 | 3 | 461 | STISLYCGLKTCPKLTCAFPVSV PDSCCRVCRGDGELSWEHSDG DFFRQPATREASHCHRSHYDP PPSRQAGGLSRFPGARSHRGAL MDSQQASGTIVRFVLNNKHKH GQVCVSNGRTYSHGESWHPNL RAFGIVECVLCTPTPID\WPQGD *GKCRHGCPTLHYVD*LPLEKQ VILATALTMILHQADRLEVCPA FLGPEVTGELLWIPSKHQEPLC DLSSITNTSMDKCVFPMEGPIL MASPGTQTSGLLALWSVCYVL PPPSIVPQGD |
| 22361 | 52729 | A | 22489 | 656 | 1495 | TGDGELSWEHSDGDIFRQPANR EARHSYHRSHYDPPPSRQAGGL SRFPGARSHRGALMDSQQASG TIVQIVINNKHKHGQVCVSNGK TYSHGESWHPNLRAFGIVECVL CTCNVTKQECKKIHCNRYPCCK YPQKIDGKC*QNSTCFLIPEELP GQSFDNKG YFCGEETMPVYES VFMEDGETTRKIALETERPPQVI CSTFCLA\QGILQHFHIEKISKR MFEELPHGHFAFVCLLGQWKIF TEGEAQISQMCSSRVCRTELED LVKVLYLERSEKGHC |
| 22362 | 52730 | A | 22490 | 1 | 477 | |
| 22363 | 52731 | A | 22491 | 1 | 294 | |
| 22364 | 52732 | A | 22492 | 56 | 4042 | VFFTSMGEHLQKLIPASPACLA* IPQACQP*PPTPPAWQCRNLRL AASRHQEPGEVGGPLGHGAE RILAVPVRTDAQGRLVSHVSA ATSRAGVRARRAAPVRTSPFPG GNEEPPGSHLFYNVTVFGRDLH LRLRPNARLVAPGATMEWQGE KGTTTRVEPLLGSCLYVGDVAG LAEASSVALSNCDGLAGLIRME EEFFIEPLEKGLAAQEAQGR VHVYRRPPTSPPLGGPQALDT GASLDSLDSLRAL |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22365 | 52733 | A | 22493 | 173 | 1148 | QALGLPSLLAVLALSTTDRAF SAVISRSPQRTVSSSTRKEQRPLV FAFSALRLGTNACKMDGFCSTF LGAPGIRLKLTPAGTHKSERD RTATPTRHHEKRLFCSSLSIGRQ AEEAWRADHPLPESRLFGLVPL GGAAWCRLAGSFCVCSLRLPRP IELVRAASGALLGAVRRRNHGP PHCFSTATLLCKAYRGGHLTIR LALG\GAPNRPFYRIVAAQNKC PRDGFP*SKLGPPYDP/LLPPNS HGEKTPCPLN\LDRI\RHWIG\CG APLLSPMEKLLGLAGFFPLHP\ MMITNAERLRRKRAREVLLAS QKTDAAETDTEATET |
| 22366 | 52734 | A | 22494 | 2 | 4985 | AGATTALELPGQPSVTGVPPEL GLPSATRALELSGQPVATGALE LPGPLMAAGALEFSGQSGAAG ALELLGQPLATGVLELPGQPGA PELPGQPVATVALEISVQSVVT TSELSTMTVSQSLEVPSTTALES YN/DERSMMSSYERSMMSYER SMMSPMAERSMMSAYERSMM SAYERSMMSMPAERSMMSAYE RSMMSAYERSMMSMPADRSM MSMGADRSMSSYSAADRSM MSSYSAADRSMSSYTADRSM |
| 22367 | 52735 | A | 22495 | 18 | 174 | ALIKKHFI*IAAAKPTPPKSQV TLTKEFPVSSGSQHRKKEADSV YGEWVL |
| 22368 | 52736 | A | 22496 | 3 | 595 | IKKHFI*IAAAKPTPPKSQVTLT KEFPVS\SGPQHRKKEADSVYG EWVPVEKNGEENKDDDNVFS NLPSEVSRRNIMYFSFFIPESAH FIVMLCLIWDSVSLFLRAGVKR QGRV*DGQMKQPAASHLTVT RM/CNSLCG\TKATKWRLRFA ENSVITSLPNIGPSLHLWEGSP WYSIPFSFPSLLLLKVGEVEFKR |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22369 | 52737 | A | 22497 | 3 | 5618 | SSELPGPSVTPVPQLSQELPGLP APSMGLEPPQEVPEPPVMAQEL PGLPLVTA AVELPEQPAVTVA MELTEQPVT TTELEQPVGMTTV EHPGHPEVTTATGLLGQPEATM VLELPGQP VATTALELPGQPSV TGVPELPGLP SATRAELSGQP VATGALELPGPLMAAGALEFS GQSGAAGALELLGQPLATGVL ELPGQPGAPELPGQP VATVALE ISVQSVVTTSELSTMTVSQSLEV PSTTALESYNTVAQ |
| 22370 | 52738 | A | 22498 | 1 | 4685 | MAPESHILASNTMETHILASNT MDSQMLASNTMDSQMLASNT MDSQMLASSTMDSQMLATSSM DSQMLASNTMDSQMLASNTM DSQMLASSTMDSQMLATSSMD SQMLATSSMDSQMLATSTMDS QMLATSSMDSQMLATSSMDSQ MLATSSMDSQMLATSSMDSQM LATSTMDSQMLATSTMDSQML ATSSMDSQMLASGTMDSQMLA SGTMDAQMLASGTMDAQMLA SSTQDSAMLGSKSPDPYRLAQD PYRL |
| 22371 | 52739 | A | 22499 | 291 | 7655 | KRAPEKV DAYLYKQILLMKLP TKKSKKHKHKHKNKKKKKKKE KEKKYKRQPEESES KTKSHDD GNIDLESDFS LKFDSEPSA VALE LPTRAFGPSETNESPAVVLEPPV VSMEVSEPHILETLKPATKTAE LSVVSTSVISEQSEQSVAVMPEP SMTKILDSFAAAPVPTTTLVLK SSEPVTMSVEYQMKSVLKS ESTSPEPSKIMLVEPPVAKVLEP SETLVVSSETPTEVYPEPSTTT MDFPESSAIEALR |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22372 | 52740 | A | 22500 | 90 | 2166 | SQHFGRLRRVDYLRTSKMQTSS SRSVHLSEWQKNYFAITSGICT GPKADAYRAQILRIQYAWANS EISQVCATKLFKKYAEKYSIID SDNVESGLNNYAENILTAGSQ QTDSKWKQSGLSINNVFKMSS VQKMMQAGKKFKDSLLEPALA SVVIHKEATVFDLPKFSVCGSS QESDSLPSAHDRDRTQDFPES NRLKLLQNAQPPMVTNTARTC PTFSAPVGESATAKFHVTPFLG NVKKENHSSAKENIGLVFLSN QSCFPAACENPQRKSFYGS GTI DALSNPILNKACSKTEDNGPKE DSSLPTFKTAKEQLWVDQKK YHQPQRASGSSYGGVKKSLGA SRSRGILGKFVPPPKQDGGEQN GGMQCKPYGAGPTEPAHPVDE RLKNLEPKMIELIMNEIMDHGP PVNWEDIAGVEFAKATIKEIVV WPMLRPDIFTGLRGPPKGILLFG PPGTGKTLIGKCIASQSGATFFSI SASSLTSKWVGECEKMRALF AVARCQQPAVIFIDEIDSLLSQR GDGEHESSRRIKTEFLVQLDGA TTSSDRILVVGATNRPQEIDEA ARRRLVKRLYIPLPEASARKQI VINLMSKEQCCLSEEEIEQIVQQ SDAFSGADMTQLCREASLGPI AV/SQTADIATITPDQVRPIAYID FENAFITVRPIVSPKDL*LYENW |
| 22373 | 52741 | A | 22501 | 3 | 523 | FFFFPAFKMSKRG\RGWVPSG CRKFDPFPLGLP\VGTL*SNWCL TNT\GAQKTLY\NSREGGIKGTG LTRLPRLPVG\DMVMAHSSRK ANPELQKKGYIPA\VIRQRKVI TVGKRWRCCFFIFED\NAGVIGD\ NKG\EMKGFAITG\PRAKECAD LWPRDCIQMLGSIAWFSQYIL |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22374 | 52742 | A | 22502 | 3 | 946 | GPSASVSFWLWSQQHSPRIRHP RPGERRLLHGIPHPTAEKQPA PLRPERRGGRRRRPAGRRGCA* /GGARPCSSRSS*PASTPAPRAA PPCRSPCSARPTGPRTGAGRPR AP/HDGPPCATPDPRDQAS\PLPP RGPRPRVAPGSP\PEGHPRELPS EGSPGPRAPGQRHVPRPRAVLR PRGLRGGGCPGPAHPAPRLQRR RAPGEAAAPGPRWPGRPGRGR AQALVPAARSRCFWKLWEAVF CLPVAAAPTRRFGARQRPQLW LHGKGGQVGEVSSHSAAGEEH LVPHAAPKRAREPHGRSGSPGG IASSWQDGS |
| 22375 | 52743 | A | 22503 | 34 | 823 | |
| 22376 | 52744 | A | 22504 | 424 | 2339 | LLRGTLSYAWTSVIPDIATELR DAPEKTLACMGLAIHQVTICLM HTFV*TFLMFAHTCTPCLTMVN VPHIHAR*GI*CIKVLLRMGH*R PFKNENAHRGTVVRVSNIKPLC TKMAFLCAACGEIQSFPLPDGK YSLPTKVIRSLTASLFILVKKAN QNTENISRQSIK*AIRLLHKRQA LDVTLLRKSIIILLHDLVDSCVPG DTVTITGIVKVSNAEEGRVQLF SLFVSQ**FINVHLF*DAPPHILV VGDPGLGKSQMLQVDNQSFVS CSFACKMR**FTSEFSPLSKDSS SGDFALEAGALVLGDQGERPK GIISDSGTF*KAFSFSVNFLSISL AKAGVVCSLPARTSIIAAANPV GGHYNKAKTVSENLK*VSSNIY TFNVLNHFNSIRKRNSSHLLSEH VIAIRAGKQRTISSATVARMNS QDSNTSVLEVSEKPLSERLKV *MFLLLIQFGSV*MSKFSVWLIV DVYPRLSTEAARVLQDFYLELR KQSQRNLSSPITTRQLESLIRLTE VCFFLWSCFFWLKGECCALTSL LKYR*DKNFKLF*MKYQLSSHL KLGNRPNRSTAKRFISALNNVA ERTYNNIFQFHQLRQIAKELNIQ VADFENFIGSLND\QGYLLKKG PKVY\QLQTM |
| 22377 | 52745 | A | 22505 | 73 | 214 | |
| 22378 | 52746 | A | 22506 | 1 | 503 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22379 | 52747 | A | 22507 | 3 | 1000 | ESKLEGKAAQDIKDEEPGDLGR PKPECEGYDPNALYCICRQPHN NRFMICCDRCEEWFHGDCVGIS EARGRLLERNGEDYICPNCTIL QVQDETHSETADQQEAKWRPG DADGTDCTSIGTIEQKSSDQGI KGRIEKAANPSGKKKLKIFQPG PGPVPTQLPVLWQVLEIAVSRSI SAFTLLHCISCKVIEAPGASKCI GPG\CCHVAQP\DSVYC\SNDCIL KHAA\ATMKFLSSGKEQKPKPK EKM KMKPEKPSLPKCGAQAGI KISSVHKRPAPEKKETT VKKAV VVPARSEALGKEAACESSTP\S WAS\DHNYNA\VKPEKTAAPSP VTVV |
| 22380 | 52748 | A | 22508 | 1 | 2330 | MAAAEGKERAGGRASGRGRSE PPRPGARASDAGPGLREVEGT GEHSVVAAGTVPRVGVGAAAR GEERRAGLGECGPGLGGCVAG LISGKSVQAFSVGAGRWP LLRV FGGNVTFCSSVWSLCA YTLPL GMDDKGDPSNEEAPKA IKPTSK EFRKTWGFRTTIAKREGAGD AEADPLEPPPQQQLGLSLRRS GRQPKRTERVEQFLT IARRRGR RSMPVSLED SGEP TSCPATDAE TASEGSVESASETRSGPQSASTA VKERPASSEKVKGGDDHDDTS DSDSDGLTLKELQNR LRKREQ EPTERPLKGIQSRLRKKRREEGP AETVGSEASDTVEGVLP SKQEP ENDQGVVSQAGKDDRESKLEG KAAQDIKDEEPGD\LGRPKPEC EGYDPNALYCICRQPHNNRFMI CCDRCEEWFHGDCVGI SEARG RLLERNGEDYICPNCTILQVQD ETHSETADQQEA*MGDLGDA\D GTDF\TSIGNIRSRSLRRPKGLK GRIEKAANPSGKKELKIF\QPVL EIAVSRSSAFTLLHCISCKVIEA PGASKCIGPGCCHVAQPDSVYC SNDCILKHAAATMKFLSSGKEQ KPKPK EKMKMKPEKPSLPKCG AQPVQWLLLLSSWQLGTSSGL QVTLCQPPFTEHKWLKFSVLHG ETAGPPRAHRIRKLNKYWGAC HHCMPLRPLPCLPGWPRSSPSL |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22381 | 52749 | A | 22509 | 149 | 2001 | IQPPDPRNMTLAA YKEKMKELP LVSLFCSCFLADPLNKSSYKYE\ AGVGD SVGGRMKASGKTVLT GRERRAQADTV\DLNWCVISD MEVIELNKCTSGQSFEVILKPPS FDGVPEFNASLPRRRDPSLEEIQ KKLEAAEERRKRGPD LVIYIEH SPASLPFHSSDASVLGDIPPTY SNISNSNQELLLMGGSPAPEQP HYEANILERSETTSYDNGSDAA QSFKVDGRCVFYINIPISNEGK VLWKAPEIATAKEPTWSPLGST GPRPCQILVVKSPVVHGKGPVL SGCGLDLLEQPTFALCFLVAGA VTITFLSCSGEEAREESAPKAMS ERQARRGGA EKQGA EGRGLQA VTTPELPYRMGLGA AFLKERS GVLPGSFICEDFTAALKQDEEIG TMKGKIREAYFKSFVPTPVAFS GGVMLPTGGTLEMCGNNFGGH KEQAGTVLP AFAIALRVTPSAS LVLRPLNDQAMLQGS LGLQL ADGLFWDLASIMDWTSRIQPS VSSSMKICQAFPGRPLAILLAQC AYVYGTWMKLEA IILT KLTOE QKTKHHLFSLPCCMPADISYRQ RCLGEPHCTVWNRHLESLVM MSNSTTSPCSELLIFEVPPVAPE |
| 22382 | 52750 | A | 22510 | 373 | 990 | IQPPDPRNMTLAA YKEKMKELP LVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVIFRHWKVIELN KCT/SGANSFEVILKPPSFDGVP EFNASLPRRARPIPWEEIPVRKL GRRLRERREVTREADP*KQLAE KR\EH EERGDSKRAFRETTTFIK MAK/EKNLAQKMESNRENREA HLAAMLERLQEK\DKHAEVR KNKELKEEASR |
| 22383 | 52751 | A | 22511 | 524 | 1107 | LCS PKVLGLNASCQKNFLKQK KSIKTLSTSQ/YSVSGYSLARSE NAHPEFRMAMKD GELVIWDSV HPCYTVFHEQTETFSSLWSEYH DDFRQFLHIYSQDVACYGENLA YFPKGFIENMFFVSANPWVSFT SFDLNVANMDNFFAPVFTMGK YYTQGDKVL MPLAIQVHHAVC DGFHVGRMLNELQQYCDEWQ |
| 22384 | 52752 | A | 22512 | 1 | 1413 | |
| 22385 | 52753 | B | 22513 | 1 | 2787 | |
| 22386 | 52754 | A | 22514 | 1 | 1638 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22387 | 52755 | A | 22515 | 71 | 2421 | YTVCYFLQAAEEDETQNQHDD SSSDSGTPSGPDFNYILNMSLW SLTKEKVEELIKQRDAKGRE\V NDLKRK\SPSDLW\KEDLAGIC WRDWDKV\ENSPRNEEDVLAG MSGKSNLKGVGKPKVKKKLQ LEETMPSPYGRRIPEITAMKAD ASKKLLKKK/KGVLDLDTAAVK\ VEFDEEFSGAP\VEGAGEEGIDS HQFPINK\GPKP\RREKKEPGS\R VRKTPTSSGKPSAKKVKKRNP WSDDESKSESDLEETEPVVIPR DSLLRRAADIHRLGGEGFDAGL TVFAPLFASPFPPRGAPYLKAA CQTPRSGIGATAISGEALKGAV SSGVDPRWASHLRVKLLEKSFS LQEIQSTEKVLSQQAKTSLLG EPKLSKQLTGTCIYRKTNLALC RGPAAAKSLFQGA VRNDRNKK KKETSKQECTESYEMTAELDDL TEKIRKAHQETFPSLCQLGKYT TSLQKGMQRCQILDLSVRPIV DVRPPELQDSKLVLVQAAKCA PLADHCSKPVLLKEGPEDQKD QHDVGDCWNPECQTLFDQNN AAKKEESETANKNDSSKKLSVE RVYHIKTQLEHILLRPDTYIGSV EPLSKVAEEGPAAVGGWKGWF GTESRKDPKPTGTEEVERGVW LSGREGRLLSPSVTTMVLAE SAIRFVGGKPSSDTVPKPKRAP KQKKVVEAVNSDSDSEFGIPKK |
| 22388 | 52756 | A | 22516 | 1424 | 4860 | GRDRYGVFLRGKILNVREASH KQIMENAEINNIKIVGLQYKKS YDDAESLKTLYGKIMIMTDQ DQDGSNIKGLLINFHWNWPSLL KHGFLEEFITPIVKASKNKQELS FYSIPEFDEWKKHIENQKAWKI KYYKGLG\TSTAKEAKEYFA\D MERHRLFRYAGPEDDAAITLA FSKKKIDDRKEWLTNFMEDRR QRRHLHGLPEQFLYGATKHLTY NDFINKELILFSNSDNERSIPSLV DGFKPGQRKV |
| 22389 | 52757 | A | 22517 | 87 | 292 | |
| 22390 | 52758 | A | 22518 | 1 | 903 | |
| 22391 | 52759 | A | 22519 | 3 | 311 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22392 | 52760 | A | 22520 | 1 | 1087 | MPSAAWKRPEVEGPATLRRPLGI AAASQCPSSPQPGCLIGAVNLK SSNRTPVVQEFESVELSCIITDS QTSDPRIEWKKIQDEQTTYVFF DNKIQGDLAGRAEILGKTSLK1 WNVTRRDSALYRCEVVARNDR KEIDEIAIEVTVQVKPVTVPVCR VPKAVPVGKMATLHCQGE*GP PPA\HYSWYRNDVPLPTDSRAN PRFRNSSFHLNSETGTLVFTAV HKDDSGQYYCIASNDAGSARC EEQEMEVCHTDKRGGFPWSW AAPHLWFLQDTALLPAALTGW CSVSVAFPGAQCKLSVDLSFWG LEDGGPLLTAPLGSTPVGTLCR GSDPTFPFCTALADDLYESPTPA ANFCLDIQAFSYIL |
| 22393 | 52761 | A | 22521 | 628 | 1117 | FFISVINGQVSSVQRLSGVGPAC LSCGSANPGPPPPTSPGAGAQR R*\PRADGSGSPQWPRGARVGG GRLGTGGRGRPGWRQVPRRLS PGFGR*GGTGPVGTSGKRG SRRRAPANDKAACWPRFPGQP AS*TGFRGERGVKGFSSWGS WRAWEDGGTVH |
| 22394 | 52762 | A | 22522 | 2 | 238 | |
| 22395 | 52763 | A | 22523 | 131 | 2891 | |
| 22396 | 52764 | A | 22524 | 131 | 3103 | LVSFLLFQDALPEGDASPLGPY LLPSGAPERGSPGKEHPEERVV TAPPSSQSAEVLGELVLDGTA PSAHHDIPALSPLLPEEARPKHA LPPKKKLPSLKQVNSARKQLRP KATSAATVQRAGSQPASQGLD LLSSSTEKPGPPGDPDIVASEE ASEVPLWDRKESAVPTTPAPL QISPFTSQPYVAHTLPQRPEPGE PGPDMAQEAPQEDTSPMALMD KGENELTGSASEESQETTTSTIIT TTVITTEQAP |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22397 | 52765 | A | 22525 | 474 | 2527 | SASPLGPYLLPSGAPERGSPGKE HPEERVVTAPPSSSQSAEVLGE LVLDTGTAHHDIPALSPLLPE EARPKHALPPKKKLPSLKQVNS ARKQLRPKATSAATVQRAGSQ PASQGLDLLSSSTEKPGPPGDPD PIVASEEASEVPLWDRKESAV PTTPAPLQISPFTSQPYVAHTLP QRPEPGEPPDMAQEAPQEDTS PMALMDKGENELTGSASEESQ ETTTSTIIITTTVITTEQAPGMQPP TPMGEPPPIVKHTWILDKCNVA TLQST*ALGPNEG YIDSSDYPLL PLNNFLECTYNVTVYTG YGVE LQVTPGEYPD GELL SIRGV DGP TLTVLANQTLLVEGQVIRSPTN TISVYFRTFQDDGLGTFQLHYQ GRVRPRLFRRPDSGDVTVM DL HSGGVAHFHCHLGYELQGAK MLTCINASKPHWSSQEPICSGM LQPQPHNATIGRVLSPSPYENT NGSQFCIWTIEAPEGQKLHLHF ERLLLHDKDR*SSEGPQTNKSA LLYDSLQTESVPFEGLLSEGNTI RIEFTSDQARAASTFNIRFEGEG PWELYEPYIQNGNFTTSDPTYNI GTIVEFTCDPGHSLEQGP AII ECI NVRDPYWNDTEPLCRGERIHN ASAVAGVVLSPNWPEPYVEGE DCIWKIHVGE EKRIFLDIQ/FVS V*NGSVFSQEKVRPTPEWW |
| 22398 | 52766 | A | 22526 | 131 | 3125 | LVSFLLFQDALPEGDASPLGPY LLPSGAPERGSPGKEHPEERVV TAPPSSSQSAEVLGELVLDGTA PSAHDIPALSPLLPEEARPKHA LPPKKKLPSLKQVNSARKQLRP KATSAATVQRAGSQPASQGLD LLSSSTEKPGPPGDPDPIVASEE ASEVPLWDRKESAVPTTPAPL QISPFTSQPYVAHTLPQRPEPGE PGPDMAQEAPQEDTSPMALMD KGENELTGSASEESQETTTSTIIT TTVITTEQAP |
| 22399 | 52767 | C | 22527 | 161 | 352 | |
| 22400 | 52768 | A | 22528 | 2 | 368 | LGSTHASVRINILSVDVLYFIFY RRDDNKDIDSEKEAAMEAEIKA ARERAIVPLEARMKQFKDMLL ERGVRKQSLGEIFLCISNINMS C*KVKSKVSAFSTWEKELHKIV FDPYRLLLLNLI |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22401 | 52769 | A | 22529 | 2 | 614 | KDHRWESGSLLEREEKEKLFNE HIEALTKKKREHFRQLLDETSAL TLTSTWKEVKKIKEDPRCIKFS SSDRKKQREFEEYIRDKYITAK ADFRTLLKETKFITYS*FSECE SESL*KMLGLAAPQTEVLCSSST E\RSKKLIQESDQHLKDVEKILQ NDKRYLVLDVPEERRKLIVAY VDDLDRRGPPPPPTASEPTRRST |
| 22402 | 52770 | B | 22530 | 201 | 296 | |
| 22403 | 52771 | B | 22531 | 1 | 1290 | |
| 22404 | 52772 | A | 22532 | 3 | 3369 | SSSVMAERGGVGGESERFNPGE \LRMAQQQALRFRGPAPPP\NA AMRGPPPLMRPPPPFGMMRGPP PPPRPPFGRPPFDPMPPMPPPG GIPPPMGPPHLQRPPFMPPPMSS MPPPPGMMFPPGMPPVTAPGTP ALPPTEEIWVENKTPDGKVYYY NARTRESAWTKPDGVKVIQQS ELTPMLAAQAQVQAQAQAQA QAQAQAQAQAQAQAQAQAQA QAQAQAQAQAQAQAQAQAQA QAQAQAQAQAQVQAQVQA |
| 22405 | 52773 | A | 22533 | 43 | 347 | |
| 22406 | 52774 | A | 22534 | 1 | 1776 | |
| 22407 | 52775 | A | 22535 | 3 | 433 | PLAPNHLGGGAVVLGAESHAS KDVAIDMMDSRTSQQQLQIDE QDSYIQSRADTMQNIESTIVELG SIFQQLAHMVKEQEETIQR*DR VNSAHPWDPVHLLPSTQQVFIE HLFM |
| 22408 | 52776 | A | 22536 | 304 | 1403 | SRGNATGLRTRIRVSTWVSQRH RSCPLQLLAVAAATSSPLPPPV LVPPPPDTMSCRDRTQEFLSAC KFAARPVKNGI\QTN*GQLLRW LVRQRSEIHPSLAKRHLGKDLS NTFAKLEKLTILAKR\KPLFDDK AGEIEELTYIHKQDINSLIKQIAQ LQ\DFVRAG\ISQSGRHLQTHS NTIV\VSLSQSKL\ASMSNDFKSV L\EVDRDRTLKQ\QREPEERQFS RAPV\SALPLSPTHRAGGA\VVL GAESHASKDV\AIDMMDSRTS QQQLQIDEQDSYIQSRADTMQN IESTIVELGSIFQQLAHMVKEQ/ ERETIQRIDENVLGAQLDVEAA HSEILKYFQSVTSNRWLMDKIF LILIVFFIIFVVFLA |
| 22409 | 52777 | B | 22537 | 147 | 506 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22410 | 52778 | A | 22538 | 2 | 1397 | AAPGNGLSPSSWRSELACEFQH ECTAEVRFGAVVCRGARSHSFY LEREILQ/PPGMSL/PENPVTPL RHLMYKIKSTGPITVAEYMKEV LTNPAKGYYVYRDMLGEKGDF ITSPEISQIFGELLGIWFISEWMA TGKSTAFQLVELGPGRGTLVGD ILRVFTQLGSVLKNCDISVHLVE VSQKLSEIQALTLTKEKVPLER NAGSPVYMKGVTKSGIPISW*S RICTD\VPKGYSFYLAHEF\LDV LPVHKFQKTPQGWREVFVDIDP QVSDKLRFVLAPSATPAEAFIQ HDETRDHVEVCPDAGVIEELS QRIALTGGAALVADYGHGDTK TDTRFGCDHKLHDVLIAPG\T ADLTADVDFSYLRRMAQGKVA SLGPIKQHTFLKNMGIDVR/L*R FF*INQMRPSVRQQLLQGYDML MNPKKMGERFNFFALLPHQRL QGGRYQRNARQSKPFASVVAG FSELAWQ |
| 22411 | 52779 | A | 22539 | 2 | 377 | |
| 22412 | 52780 | A | 22540 | 2 | 1427 | |
| 22413 | 52781 | A | 22541 | 2 | 568 | CSSPSN/TILGVQKLNSQWRLA QDFRLINEAVIPLYPVVNPYTL LSQIPEEAESFTVLDLKDAFFCIP LHSDSQFLFAFEDPTDHNSQLT WMVLPQGFRDSPHLFGQAQAAQ DLVHFSSPGTLVVQYMDDL ATSEASCQATLDLLNFLANQ GCKRVGIALGVLTQTHTGTPQP VAYLSKETDVAAK |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22414 | 52782 | A | 22542 | 1 | 1230 | GPRGTGPKGKARSEKGCSLSHG PQTNKPLVVQKGQKMEQANHP VGLVISVVYKDILKKIVQRETS HPLIHVRYAEAITGRRTAPEDK GSLGRDMLAKAGAIIMNMGN KLPIWCHLLEEGIYLEVWALEG QFGRAKNACPVQIRLKDPTTFP YQRQYPLRPEAHKGLQDIVKH VKAQGLVKKCSSPCNTPILGVQ KPNGQWSLVQDLRLISEAVIPL YPVVPNPYTLSSQIPEEAWEFP VLDLKDFAFFCIPLHYDSHDSQF LFAFEDPTDHTSQLIWTVLPQG FRDSPHLFGQALAQDLGHFSSP GTLVLQYVDDLLLATSSEASCQ QATLDLLNFLANQGYKASRSK AQLCLQQVKYLGLILARGTRTL GKERIQPILAYPHPKTLKQLWG FLQIT/GFCQLWIPR*SKI |
| 22415 | 52783 | A | 22543 | 1 | 211 | |
| 22416 | 52784 | A | 22544 | 1 | 472 | |
| 22417 | 52785 | A | 22545 | 1 | 393 | |
| 22418 | 52786 | A | 22546 | 59 | 411 | SWPSDKQTLVVQRGQKMEQA NHPDPTDHMSQLMWT/VLPQG FRDSPHLFGQALAQDLGHFSSP GTLVLQYVDDLLLATSSEASCQ QATLALLNFLANQGYK/LRSK AQLCLQQVKYLCL |
| 22419 | 52787 | A | 22547 | 43 | 236 | TSSLLRKEDSAPSQGKSVVFTL TSQG*VPLWRTLQLOGPFFTPSS RK*LELSSANSQQHLGCPV |
| 22420 | 52788 | A | 22548 | 1 | 1446 | |
| 22421 | 52789 | A | 22549 | 1 | 1521 | |
| 22422 | 52790 | A | 22550 | 2 | 689 | |
| 22423 | 52791 | A | 22551 | 1 | 64 | |
| 22424 | 52792 | A | 22552 | 636 | 1586 | SNDRTEDDCGKHPPFMSSPP/TEP WVCLIIEGQEIDFLDTGTTFSV LIPCLGRLSSRSVTIQGILGQPVT RYFSHLLSCNWETLLFSHAFLV MPESPTPLLGRDILAKAGAIISM KTGNKLPICCPLEGINPEVWA LEGQFGRAKNAHPLQIRLKDPI SFPYQRQYPLRPEAHKGLQDIV KHLKAQDSVRKCSSPCNTPILG VQKLNSQWRLVQDLRLINEAVI PLYPVVRNPYTLSSQVPEEAWE FTVLDLKDFAFFCIPLHSDSQFLF AFEDPTDHTSQLMWMVLPQRF RDSPHLFGQAQAQDLGHFSSPG |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22425 | 52793 | A | 22553 | 292 | 1493 | SNDRTEDDCGKHPFMSSPP\TEP WVCLIEGQEIDFLDGTTFSTV LIPCLGRLSSRSVTIQGILGQPV RYFSHLLSCNWTLLFSHAFLV MPESPTPLLGRDILAKAGAIISM KTGNKLPICCPLEGINPEVWA LEGQFGRAKNAHPLQIRLKDPI SFPYQRQYPLRPEAHKGLQDIV KHLKAQDSVRKCSSPCNTPILG VQKLNSQWRLVQDLRLINEAVI PLYPVVRNPYTLLSQVPPEAEW FTVLDLKDFAFFCIPLHSDSQFLF AFEDPTDHTSQLMWMVLPQRF RDSPHLFGQAQAQDLGHFSSPG TLVLQYSEIAKTLYTLIKEMER ANTHLVEWEPEAETAFTLKQ ALVQAPALSLPTGQNFALYVIE RAGIALGVLTQTHRTPQPVAY |
| 22426 | 52794 | A | 22554 | 2 | 307 | |
| 22427 | 52795 | A | 22555 | 3 | 400 | |
| 22428 | 52796 | A | 22556 | 2 | 78 | |
| 22429 | 52797 | A | 22557 | 395 | 1336 | SNNRTEGASSCH\PLTEPQVCLT IEGQEIDFLDGTAFSVLISCPA WGTGQDSVSKKNEKKRKEKA KGNHQANAEAKIAARWNPSLE IPTEGPLVWNNPLQEIKPQYSLT ETEWGLSQGHSFLPLGWLMT EVKVLIPASQWKILKTLHQTF QMGIENTQQMAKSLFTGPNLL WTIRHVVKACEVCQRNNPLVH HKAPLGEQRIGHYPGEDWQLD FTHMPKSKGFQYLLVCVDFTT NWIEAFPCKIEKAQEVNKLVIH ETIPRFGLPQSLQSDNDPAFKA MITQGIFQGAKDTISPSLCLEATI LREGREGN |
| 22430 | 52798 | A | 22558 | 244 | 638 | GPLNPTFLGPPCGLGGKLVFLL LRQ*VQLFRSAGSRDRCGFLDR ERNKTNQNCQKQAKKSPKDHK NPRAVGYPFNL*QEGNLAQP GYMSPSPSLI*SRSRQTWGSFQ MILIGTKRNRPKRKSEIRERLQP |
| 22431 | 52799 | A | 22559 | 210 | 600 | RGKRTWRERRNGWSRGFCPLP LTGSWLISRESPRLACLGEGLG VPGM*DLPHAWPTTLMCPVLV GSWSH*LQE*SHGPSQ*VLQLL RWCVWSLFLLMFGCVWSFFLL VSSWSRWLRSEATDLCGECYSS |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22432 | 52800 | A | 22560 | 2746 | 5211 | ETSCPLVRVHYAEAITGRCTAP EDEGSLGQKPPARRSNNRTEGA WGKRQLMSSP/STEPRVCLTIEG QEIDFLLDTGAAFSVLISCPGRL SSTSVTIQGILGQPVTRYFSHLL SCNWETLLFSHAFLLMPERPTG LLGRDILAKAGAIYMNMGNKL PICCPALLVEGINPEVWALEGQF GRAKNARPLQIRLKDPTTFPYQ RQYPLRPEAHKGLQDIVKHVK AQGLVKKCSSPCNTPI LGVQKP NGQWSLVQDLRLISEAVIPLYP VVPNPYTLLSQIPEEAESWAL TFKDAFFCIPLHSDSQFLFADF PTDHTSQTGTVLPPQGRDSPH LFGQALAQDLGHFSNPGTLVLQ YVDDLLLATSSEASCEQATPDL LNFLTNGQYKVSRLKAQLCLQ EVKYLGLILARGTRALSKE*IQP ILAYPHPKTLKQLRGFLEITGFC *LWIPGYSKIARPLYTLIKETQR ANTHLVEWEPEAETTFKTLKQ ALVQAPALSLPTGQNFSLYVRE RARIALGVLTQTHGTTQP VAY LSKEIDVVAKGWPHCLRVVAA VAVLASEAIKIIQGKDLTV*TTY DVNGILGAKGSLWSDNCLLR YQALLLEGPVLQICTCMALNPA TFLPEDGEPIKHDCQQIIVQTYA ARDDLLEVPLTNPDNLNLYTDGS SFVENGI/RKVS DV TILES KPLPP G TSAQLAELVALTWALELGKG |
| 22433 | 52801 | A | 22561 | 903 | 4440 | DHPGHIHSSPCHERPNNVSTLPF LPGEQHPILLPPRNC PGDKILEE NFRYNNYKRTMMSFKERLENT VERCAHNGNRPRQSRGFGELL STAKQDLVLEE QSPSSSNLENS LVKDYIHYNGDFNAKSVNGCV PSPSDAKSISSEDDL RNPDPSS NELIHYRPRTFNVGDLVWGQIK GLTSWPGKLVREDDVHNSCQQ SPEEGKVEPEKLKLTLEGLEAY SRVRKRNRNGIKVPPRSPRSTIG SPRPSMPSSPS |
| 22434 | 52802 | A | 22562 | 1 | 501 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22435 | 52803 | A | 22563 | 1688 | 2038 | SATHGLSDSCYWLVVSRAIGRN NLSPASPASIIHALVFLAEPQLF QPRILGLIDEESGHEGGRPAAKT RKLSGPWSRPAAFMSTLLINQP QYAWLKELGLREENEGVYNGS WGGRGEVITTYCPANNEPIARV RQA\SVADYEETVKKAREAWKI WADIP\APKPKEKLVRQIG\DAL REEDSKLLRKPWCPLDVGKIL LEGVGEVQEYVDICDYAVGLS RMIGGPILPSERSGHALIEQWNP VGLVGIITAFNFPVAVYGWNN AIAMICGNVCLWKGAPTTSLIS VAVTKIIAKVLE\DNK\LPGAICS LTCGGADIGTAMAKDERVNLL SFTGSTQVGKQVGLMVQERFG\ RHYQNWRSLELGGNNAIHAFE DADLSLVVPSALFACCGEQLGQ RCTT\SRGRLFYYMESIHDEVFK QTLKRAYGTRSRVG\NPWDPN VLYGAISHQGRQLSMFLGAVEE AKKERLAQWVYGGKVMDRPG N\YVEPTNVTSLDHDASIAHTE TFAP\ILYVFK\FKNEEEVFAWE* WK*NRGLSS*HSLPKDLGAESF RWLGP\KGTQTCG\IVKCQPFPT KWGLRLGGA\FGGEKAHLVVA RESGQ*C/WGKQYMRKVYLV FNYS\KDLPSPGQGIKFQ |
| 22436 | 52804 | B | 22564 | 1 | 1434 | |
| 22437 | 52805 | B | 22565 | 1 | 1185 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22438 | 52806 | A | 22566 | 1 | 2450 | GQACHASSSPLKGSRGSPPNFEI LYGPFI FDSLAPD*PKVIAGQVIT LRDAVTGPISSPNEAGKIYQLKP NPAVLICRVRGLHLPEKHVTW RGEAIPGSLFDLALYFFHNYQA LLAKGSGPYFYLPKTQSWQEA AWWSEVFSYAEDRFNLPRGTIK ATLLIETLPAVFQMDEILHALR DHIVGLNCGRWDIYFSYIKTLK NYPDRVLPDRQAVTMDKPFLN AYSRLLIKTKHKGAFAMGGM AAFIPSKDEEHNQVLNKVKA DKSLEANNHGDGTWIAHPGLA DTAMAVFNDILGSRKNQLEVM REQHAPITADQLLAPCDGERTE RKFNALMESEKGSQNLWKFA VYSGLRHGELAALAWEDVDLE KGIVNVRRLTILDMFGPPKTN AGIRTVTLQPALEALKEQYKL TGHHRKSEITFYHREYGRTEKQ KLHFVFMPRVCNGKQKPYYSV SSLGARWNAAVKRAGIRRRNP YHTRHTFACWLLTAGANPAFIA SQMGHETAQMVYEIYGMWID DMSDEQIAMLNARVMVYDVA SGNALFISELGPLPENVTWLSPE GEFQKWNGTAWVKDTEAEKL FRIREAEETKNNLMQVASEHIA PLQDAADLEIATEEEISLLEAW KKYRSIPLCSKVVTMMFDDRP GCPVGFPWGRGGFDRMPPG WGGRPMPPSRDMSPHRGPPPP |
| 22439 | 52807 | A | 22567 | 1 | 941 | MIPNVQGP MRGLEGPNIYIFIKIS KNRRYTMAVTSVGLASSLCRV VRPCRAPAGVVS RGSPPDDEWL FCPQARIQQQDID/NGTLPDFIS ETASIRDA/DWKIRGIPADLEDR RV/EITGPVERKMVINALNAIF MADFEDSLAPDW/NKVIDGQIN LRDAVNG/TISYTNEAGKIYQL KPN/PAVLICRVRGLHLPEKH/V TWRGEAIPGSLFDLA/LYFFHNY QALLAKGSGP/YFYLPKTQSWQ EAAWWS/EVFSYAEDRFNLPRG T/IKATLLD*TLAGGFQMVDP LGG* TGPWDHLRYIKVENIPKV GEEGDAETTGGTAV |
| 22440 | 52808 | A | 22568 | 2 | 393 | |
| 22441 | 52809 | A | 22569 | 1066 | 1824 | |
| 22442 | 52810 | A | 22570 | 2 | 165 | |
| 22443 | 52811 | A | 22571 | 3 | 902 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22444 | 52812 | A | 22572 | 1 | 2034 | |
| 22445 | 52813 | A | 22573 | 176 | 873 | RLFGEMSKLN/HNLSEVMSKLE KQHSSKV FVVKRLSSSSRRSLVI SPPVRTSTVSSPLTSPSTLSS KSKSESVSATEDLAPDAAQGED NSEIKELLEDEEIGKEGSEASSS EEEEPLLCNGPSQAQPSPIIESA RSQEEVPPSPALSPGGALSPSG HPLSSAAEVVLRTRTAVPQAKG NNVITSYMTNRGFFEDKKATF APSFLMNIKGNKTSVVKNSILE QGQLTVN |
| 22446 | 52814 | A | 22574 | 1 | 1890 | |
| 22447 | 52815 | A | 22575 | 2 | 1279 | LSVFPRVRNFTTQAECH/KLFFK VLKNFLIAGGGVHESSKRAS*T LQFIYY\SEWYGHEELKAIVWN NDLLWEDYEEKLADQAVRTM EIYVAQFSEIKERIAKRGRKLVD YDSARHHLEAVQNATKKDEAK TAKAEFEFNKAQTVFEDLNQEL LEELPILYNSRIGCYVTIFQNISN LRDVFYREMSKLNHNLYEVMS KLEKQHSNKVFVVKGLSSPSTL SLKSESESVSATEDLAPDAAQG EDNSEIKELLEEEIEKEGSEASS SEDEPLPACNGPAQAQPSPTT ERAKSQEEVLPSTTPSPGGALS PSGQPSSSATEVVLRTRTASEGS EQPKKRASIQRTSAPPKPPEKPV RTPEAKENENIHNQNPEELCTSP TLMTSQVASEPGAEKKMEDKE KDNKLISANSSEKYIFQRPSVLI |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22448 | 52816 | A | 22576 | 1 | 1791 | MPGARTSSSGASENHRARGQG GGPQGVGRMAEGKAGGAAGL FAKQVQKKFSRAQEAL*KLG KAVETKDERFEQSASNFYQQQ AEGHKLYKDLKNFLSAVKVMH ESSKRVSETLQEIYSSEWDGHE ELKAIVWNNDLLWEDYEEKL\ ADQAVRTMEIYVAQFSEIKE\RI AKRGRKLVDYDSARHHLEAVQ NAKKKDEAKTAKAEFEFNKAQ TVFEDLNQELLEELPILYNSRIG CYVTIFQNISNLRDVFYREMSK LNHNLYEVMKLEKQHSNKVF VVKGLSSSSRRSLVISPPVRTAT VSSPLTSPTSPSTLSLKSESESVS ATEDLAPDAAQGEDNSEIKELL EEEEIEKEGSEASSSEDEPLPA CNGPAQAQPSPTTERAK\SQEE VLPSTTPSPGGALSPGQLSSS ATEVVLRTRTASEGSE\RPKKT ASIQRTSAPRRPPPPRATASPRP CSGNIPSSPTASGGGSA\TSPRAS LGTGTASPRTSLEI*PNPEPPEK PVRTPEAKENENIHNQNPEELC TSPTLMTSQVASEPGEAKKME DKEKDNKLISADSSEGQDQLQV SMVPENNNLTAPEPQEEVSTSE |
| 22449 | 52817 | A | 22577 | 2216 | 2568 | RPSLGLGM/C/TIWQ/TSLA/GKH RRTIETHDDYRISLEQGTPLGLE PPLNALTAISKKIGCNGFFPFQIR PGKNETDGRMFSPAIGIVEDPV TGNANGPMGAWLVHHNVLP DGNVLRVKGH |
| 22450 | 52818 | A | 22578 | 108 | 532 | WGSKGNLLYSHQTHSVSHQFS LVACCLELEYSPFSFPYACLLSS LMRLEKHQELNLWPAHQRSRMR HPQDTLVVFS/HHGRVLL*DKT SRGTIRQQHSRFTKICCSAATAA VTQANRVWSGPLANSNRPAAE GPVLAAFMGWL |
| 22451 | 52819 | A | 22579 | 1 | 1125 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22452 | 52820 | A | 22580 | 1 | 985 | MCARGSLWGCYSGLERKCEAA LPDRVVSSKSACGAVSQDLLQ AQGRRAGPPSWLYADPVHTGT IECGGHWCLNAALLDFQSPQRL LTYLHCGLQRPME SDPPELAPM VHHQEGIYLNIRKAMYDKPTA NKL NWDKSNVSSLITGTRQEET TANGTTFATIHLOFFIQIPAVPR KTLLNRADYYFPEHNPSLTLVI NRRITKFSEPNWEAPPSRGRLTP HTAGYSSETKIPEERSDSSIRGS RKSAVLQPLLLDSQANRVWSG PLANSNRPA AEGPVC*LWWVT LHGPKLATMQVCQQLW |
| 22453 | 52821 | A | 22581 | 294 | 934 | YPPSPAELTVCLRLQLRDLV YCIA YPSGPGVKPFRGNSA/G/V VFPADNLSEAQMQLI/ARELGH SETAFLHSD/DSDVRI/RFTPTV EVPI/CGHATVAAHYVRKVL/ GLGNCTIWQTS LAGKHR/VTIE KHND DYRISLNALTAIS/KKIGC NGFFPFQIRPG/KNETDGRMFSP AIGIVE/DPVTGNANGPMGAWL VH/HNVLP HDGNVLRVRQ*GPR |
| 22454 | 52822 | B | 22582 | 1163 | 5585 | |
| 22455 | 52823 | A | 22583 | 2 | 429 | AACAAAMSLVPEKFQHILRVL NTNIDGRRKIAFAITASSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSVNLLSNGLYL/VKG VGRRYAHVVL RKADIDLT KRA GELTEDEVERVITIMQNP RQYKI PDWFL |
| 22456 | 52824 | A | 22584 | 84 | 424 | GVHAASDKPCWITTSQTPDVQ HRW/WLLISSML*TAPNRRSDK AFTPHPTNHAGSQLRKHPTCSI DGVIDIFHAVNTFVQHHMEETL KAFHVTGHHILIARHGLGVGKE NTEHAANVVNDQRNSGFFCRF QQTF CQTCCQLIQR FVNARLRD FISC |
| 22457 | 52825 | A | 22585 | 88 | 381 | IQVLANGLDNKLREDLERLKKI RAHRGLRHFVG*VGGLISLPTS TQHSSYSLFFFPNLLFLLCMTCD SSLFTCSLRVRGQHTKTTGRRG RTVGVS KKK |
| 22458 | 52826 | A | 22586 | 355 | 699 | FIDTTEAGSHFLYALVRFAATIT TITDDGARRLRTL FQRQQADLV SVKSGFFTADCTHTNALIDVV RTIFNNAVF*NPGFVIARLKIEIA I IKATFGQLTEDREQVLMFQAV RR |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22459 | 52827 | A | 22587 | 1389 | 1532 | SVLPGRPDARQYRQTRQSW*R WSLRLRGSYPVAGRSLRHRHQ TERF |
| 22460 | 52828 | A | 22588 | 1 | 427 | LVHQQWIQTKKSLIYPFCHSP SQRVVEVAALDQWLAMLYPR VEHQAFLAVVVVVVGPLVVRP YHTRRDAVRLLRQPAVFIVAV DIVRILRDAVIRPHCECTVRV\R SGSGSRLPAGSVAYGMRMSRS GARVRTLSILPVAL |
| 22461 | 52829 | A | 22589 | 1 | 915 | |
| 22462 | 52830 | A | 22590 | 1166 | 1321 | |
| 22463 | 52831 | A | 22591 | 813 | 977 | |
| 22464 | 52832 | A | 22592 | 3485 | 4237 | |
| 22465 | 52833 | A | 22593 | 1 | 499 | ARAAACAAAMSLVIPEKFQHIL R\VLNTNIDGRRKIAFAITAIG VGRRYAHVVLKADIDLTKRA GELTEDEVERVITIMQNPT\QYK IPDWFLNRQKDVKD GK\FQPGS *ANGLSTTKL\RENKPLKEDSG PIKGLRQLP/WGLRVRGQHTKT TGRRGRTVGVSKKK |
| 22466 | 52834 | A | 22594 | 1 | 1197 | |
| 22467 | 52835 | A | 22595 | 1 | 1905 | |
| 22468 | 52836 | A | 22596 | 37 | 514 | WTWWLRCYENRHRHCHLLQQ LPTSPHQHAVATPTTVAVPTAP AATPPVVAVVVAPVVVVVVP VVPVVASVPFVEPGSDVIVCAE MDEQWGYVGAKSRQRWLFYA YDSLRLKTVVAHVFGERTFDVVI WMTDGWPLYESRPAFTGRDC VDDAFFAVAGV |
| 22469 | 52837 | A | 22597 | 1 | 471 | |
| 22470 | 52838 | A | 22598 | 2 | 323 | SRIQPGSDVIVCAEMDEQWGY VGAKSRQRWLFYAYDSLRLKTV VAHV/FGERTIRTLTRRLFRCLR SSHDLVSSPVSHRRRRAGSRQR HRRARGGENVEYQWGALRHG |
| 22471 | 52839 | A | 22599 | 2033 | 2310 | ARYVGNAGCTGGALFGRSQT REAVG/ERRLAESRDVAALDTP CDPEIKMAEWMQTLKETGSTS GHIVTRRISVRISHVTPGPASQD GPDVQQR |
| 22472 | 52840 | B | 22600 | 1 | 4891 | |
| 22473 | 52841 | B | 22601 | 7 | 1233 | |
| 22474 | 52842 | A | 22602 | 193 | 492 | |
| 22475 | 52843 | A | 22603 | 1 | 486 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22476 | 52844 | A | 22604 | 62 | 443 | RSDRLLIHGFSFPAMGFRLRKT VVAHVFGERTMATLGRMLSL SPFDVVIWMTDGWPLYESRLK GKLHVISKRYTQRIERHNLNLR QHLARLGRKSLSFSGTACCG HCLTRDIPMLHHQGNQLF |
| 22477 | 52845 | A | 22605 | 971 | 1444 | SMGSGDMRSPSRAAALRQLPR PFRQLAVRMEMISRFRSAKEQT KSLRKWRKAKSIF*SVAQTGFN VLVCTTIIETGIDSRQPTLLSLNA RITSVCAAAPVTRSRRTFASSGY AWLLTPHPKAMTTDAKNVLKQ LPRWKISGQVRAGTARSGDSRR W |
| 22478 | 52846 | A | 22606 | 1 | 1047 | |
| 22479 | 52847 | A | 22607 | 318 | 598 | LTGFRRLCDLRFGGGAVRSVLA RSREFILQH*FRRIVTGSMGRSL VPSAPLR/PSIVLVLFKAW*LV KTQRKMHVVSIVQKKASCWYP LLGCL |
| 22480 | 52848 | A | 22608 | 1 | 2652 | |
| 22481 | 52849 | A | 22609 | 1 | 852 | |
| 22482 | 52850 | A | 22610 | 1 | 807 | |
| 22483 | 52851 | A | 22611 | 1 | 1740 | |
| 22484 | 52852 | A | 22612 | 1 | 3144 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22485 | 52853 | A | 22613 | 173 | 1983 | PVQNGSSPLGALPGAPLIFGPSV PAISRPGSCSPEWPTLDTSGYSA PR/WLFTAYAGSEAVFAHVFGD ALGDAGLLMSLLSPFDVVIWM TDGWPLYESRLKGKLHVISKRY TQRIERHNLNLRQHARLGRKS LSFSKSV EQHDKLES LPGAQIDKS LDEASLSLRAGSLRTITHILLPLL RPAILSALIYSFVRAITTVSAIVF LVTPDTRVATAYILNRVEDGEY GVAIAYGSILIVVMLAIIFIDWL IGESLLSRFEKTVDHDSQSRLPA EGSILSQDISGVKLFSLTLPARG YVPIRAPCPFLCASYRFFCVARQ QGLDAALIDAPLAVDALTPLE LLSHVGQAPCSVPVVDQDY VGIISKGMLLRALDREGGVRVP VDYILNGFHPDLLGMPAPLAIV FALIACRFPGSNGRIRSRIRH LHKMPDATLSASYQAYVRHQT NVTALVLRSSHFRKDRHCWG FVFLQQPILRATGQFEIQTFRYL SVFSVQRHKTNGKTALMSGNV ADKAVNRATGPTACVWLFSLR NSSMVTTRFCGLCEWADQQGA RPARISENGKRGYSYLYDVHM GAQSGETRGRQGEYASKPPSRE |
| 22486 | 52854 | B | 22614 | 1 | 2149 | |
| 22487 | 52855 | A | 22615 | 1 | 1815 | |
| 22488 | 52856 | A | 22616 | 2014 | 3411 | |
| 22489 | 52857 | A | 22617 | 1 | 922 | MVICQPINGGWQWPPSTGTDP APYFRIFNPTTQGEKFDHEGEFI RQWLPELRDVP GKVVHEPWK WAQKAAAPPQTRLHSTPTTIPH RVPGHTPNLKPIWEVDLPKFSH KATSHATDKPSDTTQNDQIVIA YMEPPEIVHETTTSTHPSLYIIL KRQTREL RPQSVTSRIQPGSDVI VCAEMDEQWGYVGAKSRQRW LFYAYDSLRTVVAVHVFGER MATLGRLMSLLSPFDVVIWMT DGWPLYESRLKGKLHVISKRYT QRIERHNLNLRQHARLGRKSL SFSKSVELHDKVIGH\YLNKHY |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22490 | 52858 | A | 22618 | 1458 | 2185 | YGHEWRWMPGNRPHVYGRWP QHDFPPFKKLRPQSVTSRIQPGS DVIVCAEMDEQWGYVGAKSR QHWLFYAYDRLRKTVAHVFA GERTMATLGRLLSPFDVVI WMTDGWPLYESRLKGKLHVIS KRYTQRIERHNLNLRQHLARLG RKSLSFSSKVEKITSGPTTNP GTQKTATDKRGGKKLPQIPGP ISRIASGAAINVISIGLRKFLVTA GVMLSTQRSIYDRHQVITSAGIT |
| 22491 | 52859 | A | 22619 | 493 | 1518 | |
| 22492 | 52860 | A | 22620 | 963 | 1597 | |
| 22493 | 52861 | A | 22621 | 1 | 3052 | MATDSVGLNCTPAPHARDVLL WRPSSLPVSTSCVFLGRIGDVS DESDDKTEAPTPHRLEKAREEG QIPRSRELTSLLILLVGVSIVWF GGVSLARRLSGMLSAGLHFDH SIINDPNLILGQIILLIREAMLAL LPLISGVVLVALISPVMLGGLVF SGKSLQPKFSKLNPLPGIKRMFS AQTGAELLKAILKTLVGSVTG FFLWHHPQMMRLMAESPITA MGNAMDLVGLCALLVVLGVIP MVGFDVFFQIF |
| 22494 | 52862 | A | 22622 | 1 | 1233 | MANDLPHSNSGDGQKPSSPDLF TAPLLADPTVGFLPNDAEELFIF LTEITEITIPCRVTDPLVVTLHE KKGDVLPVPYDHRGFGSGIFE DRSYICKTTIGDREVDSDAYYV YRLQAVPPVQLLTGWCVTAKA PPDISAISALTAVKHGNCSSLTP LLNPPGSDVIVCAEMDEQWGY VGAKSRQRWLFYAY\DSLRRAR RVVAHVFG*RTMATLGRLLMSL LSPFDVVIWMTDGWPLYESRL KGKLHVISKRYTQRIERHNLNL RQHLARLGKRSLSFSKSVELHD KPSPQHREGVKDVMRFNEPMY PLESRPRLYVCHLRNGAQASGR RCQLPMGCACHPVSQRNDRPN RRPERHATRKTTRQRQONSQR HKQTQKKAKPNKRRATERGKG PQQAERPKRHTHCFLKLQ |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22495 | 52863 | A | 22623 | 3 | 1386 | HEASSPLAMASLTVKAYLLGK EDAAREIRRFSCCSPEPEAEAE AAAGPGPCERLLSRVAALFPAL RPGGFQAHYRDEDGDLVAFSS DEELTMAMSYVKDDIFRI*IKE KKECRRDHRPPCAQEAPRNMV HPNVICDGCNGPVVGTRYKCS VCPYY\DLCSVCEGKGLHRGHT KLAF\SPFGH\SEGF\SHSRWL RKV\KHGHF\GWPGW\EMGPPG\ NWEPTFLPRAG\EARPGP\TAES ASGPSEDPSVNFLK\NVGESVA\ AAFSPL\NFEVDIDVEHGGKRSR LTPVSPSSSTEES\SSSQPSSCC SDPSKPGGNVEGATQSLAEQM RKIALESEGRPEEQMESDNCSG GDDDWTHLSSKEVDPSTGELQ SLQMPSEGPSSLDPSQGGNPQ GWKEAALYPHLP\PEVEPAA*F ESLSQMVPVWGFS*LKGGWVH QGSCRPRNYD\GAAL\DTIPVIQ |
| 22496 | 52864 | A | 22624 | 1032 | 1127 | FYAKAEAGDRTVA*PHKPKMF LSIHHRVAKI |
| 22497 | 52865 | A | 22625 | 121 | 561 | VFPGLGSLVDICGPSRVFPFWV VPAVLVPVQFVQRLPRFFRCPPV LVTSVIRSISTLIQALGSSPFARR YWGNLG*FLFLGVLRCFSSTGS PH*PMNSVNDVSKHT/EVTPF GNP\GNNGSYHLTDAYRRLARP SSPLT\PGHPPLYG |
| 22498 | 52866 | A | 22626 | 243 | 454 | ATAGCPSCSATEGVVRNGKST AGHQRYLCSPCRKTWQLQFTY TASQP/GARIMGVGLNTVLRHL KNSGRSR |
| 22499 | 52867 | A | 22627 | 3 | 640 | |
| 22500 | 52868 | A | 22628 | 236 | 410 | |
| 22501 | 52869 | A | 22629 | 116 | 359 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22502 | 52870 | A | 22630 | 276 | 1905 | LFLYSSHGQYGCPCSATDGVV RNGKSTAGHQRYLCSHCRKTW QLQFTYTASQPAGQ*RTAIATVI CCNNCQRRHTNSRCHTDNCRR ADSASSHATSGSSSRGCAGSGR CGASSTRRCLGPVCCFRGSKRS WRRQHEGHKDCRKLVFHNFSFI HRMDNTAVPPVQLLTGWCVTA KAPPDISAISALTAVKHGNCSSL TPLLNPPGSDVIVCAEMDEQW GYVGAKSRQRWLFYAYDSLRLK TVVAHVFGERTMATLGRLMSL LSPFDVVIWMTDGWPLYESRL KGKLVHISKRYTQRIERHNLNL RQHLARLGRKSLSFSKSVELHD KQQGLDAALIDAPLAVDAQTP LSELLSHVGQAPCAVPVDED QQYVGIISKGMLLRALDREGGV RVPVIYPKRFRRTTDCMPLSLG TCIREIEAEFPDPIFRRSVYICE HNTNGAMGIIIVNKPLENLKIEGI LEKLKITPEPRDESIRLDKPVML GGPLAEDRGFILHTPASNFASSI RISDNTVMTTSRDVLETGTDK QPSDVLVALGYASWEKGQLEQ EILDNAWLTA PADLNLFKTPIA DRWREAAKLIGVDILTMPAQD GTPDWNIIERLLKEWQPDEIIVG LPLNMDGTEQPLTARARKFAN RIHGRFGVEVKLHDERLSTVEA RSGLFEQGGYRALNKGKVDSA SAVIILESIFYEQGY |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22503 | 52871 | A | 22631 | 399 | 2337 | PEVQGLQQAGAAARRPGVGLA APRVVCEGRLRGSGLQSR LCPG ASV*ATDGVVRNGKSTAGHQR YLCSHCRKTWQLQFTYTASQP AGQ*REKEEKEEVEEEEEEEKK KRRREGEKEEKEEKEEKKKKK FKKKKKKKKKKKKKKKKKKKK KKKKKKKKQLSLVTVMSSQQCQL WRNEARTTGACLPSTVSAAP PIVSTTVTAFAAATLAKGDLRS RASSKQVPLLVLVWVWPHPG WFKAGSVALGSSPGCVLELL CKLLTGWCVTAKAPPDISAISA LTAVKHGNCSSLTPLLNPPGSD VIVCAEMDEQWGYVGAKSRQ RWLFYAYDSL RKT VVAHVFG RTMATLGR LMSLLSPFDVVIW MTDGWPLYESRLKGKLHTQER KARSKQQKDADTAPPIQVGTQ TPQTVHAARDTRQASPRASKIS QHRQADGDKRQTRHAEAQAT RTHTGRRKTIKETATQQAYADE QTRRTARTHRRTARHTAAHTH RTRVAARQTTEKDNEQSDTQPP TQKTPSATATAHTPRRTETTTNI VQARHTSARERNHTRQHQATR RETTTNAHTNTPHYHAEHTQSR SQQQTSTSTERPTTDSSTTINNNN HTPRTVRDERRMTQHKHPSRA STTTNRTTTTGAYQHTQRDTRD TRRDTHEDTTTQPHTTTPTAN EAAYTAHTTKTDDHRHTADDT |
| 22504 | 52872 | A | 22632 | 103 | 313 | ATAGCPSCSATEGVVRNGKST AGHQRYLCSPCRKTWQLQFTY TASQP/GARIMGVGLNTVLRHL KNSGRSR |
| 22505 | 52873 | A | 22633 | 620 | 832 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22506 | 52874 | A | 22634 | 453 | 1047 | AADDRGHLRPTDGLLRNGKST AGHQRYLCSHCRKTWQLQFTY TASQPAGQ*RVGTGTSERREQUIQ RLRQQGSVQVNDLSALYGVST VTIRNDLAFLEKQGIAYRAYGG ALICDSTTPSVEPSVEDKSALNT AMKRSVAKAAVELIQGHRVIL DSGTTTTFEIALMRKHTDVIAM TNGMNVANALLEAEGVELLMT AGICALLTGCCVTAKAPPDISAI SALTAVKHGNCSSLTPLLNPPG SDVPVCAEMDEQWGYVGAKS RQRWLFYAYDSLRTVVAHV GERTMATLGRMLSLSPFDVVI WMTDGWPLYESRLKGKLHVIS KRYTQRIERHNLNLRQHLLARLG RKSLSFSSKVELHDKVIGHYLN GDFLQSTLREAPLIPHTREHP |
| 22507 | 52875 | A | 22635 | 1089 | 1686 | TSPGYWRANSTDPDGRYCRTG TSGGVCHALSSLRCPSCSATDG VVRNGKSTAGHQRYLCSHCRK TWQLQFTYTASQPAGQ*RFLSK QEKTLINQLASEEQQKVTSRL SDALRNGRVWQLAIIYLTIQVA VYGLIFFLPTQVAALLGTKVGF TASVVTAPWVAALFGTWLIPR YSDKTGERRNVAALTLLAAGIG IGLSGLLSPVMAIVALCVAAGF IAVQPVFWTMTPTQLLSGTALAA GIGFVNLFGAVGGFIAPILRVKA ETLFASDAAGLLTLAAVAVIDR RGTSNLRLRNTMIALLSNPFKE RLRKGEVQIGLWLSSTAYMA EIAATSGYDWLLIDGEHAPNTI QDLYHQLQAVAPYASQP VIRPV EGSKPLIKQVLDIGAQTLLIPMV DTAEQARQVVSATRYPPYAVH PVQLLTGWCVTAKAPPDISAIS ALTAVKHGNCSSLTPLLNPPGS DVIVCAEMDEQWGYVGAKSR QRWLFYAYDSLRTVVAHVFG ERTMATLGRMLSLSPFDVVIW MTDGWPLYESRLKGKLHVISK RYTQRIERHNLNLRQHTGTGW DGSRCRSQKSGGAA |
| 22508 | 52876 | A | 22636 | 91 | 200 | SGHAFQYLLMTLKVLPVASVSI SCPSCSATDGVVRNGKSTAGH QRYLCSHCRKTWQLQFTYTAS QPAGQ*RGGA |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22509 | 52877 | A | 22637 | 2649 | 3270 | GAPVASVSISCPSCSATDGVVR NGKSTAGHQRYLCSHCRKTWQ LQFTYTASQPAGQ*RTIGRAML KNKHMTITEFVAQRMRAQQK GEISPDINTAMTSRLLLDLTYGV LADIEAEDLARKRRLLRITRDD WRYLNRILILSLFRAGDNCAR VSYQTPTREIKKLDGLWAFSLD RENCGIDQRWWESALQESRAIA VPGSFNDQFADADIRNYAGNV WYQREVFIKPGWAGQRIVLRF DAVTHYGKVWVNNQEV |
| 22510 | 52878 | A | 22638 | 1 | 2470 | MNADTDYSIAEAAFNKGETAM TINGPWAWSNIDTSKVNYGVT VLPTFKGQPSKPFVGLSAGIN AASPNKELAKEFLENYLLTDEG LEAVNKDKPLGAVALKSYEEE LAKDPRIAATMENAQKGEIMP NIPQMSAFWYAVRTAVINAAS GRQTVDEALKDAQTRITNCCRI RRESLIRPGMRKNPMDVIKKKH WWQSDALKWSVLGLLGLLVG YLVVLMYAQGEYLFATTLILS SAGLYIFANRKAYAWRYVYPG MAGMGLFVLFPLVCTIAIGFNN YRRTKQVAGMPAKSSSLRSSQ DREMPPGAKAERTRYDSPGSY GVAGPGFLGSRGGSPFGGPGKY NNTITKYALNIAPSAQNQSPHG PKLNRRQETQHALDWLDAGYT FTYSEDQALTPYFKLAYVYDDS NNDNDVNGDSIDNGTEGSAVR VGLGTQFSFTKNFSAYTDANYL GGGDVDQDWSANDLTGITAKD AQMLSVVKPLQEFGLDKCLS RYGTRFEFNNEKQVIFSSDVNN EDTFVILEGVISLRREENVLIGIT QAPYIMGLADGLMKNDIPYKLI SEGNCTGYHLPKQTTITLEQN QLWRDAFYWLAWHNRILELRD VQLIGHNSYEQFAHIFMIAAM QMGSVWGDDFSSGQHSVARKS QLHKPILRVKCHEGFTISANPNS SPRYPTIIEQAEQPRIVDFSIVRF |
| 22511 | 52879 | A | 22639 | 1 | 852 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22512 | 52880 | A | 22640 | 1 | 747 | MIIDPRYTDGAGREDEWIPIR PGTDAALVNGLAYVMITENLV DQAFLDKYCVGYDEKTL PASA PKNGHYKAYILATD/GVVRTAK STAGHQRYLCSHCRKTWQLQF TYTASQPAGQ*RYTDTGAGRE DEWIPIRPGTDAALVNGLAYV MITENLVDQAFLDKYCVGYDE KTL PASAPKNGHYKAYILATDG WCVPPKAPPDISAISALTAVKH GNCSSLTPLL NPPGSDVIVCAE MDEQWGYVGAKSRQRWLFYA YDSL RKT VVAHVFGERTMATL GRLMSLLSPFDVVIWMTDGWP LYESRLKGKLVHISKRYTQRIE RHNLNLRQHLARLGRKSLSFSK SVELHDKVIGHYLNKHYQ |
| 22513 | 52881 | A | 22641 | 1722 | 2463 | NPRLAGSEGSCPCSATDGVVR NGKSTAGHQRYLCSHCRKTWQ LQFTYTASQPAGQ*RKLTPGCL FVALKGERFDAHDFADQAKAG GAGALLVSRPLDIDL PQLIVKD TRLAFGELAAWVRQQV PARVV ALTGSSGKTSVKEMTAAILSQC GNTLYTAGNLNNDIGVPM TLL RLTPEYDYAVIELGANHQGEIA WTVTHPPRFVTKQWLCFLPDG LLLFAEARFVIWQM QPAVM AV DVAFAHLFNQQQYQRFTGRP PDSSKLPWKITCN GECVTFHW WLLGVA VRISRLLPVRVM TAL EGNYNGTEGISALPFNGI LAHS NESEWVTFRNNKNNEAFLDRV YIVKVPYCLRISEEIKIYEKLLN HIFECWQHFLN NPESLQCYIWA ANADFREARQVIFKTFFTVGVE EELGIRQTRTNDFLVTGDNLLRI FRFDVGNEDKVRQQFAVVRIH REVFLVTFHGVNQRF SRHREEF LFEFCVSVTANLTRCFFGIGFNL RLTFFVIGDDFPTLTQNFRI LIGV IDGEFRLAHKAVAANHAIGLNA QNGCRNDFVAHAAGSRALAAD GRSLEHAPT VETV VAGPLCESG DVFTQQEGGNVETRALPEVKA AVPPVQLLTGWCVTAKALPDIS AISALTAVKHGNCSSLTPLL NPP GSDVIVCAEMDEQWGYVGAKS RQRWLFYAYDRLRKT VVAHRL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22514 | 52882 | A | 22642 | 90 | 1254 | KGLCSHSEMVVPSYSATDGVV RNGKSTAGHQRYLCSHCRKTW QLQFTYTASQPAGQ*RDIVLTK LMMVWHSQSGYEKAYAHQR WWYRAILLTGWCVTAKALPD ISALSALTAVKHGNCSSLTPLL PPGSDVIVCAEMDEQWGYVGA KSRQRWLFYAYDRLRKTVAH VFGERTMATLGRMLSLSPFDV VIWMTDGWPLYESRLKGKLHV ISKRYTQRIERHNLNLSSTSILVL LNGATQFQDLGDLNKELEETY TDSKNHISCVGNDGFGNDIFSR YVEAVGREGDVLLGISTSGNSA NVIKAIAAAREKGMKVITLTGK DGGKMAGTADIEIRVPHFGYA DRIQEIHIKVIHILIQLEKEMVN FTGLVQRGGGTGPHKDGWGIT FYEAFEDVAVNFTQEEWALL DPWQKKLYRDVMLETYRNLAS VGDDDNIPSLREQVAHQRYFKT WHVEREYFSK |
| 22515 | 52883 | A | 22643 | 690 | 1233 | RLQSLHYQGRGKVPMPRSYSL FLFTISNSAGVFRCPSCSATDGV VRNGKSTAGHQRYLCSHCRKT WQLQFTYTASQPAGQ*RLLGP KNRPREQNWLLWCERGVM SRL QALYLREQGFNNVKVDNFQTK VDSCTRPLAGQQFYPCIPDDAL VQPLFGGNFVFQRREAGHITNR EDIVRHQHGGWRGANSRDDTP GTVELFNGFNQQSAIAKTLRAF NATRQHDHVIFAISHFDQRRIR QQLHAARAGNRQVTIAGDAGS GDFDTAANQQIDSGDGFSLFTT RGEANQCRCACAHHSPPFLPFQT VRVFSAVPPVQLLTGWCVTAK APDISAISALTAVKHGNCSSLT PLLNPPGSDVIVCAEMDEQWG YVGA KSRQRWLFYAYDSL RKT VVAHVFAVKPYWDTGGGFHC RWIYMQQEKELLQLSLQQGKY NQKRAAELLGLTYHQFRALLK |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22516 | 52884 | A | 22644 | 1314 | 1483 | RIQRYCGKTGCPSCSATDGVVR NGKSTAGHQRYLCSHCRKTWQ LQFTVYTASQPAGQ*RMFNADG SEVAQCGNGARCFARFVRLKG LTNKRDIRVSTANGRMVLTVT DDDLVRVNMGEPNFEPSAVPF RANKAEKTYIMRAAEQTILCGV VSMGNPHCVIQVDDVDTAAVE TLGPVLESHERFPERANIGFMQ VVKREHIRLRVYERGAGETQA CGSGACAAVAVGIQQGLLAE VRVELPGGRLDIAWKGEELQET LTELDRAVVDYLIKNPFEFFIRN ARAVEAIRVPHVVRGTVSLVE WHMARARNHIHVLEENMALL MEQAIANEGLFYRLLYLQRSLT AASSLDDMLMRFHWARDLG LAVAMPVTINKGNQIENQLDT ETITISYEFILCQHLIANTEFSYL ALPENYNRLCLPNSKNQTNRF KTLNSKAIGRLLAAGGVYNGNI EGFRDTAEKLA VPPVQLLTGW CVTAKALPDISAISALTAVKHG NCSSLYTASQPAGQ |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22517 | 52885 | A | 22645 | 1479 | 1793 | TRYRSCPSCSATDGVVRNGKST AGHQRYLCSHCRKTWQLQFTY TASQPAGQ*RRNACQYRTPAV VASRQKRWHGDLGMIGSRDV MLFISDSVGAKELDLIIPRLEDK SIALLAMTGKPTSPLGLAAKAV LDISVEREACPMHLAPTSSTVN TLMMGDALAMAVMQARGFNE EDFARSHPAGALGARLLNKVH HLMRRDDAIPQVALTASVMDA MLELSRTGLGLVAVCDAQQQV QGVFTDGDRLRWLVGGGALT PVNEAMTVGGTTLQSQSRAIDA KEILMKRKITAAPVVDENGKLT GAIKLQDFYQGRGLFNPSIPRVS TADAGLANRARNWVGSSWK QVGQIILQGGPQNAEKSGQRYT VSHDRHRDAERQVRKSGLPY AECSTYPSCPVALDLAFASHGI HMHAPGEALRMLVTAMDCAA DARTKLARLLATKGITHEIQIPD ISTKEKAQQPIGLNMEQIKPEKQ DFIKPVIPQAGKHNGVNMSVLR SLLTAGVSLASGLLWSLNGITAT PAAQASDDRYEVTQQRNPDA CLDCHKPDTEAVPPVQLLTGW CVTAKAPPDISAISALTAVKHG NCSSLTPLLNPBGSDVIVCAELD EQWGYVGAKSQRWLFYAYA QSPRTTRCCARIRLHALWRRW |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22518 | 52886 | A | 22646 | 807 | 1350 | NRGCPSCSATDGVVRNGKSTAGHORYLCSHCRKTWQLQFTYTASQPAGQ*RLLNRLIEPTRGQVLIDGVDIKISDAELREVRKKIAMVFQSFALMPHMTVLDNTAFGMELAGINAEERREKALDALRQVGLENYAHSYPDELSSGMRQRVGLARAINPDILLMDEAFSALDPLIRTEMQDELVKLQAKHQR TIVFISHDLDEAMRIGDRIAIMQNGEVVQVGTPDEILNNPANDYVRTFFRGVDSQVFSAKDIARRTPNGLIRKTPGFGPRSALKLLQDEDREYGYVIERGNKFVGAVSIDSLKTAAVPPVQLLTGWCVTAKAPPDISAISALTAVKHGNCSSTPLLNPPGSDVIVCAEMDEQWGYVGAKSRQRWLFYAYDSLRTVVAVHVGERTMATLGRMSLLSPFDVVIWMTDGWPLYESRLKGKLVHISKRYTQRIERHNLNLRQHLARLGRKSLSFSSKVELHDKVIGHYLNKHYQ |
| 22519 | 52887 | A | 22647 | 1 | 1270 | MTAATEQLNASRGLSTREMERQAEAKITTDYINSGGSEGDEKLQNMIKAQNDYYAAEDAKRADWLAGAESAFADYGDSAMDMYGNVNEIASSALNGMTDMMVQFLTGTGKANFADFANKNIISMIKMIAQMVIFNTSLRNDGRSVSSGGA AVSLAAAAGSVATSGFNASNSAPKVVTIREVERSVDVSGMEASSTSWITIRSFTAETSTFGPTMTASMTFLPTYCSIIASLLSSFKLAATDGVVRNGKSTAGHORYLCSHCRKTWQLQFTYTASQPALARNPNRDITIYWGGREEQHLYDLCELEALSLKHPGLQVVPVVEQPEAGWRGRTGTVLTAVLQDHATDGVVRNGKSTAGHORYLCSHCRKTWQLQFTYTASQPGTHQKIIDMAMNGVGCRATAR\IMGVGLNTIFRHLKNSGRSR |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22520 | 52888 | A | 22648 | 381 | 945 | GAPVASVSISCPSCSATDGVVR NGKSTAGHQRYLCSHCRKTWQ LQFTYTASQPAGQ*RTENQTPH VLTHKWELNYENPWTQGGHEL TMGLVVGWRGLQEGDPARTN LSYYQANVGSGQHRENGKPIN LGNVGKSNGERGGKSLYRCKIF LESSVTMKDRELPPVYDGVFEV LQWLLFLSAVPPVQLLTGWCV TAKAPPDISAISALTAVKHGNC SSLTPLLNPBGSDVIVCAEMDE QWGYVGAKSRQRWLFYAYDS LRKTVVAHVFGERTMATLGRL MSLLSPFDVVIWMTDGWPLYE SRLKGKLVHISKRYTQRIERHN LNLRQHLARLGRKSLSFSKSVE LHDKVIGHYLNKHYQ |
| 22521 | 52889 | A | 22649 | 354 | 1119 | RRWRRGAHEAATGGTGRGPAE EAAPGEPAAGRAAPKSGGKRL GGVLGRGGVGRSGSPDRSGA HSAAPRRCRQLPGRCPSCSATD GVVRNGKSTAGHQRYLCSHCR KTWQLQFTYTASQPAGQ*RSK GAIGEGPPDPRGIVEQNLGDIS IPCYNPRPRRSAQKTTLGPLN QPRIPSAQCAGAFPRVAAAGAG GGGGGGSGSGFCLGWRLRRR RQRRRRWRRGEGEGDGDAGH MRPRPAGRAEARRRRLRGNP PPGARLPNREGNGSGVSWAAE VSGDGRGARTEAARTRRRPGG ADNYPGAVPPVQLLTGWCVTA KAPPDISAISALTAVKHGNCSSL TPLLNPBGSDVIVCAEMDEQW GYVGAKSRQRWLFYAYDSLRLK TVVAHVFGERTMATLGRLMSL LSPFDVVIWMTDGWPLYESRL KGKLVHISKRYTQRIERHNLNL RQHLARLGRKSLSFSKSVELHD KVIGHYLNKHYQ |
| 22522 | 52890 | A | 22650 | 23 | 658 | VISRPGSSIQVRGLLSRHGLAL GSAPDLWKLPWVNLVQGMGQ QSQGSSCREGCSRQCPSAAPC GAAPAHFCSAATFWESEVQSIP R/CRATDGVVRNGKS/TAGHQR YLCSHCRKTWQ/LQFTYTASQP EVIRSSPTSAPRSDGKTVPPLM GISP*SAHRLATSDPSLCLSES LCSREPAAVPRASNQQPQGVK DVHHQFTARTSRYPKSKC |
| 22523 | 52891 | A | 22651 | 926 | 1093 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22524 | 52892 | A | 22652 | 343 | 817 | GGARSRQNPRCGPCMVVVPGQ SGRSVSADSSTEFREQGGSVAI\S FPKSINRAGPELFRFMENPFNSV *YRKNVRELTPAIMAVLPVEFR TRLAPQNDTMSLIASAMKECSE AKQAVLLNAPEHQMKKEVSEG IASLFRMLPEQVGPLMTMVT MLGVI |
| 22525 | 52893 | A | 22653 | 115 | 425 | |
| 22526 | 52894 | A | 22654 | 747 | 1173 | |
| 22527 | 52895 | A | 22655 | 1 | 2709 | |
| 22528 | 52896 | A | 22656 | 1 | 2583 | |
| 22529 | 52897 | A | 22657 | 636 | 1029 | APSDQKRDFLVPHGADSAMAK SG*CESGNDLLSSSHMNQLR/A/ ESIPEDVIAGASALVLTFIKFI AENPQWWQQFLKDHVSILAMN EDEAEALTGESDPLLASDKALD WVDLVLCTAGPIGLYMAGGGD VN |
| 22530 | 52898 | A | 22658 | 1611 | 3300 | QSAWANRHRLVDCGRPGNGSD AGVAARSGRNDGTGRCLCHS CSRYGDHHRQSDRIYRHYDAG RSPSGAVDYGTRQGNRFSRAV YPVGA/RRWR*GLPLV/QQFQPE NETSAAWVVGINQPLVDIEAK VDDEFIERYGLSAGHSLVIEDD VAEALYQDVQQKNLITHQSAG GTIGNTMHNYSVLADDRSVLL GVMCSNIEIGSYAYRYLCNTSS RTDLNQLQGVDPGPIGRCTLIG ESGERTFAISPGHMNQLRAESIP EDVIAGASALVLTSYLVRCKPG EPMPEATMKAIEYAKKYNVPV VLTGTFVIAKNPQWWQQFL KDHVSILAMNEDEAEALTGESD PLLASDKALDWVDLVLCTAGPI GLYMAGFTEDEAKRKTQHPLL PGAIAEFNQYEFSSRAMRHKDC QNPLRVYSHIAPYMGPEKCN LGRSGWLLYGRGLDKQRLTQY QSKLGAAMVIVAAWCVEDYQ VIRLAGSLTARATRLAHEAQLD VAPLGKIPHLRTPGLLVMDMDS TAIQIECIDEIAKLAGTGEMVAE VTRTGDARRTRFYRQPAQPCG |
| 22531 | 52899 | A | 22659 | 430 | 586 | |
| 22532 | 52900 | A | 22660 | 1 | 131 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22533 | 52901 | A | 22661 | 1 | 1282 | MLPAHLDACVTTLQKIRWTL VVDPTLALRVPLPALSIRDDPPL RAYLPGRGALKVIRFDDMDFA TIDGINRMLVDIDTNYLFLPRVT SSTIRCLSVPTRRTVPAVTASGR SVKYYPPDFDPSKIPKLKLPKD RQYVVRLMAPFNMCRCKTCGEY IYKGKKF\NARKETVQNEVYLG \LP\FRFYIK\CTRCLGRDSPFKT DP\ENTDYTE\ESLGATRNFQG* EASWEEEEKRV\QK\EREDE/ES LNNPMKVLENRTKDSKLEMEV LENLQELKDLNQRQAHVDFEG\ MLRQHRLSEEERRSQQQEEFEQ KTAALLEEARKRRLLEDSDSED EAAPSPLQPALRPNPTATLDEA PKPKRKVEVWEQSVGSLGSRPP LSRLVVVKAKADPDCSNGQP QAAPHPRSPAEGGQPYTPDA WRVLPEPTGCIPGQ |
| 22534 | 52902 | A | 22662 | 1 | 412 | |
| 22535 | 52903 | A | 22663 | 298 | 532 | MGWSLPGRTLWKEKVRFLKS KERTNPGSNFFSFPQSHTREER SQECLSLPVLPSYLATRLSLPDS CPLKGRKAH*QRHSEI*LMGFE PGWPGKL*GWIELAFLGCLHL TLPLCPTPLPPKSTKSGCFSLSI ALCFNKQFAVTK |
| 22536 | 52904 | A | 22664 | 1 | 193 | |
| 22537 | 52905 | B | 22665 | 55 | 281 | |
| 22538 | 52906 | A | 22666 | 86 | 159 | |
| 22539 | 52907 | A | 22667 | 63 | 1036 | VRGGLAAGRGRGSAGAAPVVV AAMLGAWAVEGTAVALRLRL LLLLPPAIRGPGLGAVAGVAGAA GAGLPESVIWAVNAGGEAHVD VHGIHFRKCIPL*GRVGRALYY GMKLPILRSNPEDQSCYQTERS NEETFGYESPIQREGGLTCWSL KFAE\VFYFAQSQQKVFDVRLNG HVVKDLDFDRVGHSTAHEI IPMSIRKGLSVQGEV\ST\FTQG KLLPLSFSKGYL*PIPKVCAL\YI MAG\TVDDVPKASAFNPGLEK KEEEEEEEYDEGSNLKKQTNK NRVQS\GPRTPNPYALDNSSLM FPILV\AFGVFIPTLFLCLRL |
| 22540 | 52908 | A | 22668 | 1570 | 1773 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22541 | 52909 | A | 22669 | 62 | 454 | NKQLNKKRRRTMIALIQRVTRAS/VTVEGEVTGEIGAGLLV/LLGVEKDDDEQKAN/RDAEGQM/NLNVQQAGGSVLVVSQF/TLAADTERGMRPSFSQGHHRIRAQAFYDYFVES/CRQQR*YAQGGLSAEFRLLS |
| 22542 | 52910 | A | 22670 | 1 | 1930 | MAGKPEYDKTISTSIVLNALNALGVSAEASGRNDLVVKTVEGDRKVS GSAYRETKDRGFHHGTL LLNADLSRLANYLNPKKKLA AKGITSVRSRVTNLTLLPGITH EQVCEAITEAFFAHYGERVEAE IISPNKTPDLPNFAETFAQQSSW EWNFGQAPAFSHLLDERFTWG GVELHFDVEKGHITRAQVFTDS LNPAPLEALAGRLQGCLFSLYN SDLNTVIDNVLRJFPLLSWISF WLLYSIVPTIRVPNRDAIVGAFV AALLFEAGKKGFALYITMFPSY QLIYGVLAVIPILFVWVYWTCV TVEGEVTGEIGAGLLVLLGVEK DDDEQKANRLCERV LGYRIFSD AEG\KMNLNVQQAGGSVLVVS QFTLAADTERGMRPSFSKGVID DIGFNTEISQTRFHQASHLFKRK GIYRLHFARRRCQQIQRQR RR FMQRTAVAITHQQRMKQGIL RLWRNWLLWLLILLRRNRLL RLLILLWRNRLLRLLILWLRR NRLLWLLILRLRRNWLLRLLIL LLRCNRLLRLLYRFNNWRKQR FVWTIIQQR FHWRFKIIQRERI RPSRLFAGITLLSLRKLTSQFS LCRSICIFCVYGHIMLILFAIAL LCLGELTCQFILLHRIDFIIVVLI |
| 22543 | 52911 | A | 22671 | 377 | 463 | QTISQTTVQSN*NSGLRISPKTAQLHGD |
| 22544 | 52912 | A | 22672 | 129 | 615 | KARQKSCQPVTDTQCRHTSSS IGKRLAFCQNLQIHTESTMKP WILLVVMFISGVVMLLPVLGSF WNKDPFLDMIRETEQCWVQPP YKYCEKRCTKIMTCVRPNHTC CWTYCGNICLD/IRRAP*/HQC* TPRFYWPITTVG*RMTIWSKKS AAYFLLGTPTWL |
| 22545 | 52913 | A | 22673 | 3 | 412 | |
| 22546 | 52914 | A | 22674 | 2 | 390 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22547 | 52915 | A | 22675 | 180 | 507 | CCGGRARSELCLLNLCIKGAD*I QAW*KFCQWPCERADGRGCRK AER\CPCPKGAYSL/YCRESVCC LPSFVNKNSSSLCVAHNWGRH CYLWTAADV KQFISSHMFPVE HL |
| 22548 | 52916 | A | 22676 | 3 | 227 | GGGRARSELCLLNLCIKGAD*I QAW*KFCQWPCERADGRGS*F DRGA EVCNQT DWQSIRSSQGG RDQRFSTERA |
| 22549 | 52917 | A | 22677 | 567 | 842 | |
| 22550 | 52918 | A | 22678 | 1 | 1400 | MGWGQGP DVQLMNGHERSPS HSPREAKKSGSPLPTDIHCFSPQ SQPAMVITGVPTAPAGASAKM GLCATPITGACPLWLRGFRGWR CEDRCEQGTYGNDCHQRCQCQ NGATCDHVTGECRCPPGYTGA FCEDLCP PGKHGPQCEQRCPCQ NGGVCHHVTGECSCPSGWMLS FPGWRPI*FSKSL*MQGTVC GQ PCPEGRFGKNCSQECQCHNGGT CDAATGQCHCSPGYTGERAAV PDVRK\CQDECPVGTYGVLCAE TCQCVNGGKCYHVS GACLCEA GFAGERCEARLCPEGLYGIKCD KRCPCHLENTHRGDDREKAEF GHLLIALEVQYTEISNCIEKSQE ASCYDIRMLKQPYGETNTEEEL AVNYVYSIYASKEQIRYKHGRS FANGHVKELMEGPSRRIAGSGG EKYKRDEEKNTLLRGQNRGGR GKNPKKTKAWVKIQQNKIEIS GVGADRKRFFREK |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 22551 | 52919 | A | 22679 | 1 | 2210 | MEQKGEFKNDTLIYEFFHIVAK PHPLPIKSSTYTTFQSARVTRFF LDAEKECRCQEGQVEAALIAM GGTCQGTQRLSTAGESESATH MREPAVQCRRDSQCVSVLAGR RRFFQGAASPLHPASVALTQLH VRWASTATIGQVSGFPGKIRVS PTTNLGSDYIFTASHWGLGHY GPAVHVHSQGGIDERGSNDG RLYVTNPCGNVPSWTPNIDRLA EDGVKLTQHISAASLCTPSRAA FLTGRYPVRSGMVSSIGYRVLQ WTGASGGLPTNETTFAKILKEK GYATGLIGKWHLGLNCESASD HCHHPLHHGFDHFGMPFSLM GDCARWELSEKRVNLEQKLN LFQVLALVALTLVAGKLTHLIP VSWMPVIWSALSALLASSYF VGALIVHADCFLMRNHTITEQP MCFQRTTPLILQEVASFLKRNK HGPFLLFVSFLHVHIPLITMENF LGKSLHGLYGDNVEEMDWMV GRILDTLDVEGLSNSTLIYFTSD HGGLENQLGNTQYGGWNGIY KGGKGMGGWEGGIRVPGIFRW PGVLPAGRVIGEPTSLMDVFPT VVRLAGGEVPQDRVIDGQDLL PLLLGTAQHSDFEFLMH\YCER VLHAARWHQRDRGTMWKVHF VTPVFQPEGAGACYGRKVCPCF GEKVVHHDPPLLFDLSRDPSET HILTPASEPVFYQVMERVQQAV |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22552 | 52920 | A | 22680 | 185 | 2091 | GSTERDNMLHLHHSCVCFRSW LPAMLA VLLSLAPSASSDISASR PNILLMA\DDHGVGDIGCYGN NTMRTPNIDRLAEDGVKLTQHI SAASLCTPSRAAFLTGRYPVRS GMVSSIGYRVLQWTGASAGFT TN\ETTFAKILKEKGYATGLIGK WHLGLNCESASDHCHHPLHHG FEHFYGMFPFLMGDCARWELS EKRVNLEQKLNFLFQVLALVA LTLVAGKLTHLIPVSWMPVIWS ALSAVLLLASSYFVGALIVHAD CFLMRNHTITEQPMCFQRTTPLI LQEVASFLLKRNKHGPFLLFVSF LHVHIPLITMENFLGKSLHGLY GDNVEEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLNQL GNTQYGGWNGIYKGGKGMGG WEGGIRVPGIFRWPGVLPAGRV IGEPTSLMDVFPTVVRLAGGEV PQDRVIDGQDLLPLLGLTAQHS DHEFLMHYCERFL\HAARWHQ RDRGTMWESPTL*PPCVSSQEG AGAC\YGRK\VCPCFGEK\VVHH DP\PLL\FDLSRDPSETHILTPASE PVFY\QVMER\VQQA VWEHQR TLSPVPMQLDRLGNIWRPWMQ PCCGPFPLCWCLREDDPQINVC SEKLEPRFLNFVTQIETNQLAM |
| 22553 | 52921 | A | 22681 | 209 | 392 | |
| 22554 | 52922 | A | 22682 | 1 | 513 | |
| 22555 | 52923 | A | 22683 | 3 | 613 | |
| 22556 | 52924 | A | 22684 | 1 | 2115 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22557 | 52925 | A | 22685 | 53 | 1966 | VGQPRGLRTLEKLTASVAGGA ANFFGDIERDLGPRDTSRGIRG GNLGDRCSSAEMAYASWQR WSPVEWARWMWTAVTSSGDS SLLVLQGD SGKRSSDSEAFET PESTTPVKAPPAPPPPPPEVIPEP EVSTQPPPEEPGWGSETVPVPD GPRSDSVEGSPFRQTQAHSGVF DEDQPIASTGTDILDFDNIELVD TFQTLPRASDAKNQEGKVNT RRKSTDSPISKSTLSRSLSLQA SDFDGASSSGNPEAVALAPDAY STESAKRVVPPASGGGRVQNSP PVGRKTLPLTTAPEAGEVTPSD SGGQEDSPAKGLSVRLFYSE DKSSWDNQENPPPTKKIGKKP VAKMPLRRPKMKKTPEKLDNT PASPPRSPAEPNDIPIAKGTYTF DIDKWDDPNFNPFSSTSKMQES PKLPQQSYNFDPDTCDESVDPF KTSSKTPSSPSKSPASFEIPASA MEANAV\DG DGLNKPAKKKKT PLKTMVEDVMSVCSLFDTRV KKSPKRSPLSDPPSQDPTPAATP ETPPVISAVVHATDEEKLAVTN QKWTCMTVDLEADKQDYPQPS DLSTFVNETKFSSPTEELDYNF YEIEYMEKIGSSLPQDDAPKK QALYLMFDTSQESPVKSSTVR |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22558 | 52926 | A | 22686 | 662 | 2927 | HLRRKRNLP RREG LSPALLEET PLEPA VGPKAACPLDSESAEGV VPPASGGKRCLFTTAPEAGEVT PSDSGGQEDSPAKGLSVRLEFD YSEDKSSWDNQQENPPPTKKIG KKPVAKMPLRRPKMKKTPEKL DNTPASPPRSPAEPNDIPIAKGT YTFDIDKWDDPNFNPFSSTSKM QESPKLPQQSYNFD PDT CDES V DPFKTSSKTPSSPSKSPASFEIPA SAMEANGVDGDGLNKPACKK KTPLKTD TFRVKKSPKRSPLSD PPSQDPTPAATPETPPVISAVVH ATDEEKLAVTNQKWTCMTVD LEADKQDYPQPSDLSTFVNETK FSSPTEELDYRNSYEIEYMEKIG SSLPQDD DAPKKQALYLMFDT SQESPVKSSPVRMSESPTPCSGS\ SFEETGSPLRNTAA\KNQ\HPVP TRDWAP*PRSSHLAGCQRKSSQ E/VELGGPWGLGHPFQEGDLKF TASPRGSFASADALLSRLAHPV FSL/CGALDYL\EPNFRQKRNP LFAQKLQREA\ VHPTDVS\SKT ALYSRIRTTEVEKPAGLLFQQP DL\DSALQIARAEI\TKEREVSE WKDKYEESR\REVMEMRK\LA EYEKTIAQMIEDEQREKSVSHQ TVQQLVLEKEQA\LADLNSVEK \SLADLFRRYEKMKEVLESFRK NEEV LKRC AQEYLSRVKKEEQ RYQA\LKVHA\EEKLDRANAEM |
| 22559 | 52927 | A | 22687 | 374 | 1268 | AETNMVWYDWMRPSHAQLHS DYMQLPTEAKAKSKNKVRGV QQLIQRLRLIKSPA EIERMQIAG KLTSQAFIETMFTSKAPVEEAF YAKFEFECRARGADILAYPPVV AGGNRSNTLHYVKNNQLIKDG EMVLLDGGCESSCYVSDITRTW PVNGRFTAPQAELYEAVLEIQR DCLALCFPGTSL ENIYSMMTLI GQKLKDLGIMKNTQGK*CL/RR LLE/QYCPHHVGHYLGMDVHD TPDMPRSLPLQPGMVITIEPGIYI PEDDKDAPEKFRGLGVRIEDDV VVTQDSPLILSADCP |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|---|
| 22560 | 52928 | A | 22688 | 329 | 1389 | RIWKTQMMRMKKMMMMMM MMMRITLFFQQESQEAIFFPFD LFPMCPFGCQCYSRVVHCSDLG LTSVPTNIPFDTRMLDLQNNKI KEIKENDFKGLTSLYGLILNNN KLTKIHPKAFLTTKKLRLRLYS HNQLSEIPLNLPKSLAELRIHEN KVKKIQKDTFKGMNALHVLEM SANPL**/SMGIEPGA*RG*RCS /YIRIAEAKLTSVPKGLAPPTLLE LHLDYNKISTVELEDFKRYKEL QRLGLGNNKITDIENGLANIPR VR\EIHLGNILKKIPSGLPKLY LQIIFLHSNSIARVGVNDFCPTV PKMKKSLYSAISLFNNPVKYWE MQPATFRCVLSRMSVQLGNFG |
| 22561 | 52929 | A | 22689 | 1 | 4608 | |
| 22562 | 52930 | A | 22690 | 1 | 465 | |
| 22563 | 52931 | A | 22691 | 1 | 1542 | |
| 22564 | 52932 | A | 22692 | 1 | 4226 | EAVLCSSRGRPDSSMPDCCRNA ALEARSCQSMSTLFSNTVSPTQ DGTSSLPRRQSSFAKPLRALY DLIAPMEGGVVESTEPLGTSR SGFASGTALFWLGDNGKAASP PGVSVSSLENNEDNTQCNRLAQ GYREAAVPDWTQDLALCLLPT LQSLKARTAPHLCPVSSCYKA WYTLAVSKVSGMVEGKAWIIL LLLAATHALLQRPQEGDITPL AGSRAAAVSCQARPFSTFSGLM HSSGPVGRHRQLILVLE |
| 22565 | 52933 | A | 22693 | 2 | 4197 | ALDFPGRFRPTASFIWASVLFE TIRHEAEVSTDYKLSLFDLQTSS YQALQRVLVSLGHHDEALAVA ERGRTRAFADLLVERQTGQQD SDPYSPVTIDQILEMVNGQRGL VLYYSLAAGYLYSWLLAPGAG IVKFHEHYLGENTVENSSDFQA SSSVTLPTATGSALEQHIASVRE ALGVESHYSRACASSETESEAG DIMDQQFEEMNNKLNSTVDPT GFLRMVRRNNLFNRSCQSMST LFSNTVSPTQDGTSS |
| 22566 | 52934 | A | 22694 | 1 | 618 | |
| 22567 | 52935 | A | 22695 | 1 | 3528 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22568 | 52936 | A | 22696 | 85 | 1193 | RPIEGQLGTCHPGSEPRTIRWRA PGKGLRLYTHPPTSDIAGRTGA AASFPAPLHLPREPRAGVDGTD AERILYPRRAAPAASGVGSRPA GEAVRADEAGAAGLGGFQSER NRSWGGESLGSRQPQKMPAFN RLFPLASLVLIY*VSVCFPVWGE VPLENGGRARANPMKLCISC MKREEVEATTVVEWFYRPEGG KDFLIYEYRNGHQEVESPFQGR LQWNGSKDLQDVSITVLNVTL NDSGLYTCNVSREFEFEAHRPF VKTTRLIPLRVTEEAGEDFTSV VSEIMMYILLVFLTLWLLIEMIY CYRQVSKAEAAQENAPGNSL EGGSQGLQINSTQDGLVTGQQ DVGSHRAREHMPDFEPPSAK |
| 22569 | 52937 | A | 22697 | 277 | 527 | VRVSWEIFCAPGPAGSPAGPG RGEEKQRLGILLIRDARSPAPPG PPVGSVRG/PKPAPAGRVRKAG RRA*GAACSLAAGAWVEPGI |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22570 | 52938 | A | 22698 | 226 | 2268 | SVKNYTKCHVRNEQICNKLTSCKSCSLNLCQWDQRQQECQALPAHLCGEGWSHIGDACLRNVSSRENYDNAKLYCYNLSGNLASLTTSKEVEFVLDEIQKYTQQKVS PWVGLRKINISYWG WEDMSPF TNTTLQWLPGEPNDSGFCAYLE RAAVAGLKANPCTSMANGLVCEKPVVSPNQNARPCKKPCSLRTSCSNCTSNGMCECMWCSSTKRCVDSNAYIISFPYGCLEWQTATCSPQNCSGLRTCGQCLEQPGCGWCNDPSNTGRGHCIEGSSRGPMKLIGMHNMVLDTNLCPKEKNYEWSFIQCPACQCNGHSTCINNVC EQCKNLTTGKQCQDCMP GYYGDPTNGGQCTACTCSGHA NICH LHTGKCFCTTKGIKGDQCQLCDSENRYVGNPLRGTCYYKTLIDYQFTFSLLQEDDRHHTAIYFIVNPKQSNKNLHISINASNNFNLNITWPC*STAGTISGEETYIVSKNNILEYRDSFSYEKFNFRSNPNITFYVYVSNFSWPIKIQIAFSQHNTIMDLVQFFVTFSCFLSLLL EAAVVWKIKQTCWASRRREQLLRERQQMASRPFASVDVALEV GAEQTEFLRGPLEGAPKPIAIEPCAGNRAAVLTVFLCLPRGSSGAPPPGQSGLAIASALIDISQQKASDSKDKTSGVRNRKHLSTRQGT |
| 22571 | 52939 | B | 22699 | 252 | 360 | |
| 22572 | 52940 | A | 22700 | I | 84 | |
| 22573 | 52941 | A | 22701 | I | 404 | |
| 22574 | 52942 | A | 22702 | 86 | 292 | NPEMRCREFCLPSCRPELALE*G*SVRDVA*AQMCSVVWAGRPLGFAA*S*GSGHSCGRCSIWGE CWG |
| 22575 | 52943 | A | 22703 | 82 | 379 | HTLQPFISMGSLTKMFKVISEGPM D*RPHPKVRPMT*HSTPAPANFMGHFFWKIMICTDRTEVATLVAGVVSGASVGGKSPPYRKWNSPEPDVKGPRVL |
| 22576 | 52944 | A | 22704 | 2 | 382 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22577 | 52945 | A | 22705 | 1 | 479 | HMPSETAPLRIVDTGTGTGTV VAYAPTE\LGLHEMHIKYMASHI LESPLRFYVTTPTVPSVSAYGPG LVYGVAN/NTATFTIVTEDAGE GGDLAIEGPSKAEPRPRLSRA PGVDGAGASPLGEDTGPQAP GLQV\TERIPGPSAPTPEFLSVG VSAVC |
| 22578 | 52946 | A | 22706 | 1 | 590 | |
| 22579 | 52947 | A | 22707 | 171 | 406 | |
| 22580 | 52948 | A | 22708 | 269 | 2477 | |
| 22581 | 52949 | B | 22709 | 167 | 7472 | |
| 22582 | 52950 | A | 22710 | 1 | 520 | |
| 22583 | 52951 | A | 22711 | 2218 | 2472 | |
| 22584 | 52952 | A | 22712 | 722 | 1555 | SRNWYEALNNTWGREDICVVD GWQSFRRQDYAFLQERGSGGD LWSSTLAQAMTLVESRHRHQ ALSTQLLDAIMPYCGNTLRLGV TGTPGAGKSTFLEAFGMLLIRE GLKVAVIAVDPSSPVTGGSILG DKTRMNDLARAEEAFIRVPSS GHLGGASQRARELMLLCEAAG YDVVIVETVGVGQ\SETEVARM VDCFISLQIAGGADDLQGIKKG LMEVADLIVINKDDGDNHTNV AIARHM/YESALHILRRPPMHR VPRNPKVNLLPGTAMANLLS |
| 22585 | 52953 | B | 22713 | 381 | 425 | |
| 22586 | 52954 | A | 22714 | 1 | 1185 | |
| 22587 | 52955 | A | 22715 | 1 | 3009 | |
| 22588 | 52956 | A | 22716 | 22 | 527 | YEGIVMKPLIIVNPADCIGC\RT CEIVACVVAHPSEQELNADVFL PRLKVQRLDSISAPVMCHQCEN APCVGACPVGALTMGEQVVQT NSARCIGCQSCVSACPFGMITIQ SLPGDTRQQIVKCDLCEQR*EG PACVESCPTQALQLLIERELRRV RQQRIVVTGENPL |
| 22589 | 52957 | A | 22717 | 187 | 325 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22590 | 52958 | A | 22718 | 1 | 2240 | MRSDPDTSVNEIETKLSALLGS ETTGEILFDLLCANGPEWNRV TLEMKYGRIMLDATAKIIDEQDV PTHILSKLTFTLRNHPEGVVMK NFEVLQPLQNSLSGLPLWVSR ILQQINQLTHYEPVIGIMGKTGA GKSSLCNALFAGEVSPVSDVAA CTRDPLRFRLQIGEHFMTIVDLP GVGESGVRDTEYAALYREQLP RLDLILWLIKADDRALATDEHF YRQVIGEAYRHKMLFVISQSDK AEPTSGGNILSTEQKQNISRKIC LLHELFQPVHPVCAVSRLHPV VALLQQFRDTERTHRYHYDS QHRLVDYTRTQYEEPLVESRYL YDPLGRRVAKRVWRRERDLTG WMSLSRKPVQVTWYGDGDR TTIQNDRSRIQTIYQPGSFTPLIR VETATGELAKTQRRSLADALQ QSGGEDGGSVFPVVLVQMLD RLESEILADRVSEESRWLASC GLTVEQMKNQMDPTEGTAW Y/AEYDEWGNLLNEENPHQLQ QLIRLPGQQYDEESGLYYNRHR YYDPLQGRYITQDPIGLKGGW NFYQYPLNPISDIDPLGLSMWE VARQMNAIASKLPEGFHIGINFS ASHIISPTFVDECLNFRDSFTRR DLNLVLEVTERDLLNVDESLVQ RLNILHENGFIALLDDFGTGYS GLSYLHDLHIDYIKIDHSFVGRV NADPESTRILDCVLDLARKLSIS |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22591 | 52959 | A | 22719 | 1 | 2301 | MALTSGVHTGEKPYKCAQCEE AFSRKSELIIHQIIHTGEKPYECT ECGKTFSRKSQLIHQRTHTGEK PYKCTKCGKSFCQQSHLIGHQR IHTGEQPYLGLSVAERPKEYED DRALKMAAPCGNSSREQPCCFL NKASEDAERAKPPS*EPGRLRT P*VAQPH*VPHFMATWVRKHP VHDRQFRLHGOIRELNWDVVR PEQFTGVATNCSGITYPQGGWL CPAELTRNVLELAQQQGLQIYY QYQLQNLSRKDDCWLLNFAGD QQATHSVVVLANGHQISRFSQT STLPVYSVAGQVSHIPTTPELAE LKQVLCYDGYLTPQNPNQHH CIGASYHRGSEDТАYSEDDQQQ NRQLIDCFPQAQWAKEVDVS DKEARCGVRCATRDHLP MVGN VPDYEATLVEYASLAEQKDEA VSAPVFDDLFMFAALGSRGLCS APLCAEILAAQMSDEPIPMAS TLAALNPRLWVRKLLKGKAV KAG |
| 22592 | 52960 | A | 22720 | 1021 | 1734 | |
| 22593 | 52961 | A | 22721 | 1247 | 2412 | RRSHHAANLDIRIMPQTRQVT LPDPELHPDSTLSMWPD/NRIAR DAHLYRYDRHGRLTEKTDLIP EGVIRTDDERTHRYHYDSQHRL VHYTRTQYEEPLVESRYLYDPL GRRVAKRVWRRERDLTGWMS LSRKPQVTWYGWDGDRLLTIQ NDRTRIQTIIYQPGSFTPLIRVET ATGELAKTQRRSLADALQQSG GEDGGSVVFPVLVQMLDRLE SEILADRVSEESRRWLASCGLT VEQM QNQMDPVYTPARKIHLY HCDHRGLPLALISKEGTTEWCA EYDEWGNLLNEENPHQLQQLI RLPGQQYDEESGLYYNRHRY DPLQGRYITQDPIGLKGGWNFY QYPLNPVTNTDPLGLEVFPRPFP LPIWPWKSPAQQQQWYPTFCC |
| 22594 | 52962 | A | 22722 | 1 | 4767 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22595 | 52963 | A | 22723 | 668 | 1922 | YPHADSPECWLSSSSSERGKSSV TADLSRPRRLRPIPTCHGKPIAC TTTKAKNAFRPIAGASATGRLA NSPIIILPNAAIRQEFGITLDPEEV FTFQGVKLYEYRYFPDCVRSRN EAGILVEQILSTLFSVGEHFSLK RAPFFKVPSLRSFYAFGGLTTG VVRNGNHGVNTPARKIHLHYH CDHRGLPLALISKEGTTEWCAE YDEWGNLLNEENPHQLQQLIR LPGQQYDEESGLYYNRHRYD PLQGRYITQDPIGLK\GGWNFY QYPLNPVQYIDSMGLASKYGH LNNGGYGARPNKPPTPDPSKLP DIAKQLRLPYPIDQASSAHNVF KTFFRALSPYDYTLYCRKWVK PNLTCTPQDDSQYPGMDTKTA SDYLPQTN/WPVPSSIVSCTTG VP*VVCQWVFAWPPDISHRRTG |
| 22596 | 52964 | A | 22724 | 25 | 510 | RITDFGVKKIIRVGSCGAVLPHV KLRDV/VI/GMGAC/TDSKVNRI RFKQGAFGGIADFAMGRTAVD PGKALGINARVGNLVSADLFYS PDGEMFDVMEKYGILGVEMEA AGIYGVAAEFGAKALTICTVSD HIRTHERQTAAERQTTFNMIKI ALESVLLGDKE |
| 22597 | 52965 | A | 22725 | 415 | 759 | HRRRVIDDTGIFRPRNTAQQLR QRPIAMSASGVVQIILEGHWRT HSLRNGFHRGFRL*SSPKVGMQ HGSRQVDHRTQRALRFFRQPGI DFLRPVFTPRRQRLAATNHFSR FVEH |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22598 | 52966 | A | 22726 | 2 | 2329 | GTLPGCGAMHTCPSGPATHLV RRRIVRLPACVVTRANVPTPSR PVNATIGAFHSG*MASQGRRLS AQYPWSPFQYA\ARPVPTVPGR LVFTGTSKAPKISVMGPGMGIP SCSISAKELITDFGVKKIIRVGSC GAVLPHVKLRDVVIGMGACTD SKVTRIRFKDHAFAAIADFDMV RNAVDAAKALGIDARVGNLFS ADLFYSPDGEMFDVMEKYGIL GVEMEAAGIYGVAAEFGAKAL TICTVSDHIRTHERQTAAESQTT FNDMIKIALESVLLGDKEEDRVI RFGKARATRYALLRPYRGIERIP VWRVDDTGKAHKFADIRLCWP QGSCLDVAKAREVIRGSQPLPA WCENWAQEV DARLTKEA QSA LRPVINLTGTVLHTNLGRALQA EA AVEAVAQAMRSPVTLEYDL DDAGRGRDRALAQLLCRITG AEDACIVNNNAAAVLLMLAAT ASGKEVVVSRGELVEIGGAFRI PDVMRQAGCTLHEVGTTNRTH ANDYRQADFQFDDFVMAFTQN INGPTQNTALHGGHGRPDLFP LLGAFHGAIDILAPGGLHGYSL PSSFFHALALSAAPGKRCKLS VHLFWGLKDGGPLLTA PLGG ALVGIVGGVGGSNLTFPFHTNF LNVRFVIRRISHRHHHFYRIAKL LMNGAQGSNMLIAAVAGVPHQ NGHFPFTVADRFAIVLSEGSIRV |
| 22599 | 52967 | A | 22727 | 1 | 702 | |
| 22600 | 52968 | A | 22728 | 876 | 1318 | RCHLANASPAAGSHAPSPDSLS/ KIR/QEVG/PPLP/PLLAPLIATPP RTSQPLSPLISSSSPSPASPVGQ VSPFRETPVPPAMSPWPEDPRR ASPPDPSPSAASASERVVPS LQFCAATPKHALPVPGRLLPCA SGHAMPCWRRAKIK |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22601 | 52969 | A | 22729 | 485 | 1455 | PVVQRARNASSCQPFSTSVWAI PSISATSVPMCGATHSILSPKKS TVSDRIGSMQISFFPLSRSAEK* ESPCSSDAFHAIFSVLSGLALHS TTTSLCSSTSGQLVCC**TSLPPT TYGMIACAAPVE*SPRCPV*PPA SAI*RCNNVEALCSTPFERQP*E PAK\SMPDHPKHECVYVVGE*D PAPHPNSREQIHPAHECLAGFP VTQESLFAPLEIVPAYCCEPGRE PRSARSFPFAPRELT*VQLELGT GL*RETLDLVVSAGWA*ARRIS GAVTATPETGTLCQLDSGAECH YRETGVELP*RSRPPVGHGSSR HSRRWRT |
| 22602 | 52970 | A | 22730 | 814 | 5001 | PENSSHRPKPIIPMIAS TLINANQ NSVSPYKRTFTRLTALMIKKA AAQIHVGTSGNQYWRKLD FNS PGGSSPVENS DCSTNSRLSFSPE NILIQNQDIVREAAVQGDGQKQ RQPQATDL DSSGTHGSEMLPAT EVTVSGGFSVEETSCGDTGRSG GEALAVANDSTSTPQNANGLW KLKSTTPGGALPECFGTTDTTFS SAFCRKHGETQDTSQSSLPGTL HCYTGIREGGDDTEVESEAFSC SEGSEQQDAPD |
| 22603 | 52971 | A | 22731 | 34 | 102 | |
| 22604 | 52972 | A | 22732 | 584 | 893 | QKLLPNRMGHPVFVKSSQDPV LLSRIAWKDASTVTWVIEQDPV LRRRRRRTRRRRTRMRRRRGR* */SKRRRMR/GRRGRR*CRRRRR RSSRSRPTRRQRNRNQV |
| 22605 | 52973 | A | 22733 | 2 | 269 | IGKLYWFMPPSANLALREL GIV LFLSVVGLKSGLSWIGYGALIT AVPLITVGILARMLAKMNYLT MCGMLAGSMTDPPA*PRFQTN DREEQHDPQLPQREVGA WRHK PVQLAD |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22606 | 52974 | A | 22734 | 3 | 958 | RCYSLLSRAPHPGIYISIAERV/*I RLNSANFTLNSLLPAEKKLAEE FAVSRMTIRKAIDLLVAWGLV VRRHGSGTYLVRKDVLHQTAS LTGLGEVLKRQGKTVTSQVLIF EIMPAPPAIASQLRIQINEQIYFS RRVRFV\EGIPLMLEDSYMPVK LFRNLSLQHLEGSKFEYIEQECG ILIGGNYESLTPVLADRLLARQ MKVAEHTPLLRLITSLSYSESGEF LNYSVMFRNATQIQGWRSFR R\LHPKKS LTVPPERAPPVFGGL IMRKNHSQRIDSGVRERRRTAG WMKIISKRQRRRIGHGTCQHPA HGQVIHFG |
| 22607 | 52975 | A | 22735 | 2 | 285 | GDEMTTSTLQKAIDLVTKATEE DKAKNYEEALRLYQHPVEYFL HA\IKYEAHSDKAKESIRAKCV QYLDRAEKLKDYLRSEKHHGK LCLKDRV T |
| 22608 | 52976 | A | 22736 | 545 | 791 | |
| 22609 | 52977 | A | 22737 | 249 | 1574 | NHKAIDLVTKATEEDKAKNYE EALRLYQHAVEYFLHA\IKYEA HSDKAKESIRAKCVQYLYRAE KLKDYLRSEKHHGKPKVKENQ SEGKGS DSDSEGDNPEK KKLQE QLMGAVVMEKPNIRWNDVAG LEGAKEALKEAVILPIKPHLFT GKRTPWRG\LLFRPPGT\GNSN RPGAGAPKATNSTFFSVSS\SDV KSKRLGETEKL V*NL FELARQ HK\PSIIFIDEVDSL CGSRNENES\ QAARRIQNGSSLVQIAGGLGIN NDGDSGFFGATNIP\WVLD\SAI R\RKV*KTKFYIPLPEKACPRPD VSRLHLGSTPHN\LRVATFHKL ARKTEGYSGADISIIVRDSL MQP VRKVQSATHFKKVCGPSRTNPS MMIDDLTPCSPGDPRAMEMT WMDVPGDKLLEPVVCM S DML RSLATTRPTVNADDLL\KVKKF SEDFGQES |
| 22610 | 52978 | A | 22738 | 52 | 567 | |
| 22611 | 52979 | B | 22739 | 1 | 1293 | |
| 22612 | 52980 | A | 22740 | 443 | 1027 | |
| 22613 | 52981 | A | 22741 | 2077 | 2430 | |
| 22614 | 52982 | A | 22742 | 1 | 504 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22615 | 52983 | A | 22743 | 3244 | 3947 | RNEITPFRAMMIIRMAHRFQT EEIKRISFIKRRVGNKDEINPGA RWRRFHDDGITFLRLLDAGLTI PSGKTIVHPLARQRRGLVKIQFL R*LLAKLTRQPLLPLQPV TARL CLNPRLRRQRKIRMPAGTKWQ RLCPLIGDR*RHRQRSVYALS VRHNPVHHILRKNNGDMYSFPIT IGNNVWIESHVVINPGVTIGDNS VIGAGSIVTKDIPPNVVAAGVP CRVILEINDRDK |
| 22616 | 52984 | A | 22744 | 742 | 1158 | |
| 22617 | 52985 | A | 22745 | 439 | 2882 | PDWQAFQSPFPASLIHHPKPAK LPGWLCIVQWSLLAITRTPPV RWAQQTETVGLVVGDVSDPF FGAMVKA VEQVAYHTGNFLLI GNGYHNEQKERQAIEQLIRHRC AALVVHAKMIPDADLASLMKQ MPADKQCESIPDQNNQTGTQY PRGKEPKLLRRLMHMNRKVGP RGPRRMLLRYLDVEFLSVALA VVHLGPQGTC SRLFLVARALV VAVSEMDKSLSAQAAQIYFASSN GPVPDLAYQVDFPRLEIGL*F/E YVDTGAETTLVPGDVLYVPAG GWNFPQWQAPATTF SVLFGKQ QLGF/SAVVQWDGKQYQNLAK QHVARRGPRIGSFLLQTLNEMQ MQPQEQQTARLIVASLLNHCR DLLGSQIQ TASRSQALFEAIRDY IDERYASALTRESVAQAFYISPN YLSHLFQKTGAIGFNENLSHTR LGHA*TLLKGYDLKVKVAHA CGFVDSNYFCRLFRKNTERSPS EYRRHRLHDNRICQFKTPTDN PENPDRYLTFRRIDKETSSLPKK VAPSCRLSVSRSSPKPSISIRRC MRLMLIEGRSSFIHPDKDVDG FHPYNVGRLCQRAPRLRPCTPR GIVTLLERYNIDTFGLNAV VIGA SNIVGRPMSMELLLAGCTTTVT HRFTKNLRHHVENADLLIVAV GKPGFIPGDWIKEGAIVMMSGI NRGVATDASCFPLVPFANRVSG |
| 22618 | 52986 | A | 22746 | 2 | 126 | |
| 22619 | 52987 | A | 22747 | 1 | 465 | |
| 22620 | 52988 | C | 22748 | 78 | 308 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22621 | 52989 | A | 22749 | 1 | 2797 | MEHPPVLAVQRVALPSRSSEPE LFLNPPTDEETEAHRGMYLDQ GPRTKDWIPVAPGVREPSPLGP GPSSLWLLVVGTVVEEGSRKH RPTCKKDFTKSKTVDQAPTLCA RHQMLNIQFLISDRDPQCNLHC SRTQPKPICASDGRSYESMCEY QRAKCRDPTLGVVHRGRCKDA GQSKCRLERAQALEQAKKPQE AVFVPECGEDGSFTQNTSCIHSS VYQIGENSSLTFLEKREESGHL QRDWFPWFPRKARVI |
| 22622 | 52990 | A | 22750 | 1 | 5295 | MNLNQEEIPDLPEKEFRRLVIKL IREGLEKGKAQCKEIQKMIQEV KREIFQEIESLKKKPPKIQKTLDI LLKMQNALESLSDRTEQAEEIN SELEDKVFKLTQSNKDEKITER KYEQSLQEVWSYVKRPNLRIIG VPEEEENTKSLENILGGIIEENFP SFARDLDIQIPEAQRRTTGKLIK RSLLRHIVFRLSKVKMKERILR AVRQKHQATVSQKNKAGGITL PDFKLYYKATVSQKNKAGGITL PDFKLYYK |
| 22623 | 52991 | A | 22751 | 1 | 891 | GSPFEVMPRDDVFFIVDVKI*DI GVYSCTAQNSAGSISANATLTV LETPSFLRPLDRTVTGETAV LQCIAGGSPPKLNWTKDSDSPL VETERHFFAAGNQLLIIGDSDV SDAGKYTCEMSNTLGTERRGNV RLSVIPTPTCDSPQMTVL/HLLD DDGWGHCGLYVIIAVVCCVVG TSLVWVVIYHTRRRNEDCSITN TDETNPADIPSYLSSQGTADR QDGYVSSSESGSHHQFVTSSGAG FFLPQHDSSTCHIDNSSEADVE AATDLFLCPFLGSTGPYVFEGK CVWAQNPF |
| 22624 | 52992 | A | 22752 | 1 | 2947 | MSAPSLRARAAGLGLLLCAVL GRAGRSDSGRGELGQPSGVA AERPCPTTCRCLGDLLDCSRKR LARLPEPLPSWVARLDLSHNRL SFIKASSMSHLQSLREVAGNRIV EILPEHLKEFQSLETLDLSSNNIS ELQTAFPALQLKYLELNRNLIK NVDGLTFQGLGALKSLKMQRN GVTKLMDGAFWGLSNMEILQL DHNNLTEITKGWLYGLLMLQE LHLSQNAINRISPDWEFCQKL SELDLTFNHLRLDD |
| 22625 | 52993 | A | 22753 | 2 | 417 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22626 | 52994 | A | 22754 | 1 | 262 | VLDIGS/SLTVPDEFKQE/RAD GMWWKQLVAGAVAGAVS/RT GTAPLDRLKVFMQIKRAILGQQ ETLMCRSASWLAPWLVPQPNH HLPYG |
| 22627 | 52995 | A | 22755 | 1 | 762 | |
| 22628 | 52996 | A | 22756 | 1 | 1527 | RLAAAGADPAGSRGGRGSREA PTEAARCRASPPPRAGAMRGSP GDAERRQRWGRLFEELDSNKD GRVDVHELRLQGLARLGGGNPD PGAQQGISSEGADPNGLDLE EFSRYLQEREQRLLLMFHS�DR NQDGHIDVSEIQSFRALGISIL LEQAEKNFAQA/VDRDGTMTID WQEWDRHFLHSLNVEDVLY FWKHSTVLDIGECLTVPDEFK QEKLTGMWWKQLAAGAVAG AVSRTGTVPLDRLKVFQVHA SKTNRLNILGGL*SMVLEGGIRS LWRNGINVLKIAPEAIKFMA YEQIKRAIPGE*ETLPVLERFVA GSLAGATAQTIIYPMEVLKTRL TLRRTGQYKGLAGLRRGGILER EGPRAFYRGYLPNVLGIIPIYAGI DLAVYETLKNWWLQQYSHDS ADPGILVLLACGTISSTCGQIAS YPLALVRTRMQAQASIEGGPKL SMLGLLRHILSQEGMRGLYRGI APNFMKVIPAVSISYVVYENMK |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22629 | 52997 | A | 22757 | 1 | 2127 | MDQSGLLALRAAVGAVVGSTL AVDIGILVKDWHPRPLGGKHC QLLGAFCRCRQHRRGKEERRGE TKEKKGERENERGKRRRIEGER DKYVKENEKQTCVQKERHSCT GNSPNHMATVQAERGALDSHG GWHWPWDYCAVQQGRYHQLLL TKEEIEVQRSKKMCLLQAFLIC CQKSHFLGPGCTRSMVPASASG ESLKLLPLMVEDEGEPTEREVR KREGERERGRERERRRRRKRK RRRKRRRKRRRRRRRRRG*EFLS LG*NERGKRRRIEGERDKYVKE NEKQTCVQKERHSCTGNSPNH MATVQAERGALDSHGGWHPW DYCAVQQGRYHQLLLTKEEIE VQRSKKMCLLQAFLICCQKSHF LPGCTRSMVPASASGESLKLL PLMVEDEGEPTEREQEEGGGE RERERERKKEKEKEKEKEKEEK EKEKEKEEERIRVPLPRVELRLT NIAAKQVGNTILDVAAPADHPS ESSCVYVRFVIKIPVAASFRFKK SYVTNNVESCEDGIHYFWKSH MHSENSCCKLPCPHLPAAER LGDALEPLLPTMRRQRQCQNT GDGCDGRRQIGTRETEMHRDTS VAVKTQVDTSREGMGEVEPN CFWRDTHMASGVGAAFEELPH DGTCDCEPDEAPGAEEVCREC GFCYCRRHAEAHQRKFLSHHL AEYVHGSQAWTPPADGEGAGK |
| 22630 | 52998 | A | 22758 | 348 | 881 | WRQPRWPHHQACLWQRAGSS YSQHKDPHFTSFSTPRAVQNFD GFPCPFLRETTTLVLIPSVPLTDP GSFYRAWSFQCGPRSPRPLLGR TLSQKFLRLRLGRPRRPYMSTL TPF*STRIFERAFCQVMGAESGG RIEKTTLCKRSLGPLMEPRV |
| 22631 | 52999 | A | 22759 | 1 | 347 | MVPASASGESLKLLPLMVEDER EPVTERE/REKGRGREREGERE KEREGERERERERGERKGERER RRG*QPPFHNRFSEGQGRSFLCS RRPRVSRRGHTSRGPARKAAE RRGLG |
| 22632 | 53000 | A | 22760 | 145 | 258 | PENGLIGLS*KIVLSLNIPVNN DMKVDEVLYEDSSTA |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22633 | 53001 | A | 22761 | 1 | 1479 | MALKEIFCPVRETETCTINCGTR ISPSILHVGLPYPSTPNVKPERE GCGGGVSGNSKQPGALETAESE GKKEGRREEGSRPESASSLSLLL SLAYDVKSAQICTRIHSSVPLE AVYPGYIHQSIINQADLSALAPY DPCVCQIHKYHGAYNCLQYSV QNTLYSPTTEQYKRCQAPWVL PAIFTIPASGAAASAVPVRAQA QGGQAAGQRRRLATAPLTGEG EPDHGDRTRAGSQGPPEARPRIH LGAARGGDRTRGRPGRGRDW TRLGREMAAAAVSSAKRSLRG ELKQRLRAMSAEERLRQSRVLS QK\VIHSEYQKSKRISIFLSMQ DEIETEEIHKD\ICQRGK\ICFIPPV RFSRAITMDMVRIGSP\EGNFFN FPKTSWEYSLRLGEG\DVREEG LVPPGGL/EILILPCPQALGLDQ NHGQPRLG\RGQGA*YL*CLS*K RLFCSHSGKLPPTPPGGWLFK EQICPPRSPVNENDMK\VDEVL |
| 22634 | 53002 | A | 22762 | 1 | 813 | |
| 22635 | 53003 | A | 22763 | 1 | 368 | |
| 22636 | 53004 | A | 22764 | 327 | 4281 | SASASRCDPGSGSRREEREELQ WRRRRRRRRRRRRRRRRRQRQRA AAPAAPAGGIEAVNMASASYHI SNLLEKMTSSDKDFRFRMATND LMTLQKDSIKLDDDSERKVV KMILKLLEDKNGEVQNLAVKC LGPLVSKVKEYQVETIVDTLCT NMLSDKEQLRDISSIGLKTVICE LPPASSGSALAANVCKKITGRL TSAIAKQEDVSVQLEALDIMAD MLSRQGGLLVNFHPSILTCLLP QLTSPRLAVRKRTIIA |
| 22637 | 53005 | A | 22765 | 2 | 271 | |
| 22638 | 53006 | A | 22766 | 299 | 451 | IVALFRSLVRHLRGTMAVESTA TAAVAAEL/VSADKIEDAPAPST SADKVES |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22639 | 53007 | A | 22767 | 1 | 1122 | MATESTATAAIAAELVSANKIE DVPAPSTSADKVERIENGVLGN TLDGVHVEEEEGEKTEDSLVE NNDSIDEEARKELREQVYDSM GEKEEAKKTEDKSFAPETDKE QDCMEKGGREDMDISESAEEP QEKVDLTGWLTEISEGAKGG GAPEGPNEAEVTSKGPEQVDP VEEEKSVSETDVQKECREKGG WEKHREVIVSIEEKPEVSEEQP VVILEKQGTAVEVAAESLDPTV KPVDVGGDEPEEK/GTVPGLSR PSPCRDPLPAGLGLWVQLSV** GSGTVQQIY*SH*EENGCTKRA GEGG*RIVC*IQERN*GTEGTAT RNYRKDRRCKGVSDYWECS*T GSESYSGGELYFRFHS*WRRLF |
| 22640 | 53008 | A | 22768 | 223 | 339 | |
| 22641 | 53009 | B | 22769 | 341 | 496 | |
| 22642 | 53010 | A | 22770 | 12 | 1099 | VSGVPNCLFFSQALFRSLVRHL RGTMAVESTATAA VAAELVSA DKIEDVPAP\STS\ADKVESLDV DSEAKKLLGLGQK\HLVMGDIP AAVNAFQEAASLLGKKYGETA NECGEAFFFYG\KSLLLELARME NGVLGNA\LEGVHVEEEEGEKT EDESLENNDNI/D*N*RLGRG* *RK**D*RNAK*FSP*KQVSSRK *GGGDWEPRACLG YAGFSKDH F*KARNKRSTALCCPGTS*TRRS *C*I*KLCASC\GGVPVLP*PTGP VPGSPRPSPCRDPLPAGLGLWV QLSV**GSGTVQQIY*SH*EQNG CTKRAGEGG*RIVC*IQERN*GT KGTATR N*REDRRCKGVSA*W ECS*TGSESYS |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22643 | 53011 | A | 22771 | 11 | 2485 | VSGVPNCLFFSQALFRSLVRHL RGTMMAMESTATAAVAADVVS ADKIEDVPAPSTSADKVESLDV DSEAKKLLGLGQKHLVMGGIP AAV\NAFQGAA\SL\GKKYGET ANE\CGEAFFFYG\KSLLLEARM ENGVLGNALEGVHVEEEEG\EK TEDESLVENNDN\IDEEAREELR EQVYDAMGEKEEAKKTEDKSL AKPETDKEQDSEMEKGGREDM DISKSAEEPQEKVDLTLDWLTE TSEEAKGGAAPEGPNEAEVTS KPGQ\QVEVPDAEEEEKSVSGTDVQ EECREKGGQEKQGEVIVSIEEK PKEVSEEQPVVTLEKQGTAVEV EAESLDPTVKPVDVGGDEPEEK VVTSENEAGKAVLEQLVGQEV PPAESPEVQTEAAEASAVEAG SEVSEKPGQEAPVLPKDGAVN GPSVVGDTPIEPQTSIERLTET KDGSGLEEKVRAKLVPQSQETK LSVEESEAAAGDGVDTKVAQGA TEKSPEDKVQIAANEETQEREE QMKEGEETEGSEEDDKENDKT EEMPNDSVLENKSLQENEEEEI GNLELAWDMLDLAKIIFKRQET KEAQLYAAQAHLKLGEVSVES ENYVQAVEEFQSCNLQEQYL EAHDRLLAETHYQLGLAYGYN SQYDEAVAQFSKSIEVIENRMA VLNEQVKEAEGSSAEYKKEIEE LKELLP\EIREKIENAKE\SR\SG |
| 22644 | 53012 | A | 22772 | 52 | 161 | FQNPTGLY/CDTEYN\RLQKQQ TEKTKQKKTQFHPICN |
| 22645 | 53013 | A | 22773 | 3 | 115 | FFQNPTGLY/CDTEYN\RLQKQQ TEKTKQKKTQFHPICN |
| 22646 | 53014 | A | 22774 | 229 | 358 | |
| 22647 | 53015 | A | 22775 | 257 | 386 | |
| 22648 | 53016 | A | 22776 | 259 | 294 | |
| 22649 | 53017 | A | 22777 | 217 | 398 | KAWWNLLRKSEPKSCGS*GGL STSRERLVECSSPLGLGYCG**L CHLQEPHYGSLHRMSS |
| 22650 | 53018 | A | 22778 | 1 | 3386 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22651 | 53019 | A | 22779 | 391 | 2100 | SRRTAGVRLDILCKDPIMWVSA DGHSYQPQYPKAKRATEFHFF NFKALLARA AVGAARGIHIHRC GLTKRPDARRRRVAGA QGREP AISLPGDRAAGARATRTRGPGP APKMPAIAVLAAAAAA\WCFL QVESRHLDALAGGAGPNHG\NF L\DNNDQ\WLSTVSQYDRDKY\W NRFRDEVEDDYFRNW\NPNKPF DQAL\DP SKDPCLKVKCSPHKV\ CVTQ\DYQTAL\CVSRKHLLPR QKEWGTWAQKHWGLDL*ILV K\CKPCSRGRSSAMGLAGSDGP LLTAFQVANLEFHACSTGQK/S FATLCDG\PCPCSSQSLEPPKHK GRKGVPCTDKELRNLASRLKD WFGALHEDANRVIKPTSSNTAQ GRFDTSLPICKDSL GWMFNKL DMNYDLLLDPSEINAIYLDKYE PCIKPLFN SCDSFKDGK PFLNNE WCLLP SQNP GGLP/CAQNEMNR IQ\KLSKGK SLLGAFIPRCNEEG YYKATQCHGSTGQCWCVDKY GNELAGSRKQGAVSCEEEQETS GDFGSGGSVLLDDLEYERELG PKDKEGKLRVHTRAVTEDDED EDDDKEDEVGYIW |
| 22652 | 53020 | A | 22780 | 2 | 441 | HGVQGAGCGEVA AVSIELGAG GPVWRAAPRAC SRLQLLRGFG LEGQWFGESCCRRGAS*EGSTR *PPRRQPWPEWVMSWVPPET REPARISPAPAKQN*PPPAPKSP AAPA\PQA AVAATPSPGEISEA WDSLESFSKPAFFSQ |
| 22653 | 53021 | A | 22781 | 3 | 121 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22654 | 53022 | A | 22782 | 2 | 1488 | FVNNMADGEEPEKKRRRIEELL AEKMAVDGGCGDTETWKDR\ WNHVKK\FLERSGPFTHPDFEP\ STESLQFLLDTCCK\VLVIGAGG\ LGCELLKNLALS\GFRQIHVID\ MDT\DVSN*IRQFLFRPKDIGR PKAEVAAEFLNDRV\PNC\NVV PHF\NK\IQDFNDTFY\RQFH\IV CGTGTLS CARRWINGMLISL\LN YERMVS*DPSSIVPLID\GGTEGF \KENARVIL\PGMTACIECTLEL YPPQVNFP MCTIASMPRLPEHCI \EYVGMLQWPKEQPFGEQ\VPL DGDDP\EHQWIFQKSLERASQY NIRGV TYRLTQGVVKRIIPAVA STNAVIAAVCAT*/EVFKIATSA YIPL*IITWVFNDV\DGLYTYTFE GRKGK\ENCPAC\SQLPQNISVF LHQAKLQ\EVLGIILTNSASLQN EILPAITATLGGEKIGTLYLQSV TS\EERNRANFFQTIERNWGLL DGPKTGRLLDVTP\QTVLFQTS ILLKKGKSPT |
| 22655 | 53023 | A | 22783 | 1 | 1719 | |
| 22656 | 53024 | B | 22784 | 199 | 460 | |
| 22657 | 53025 | A | 22785 | 226 | 1620 | NGSGLALATGNRDPGLCPLSAP SCPWR*KSAGASTQQAYSSQSQ /HPAYHRITPTLTNFALRLYKEL AADAPGNIFFSPVSIS\TTLCLLC LGAQANNSALILEGLGFNL TET PEADIHQGFRLHLTLVLPSPKL ELKVGNSLFLDKRLKPRQHYFD SIKELYRAFAFSAHFTDSVTTGR QINDYL*RRTYWPGVDLPFRS/L ARDTFMVLA\NFILEFSKAKVKA TLSSRVDPKSRPVFLVDERTSF \QVPMMHQKEMHRFLYDQDLA CTVLQIE\YRGNALALLVLPDPG KMKQVEAALQPQTLRKWGQL LLPSLLDLHLPRFSISGTYNLEDI LSPNWFSP TYTLNKITSLQSVG G*LNK SISKVSHKSMVDMNEK GDQRPGLLQASSPSPHL*/YTMS DPHAHFNRPFLLLLWEVTTQSL LFLGKVVPVWVWVTMVGQGE LSYLILDQTDRPEPACILGLLCG |
| 22658 | 53026 | A | 22786 | 64 | 288 | |
| 22659 | 53027 | A | 22787 | 1 | 1923 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22660 | 53028 | A | 22788 | 309 | 2286 | CAVCHISFQDTPVLVSSNVTMQ FGSKPLFENISVKFGGGNRYGL\ IGANGSGKSTFMKILGGDLEPT LGNGSLDPNER\IGKLRQ\DQFA FEEFTVLDTVIMGHKEL\WKVK QERDRIYALPEMSEEDGYKVA DLEVKEYGEMAGYSAEARAGEL LLG\VGIPVEQHYGPMSEVAPG WKLRVLLAQALFADPDILLDE PTNNLDIDTIRWLEQVLNENNS T\MIISHDRHFLNMVCTHMAD LDYGELRVYPGNYDEYMTAAT QARERLLADNAKKKAQIAELQ SFIDKIKLEEVKASSRQNPFIREF QDKKLFRNALEVEGLTKGFDN GPLFKNLNLLLEVGEKLAVLGT NGVGKSTL\KTLVGNLQPDG TVK WSENARIGYYAQDHEYEF ENDLPVFEWMSQCKQ*GDDEQ AVRSIFGRLLFSQDVIKKPAKVL SAPFCKDSILEAIDAGIKLIITITE GIPTLDM LTVKVKLDEAGVRMI GPNC PGVITPGECKIGIQPGHIH KPGTGELNITTGGIVKARDTQIA LNDKSKGDVRVDGQNSLLET NMYVGTSGTGTLTLTNNGTLN VEGGEVYLGVFEPVAVGTNLNIGA AHGEAAADAGFITNATKVEFG LGEGVFVFNHTNNSDAGYQVD MLITGDDKDGKVIHDARHTVF |
| 22661 | 53029 | A | 22789 | 1 | 553 | |
| 22662 | 53030 | A | 22790 | 1633 | 2207 | ILFFDKGMPAQTPSLQKRWEK M*LVLW*GDREGIKAI/ISEESW GARAPIFLLR/MMEDQGLYSIR MGGARGLPKSLAL*GAGRGF YSGERTWTLSPSGNCAPYQR GGWWYHACA\HSNLNGVWHH GGHYRSRYQDGVYWAEFRGG AYSLRKAAMPHLAPEAVTLCSE GPLGPRGHWSAGAPSCSGHTFF |
| 22663 | 53031 | A | 22791 | 34 | 210 | AAADPLRHLRRGAFIKAGRHA G/PSLPVCLQATA\H*MDLARLA LVLVVRTSASTKSSTRE |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22664 | 53032 | A | 22792 | 397 | 1168 | LLSRISKVSSKLPVRGGAGSLCT GDQRK\RRKFL\ETVELQISLKN YDPQEGQSAFSGHPSRL*\VPSP PLSSLVCVLGGPSKHL*RRLRP VGYPPTMDIEGA*KKLNQELKN LVKKAGPRKYDCVFWPQESLD SSKIPPNPSPGPGFK*RAGKVPFP CLTHNGKHGLAQSGIEVEVPTF/ LSFQMKKG VYVWAVVWSRE R*QTNELVYNIHLACQLSWVSL LKEKNWQ\NVPGPYIHKSTMGG SPSSHILRHIRINSITS |
| 22665 | 53033 | A | 22793 | 1 | 377 | SVSRVPTSLRTSTWRLAQDQT QDTQLITVDEKLDITTLTGVP HIKTRKVRIFVPARNMQSGVN NTKKWKMEFDTRERWENPLM GWASTWSYDIEERKVPKPKSK SYGANFSWNKRTRVSTK |
| 22666 | 53034 | A | 22794 | 183 | 368 | |
| 22667 | 53035 | A | 22795 | 3 | 623 | ILAFACSKMAAVSMSV\VLRT LWRRRAVAVAAL\SVSRVPT/R RSLRTSTWRLAH\DTQDTQLI TS**KIGISLTFNWPFP EIKNL EKS GIVPCSPITCQSGVNNTK\ KWK\MEFDT\RRER\WEN\PLMG\ WASTGLIPLS\NMVLNLPVLKE DAVS\FAEK\NGWELWTLEERK\ VPKPKSQVFMGANFS\WNKRTR VSTKIGLALTISPA |
| 22668 | 53036 | A | 22796 | 1 | 798 | MNKVNPTQQDKEDHPELIITSIG DKRQLTLEAASGVCHRGQT VKEESKKFLISMSFRGGKPVHK VVERACVCTCLHHTSVPATHN TQRRHTTPTTRKNGRKRGGK EREKRKDREHNTGRRTKRKKT RNIGGQRTQQKQKQSEDKARR EPGGGRKQGRGREDGTRQRRG GRTRNREEGAQRGRNGR/RGEG RRTTEETHMA*APDITATQQT E QQGHGTRQRDTTLRRHTAEDA QPSEHASADQAHTKKTE*SVSR TNGQYLLT |
| 22669 | 53037 | B | 22797 | 85 | 322 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22670 | 53038 | A | 22798 | 165 | 4733 | AATALLTHGQEEGQVEGQDED IPPITCVQNGLRYHNRDVKPE PCRICVCDNGKVLCDVICDET KNCPGAEVPEGECCPVC PDGSR VTHRPKKPPGVEGPKGDTGPPR PKGTPGPPGRDGIPGQPGLPGP PGPPGPPGPPGLGGKLLLPKLSY GYDEKSTGGISVPGPMGSPGPR GLPGPPGAPVSIQDVFICLLGLW SFGGKTGMRAGEMLRDLLGPQ GFQGGPPGEPGEPGASGPMGPRG PPGPPGKNGDDG |
| 22671 | 53039 | C | 22799 | 88 | 392 | |
| 22672 | 53040 | A | 22800 | 37 | 293 | |
| 22673 | 53041 | A | 22801 | 55 | 1917 | GGGGVRRRRGTRRSEPGDSRSA MAPIGLKAVVGEKIMHDVIKK VKKKGWVKLVVDQLSMRML SSCKMTDIMTEGITIVEDINKR REPLPSLEAVYLITPSEKSVHSLI SDFKDPPTAKYRAAHVFFTDSC PDALFNLVKSRAAKVIKTLTEI NIAFLPYESQVYSLDSADSFQSF YSPHKAQMKNPILERLAEQIAT LCATLKEYPA\VR YRGEYKDN ALLAQLIQDKLDAYKADDPTM GEGPDKARSQLLILDRGDFPSSP VLP* *LFQMSY*SCLPIENDV\ YKYETSGIGGGHGVKGGASGT EDDDLWIALR\HKHIAEV\SQE VTRSLKDFSSSKRMNTGEKTT MRDLSQMLKKMPQYQKELSK YSTHLHLAEDCMKHYQGTVDK LCRVEQDLAMGTDAEGEKIKD PMRAIVPILLDANVSTYDKIRIIL LYIFLKNGITEENLNKLIQHAQI PPEDSEIITNMAHLGVPIVTDST LRRRSKPERKERISEQTYQLSR WTPIIKDIMEDTIEDKLDNK\HY P\YISTRSSASFSTTAV\SARYGH WP*GTRPPGEYRSGP/RVFIIFHP LGGVSLNEMRCALRR*PRANG KWGGA**GSTHILQPHRNLP GH |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22674 | 53042 | A | 22802 | 46 | 1931 | GGGGVRMLCGTRRSEPGDSRS AMAPIGLIAVVGEKIMHDVML NDLNMGEWKALLVDQLSMRM LSYCCLMTDIMTEGITEDINK RR*PLPSLEAVYLITPSEKSVHS LISDFKDPPTAKYRAAHVFFTD SCPDALFNELVKSRAAKVIKTL TEINIAFLPYESRVYSLDSADSF QSFYSPHKAQMKNPILERLAEQ IATLCATLKEYPAVRYRGEYKD NALLAQLIQDKLDAYKADDPT MGEGPDKARSQLLILDRGFDPS SPVLHELTFQAMSYDLLPIEND VYKYETSGIGEARVKEVLLDED DDLWIALRHKHIAEVSQEVTRS LKDFSSSKRMNTGEKTTMRDL SQMLKKMPQYQKELSKYSTHL APCLRTCMKHYQGTVDKL\CR VEQDLAMG\TDAEG\EK\KDP MRAIVPILLDANVQTY*QIRIILL YIFLKNNGITEENLNKLIQHAQIP PEDSEIITNMAHLGVPIVTDSTL RRRSKPERKERISEQTYQLSRW TPIIKDIMEDTIEDKLDTKHYPYI STRSSASFSTTAVSARYGHWK NKAPGEYRSGPRLIIFILGGVSL NEMRCAYEVTQANGKWEVLIG STHILTPTKFLMDLRHPDFRESS RVSFEDQAPTME |
| 22675 | 53043 | A | 22803 | 2 | 51 | |
| 22676 | 53044 | A | 22804 | 236 | 451 | LHLPLFLGAIRSGQYGLWNLFR VLGWTCSLGIYLGWRVS*NFG RGTKALKVLSTIS/E*RNHHCHP *NNIFVY |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22677 | 53045 | A | 22805 | 3 | 1173 | GAGAPAAGQAGLTSTSAVRAR PVSPARQSQDPAASLSLHLSLPP APGAGCARWRRRGPPQAAMAA GAGAGSAPRWLRALSEPLSAA QLRRLEEHRYSAAAGVSLLEPPL QLYWTWLLQWIPLWMA PNSIT LLGLAVNVVTTLV LISYCLTAT EEAPYWTYLLCALGLFIYQPLD AIDGKQARRTNSCSPLGELFDH GCDSLSTVFMAVGASIAARLGT YPDWFFSRSFYLGCLVFYCAH WQTYVS\GMLRFGKVDVTEIQI AL\VIVFVL\SAFG\GATM/WGD YTIPILEIKLKILPVLGFLGGVIFS CS\NYSHVILHGGVGKNGSTIA GTSVLSPGTPH/MGLIIL\AIMIY *KVRQLMVF*K SIPCL*YPQCLG CVFAKVSQKISGSSHDQK |
| 22678 | 53046 | A | 22806 | 2 | 1091 | CPGRRRRRRPGRSRARATALPT PGPRKRGGPAGRKRRPERCSS SSGGSSSGDEDGLELDGAPGR GKRAAQPVAAAGKVGGA AVVV AEPEHTKKHVKLETLLITTEGK LWSWGRNEKAQLGHGDTKRV EAPRLTEGLSHEVIVCTCARNH TLALTETGVSFAFGENKMGQL GLGN*TD AVPSPVQIMYNSLPIT KMA/CGYGWLGYTEQKDEM V PRLVKLFDFPGHGASQIYAGYT CSFAVSEVGG LFFWGATNTSHE STMYPKAVQDLCSWRIWSLAC GKSSIIVAADESTISWGSPSTFG ELGYRDHKPKSSTA AQEVKTL HGIFSEPVAMGYSHSLVIARDE SETEKEKIKKLPEYSPQTL |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22679 | 53047 | A | 22807 | 1 | 1409 | MSLGLASERLWAGLGLPALPL ADEGGECGETLFVWRSQKLEG SKCKGQLLIFGATNWDLIGRKE VPKQQAAYRNLGQNLWGPHR YGCLAGVRVRTVVSGSCAAHS LLITTEGKLWSWGRNEKGQLG HGDTRKVEAPRLIEGLSHEVIVS AACGRNHTLALTETGSVFAFGE NKMQLGLGNQTDVPSPAQI MYNGQPITKMACGAEFMIMG LQRKPLFLWGALNMGQLGTQL RMGKFHSPGAQRIEYDCELVPR RVAIFIEKTKDGQILPVPNVVVR DVACGANHTLVLDSQKRVFSW GFGGYGRLGHAEQKDEMVPRL VKLDFDPGRGASQI/SCWL/HTC SLCCQ*NGWSVFLGGHQHLP*I YHVPQKQCRTSAAGESGTLAC GKSSIIVAADESTISWGPSPTFG ELGYGDHKPKSSTAQEVKTL DGIFSEQVAMGYSHSLVIARDE SETEKEKIKKLPEYNPRTL |
| 22680 | 53048 | C | 22808 | 277 | 518 | |
| 22681 | 53049 | A | 22809 | 2 | 192 | |
| 22682 | 53050 | A | 22810 | 1 | 2946 | MAEAGLRGWLLWALLRLAQ SEPYTTIHQPGYCAFYDECCKN PELSGSLMTLSNVSCLSNTPAR KITGDHLILLQKICPRLYTGPNT QACCSAKQLVSLEASLSITKAL LTRCPACSDNFVNLHCHNTCSP NQSLFINVTRVAQLGAGQLPAV VAYEAFYQHSFAEQSYDSCSRV RVPAAATLAVGTMCGVYGSAL CNAQRWLNFGQDGTGNGLAPLD ITFHLLEPGQAVGSGIQPLNEG VARCNESQGDDVATCS |
| 22683 | 53051 | A | 22811 | 258 | 362 | |
| 22684 | 53052 | A | 22812 | 1 | 4038 | MAEAGLRGWLLWALLRLAQ SEPYTTIHQPGYCAFYDECCKN PELSGSLMTLSNVSCLSNTPAR KITGDHLILLQKICPRLYTGPNT QACCSAKQLVSLEASLSITKAL LTRCPACSDNFVNLHCHNTCSP NQSLFINVTRVAQLGAGQLPAV VAYEAFYQHSFAEQSYDSCSRV RVPAAATLAVGTMCGVYGSAL CNAQRWLNFGQDGTGNGLAPLD ITFHLLEPGQAVGSGIQPLNEG VARCNESQGDDVATCS |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22685 | 53053 | A | 22813 | 198 | 380 | ASSEDSTPCR*MAYSWPPNSN SSHCIKELPLFMGKIPAAS*DGG PQGLAIFPPGVIVGI |
| 22686 | 53054 | A | 22814 | 1 | 154 | |
| 22687 | 53055 | A | 22815 | 35 | 486 | PARRGRDEC*VLAPFRATRPPS RRTR*SKATYPTPSNDQTRTIRT SRERASMPRSAEPKRPTIPRLHP SPRGIVTVSS/RPRSHALPVSHIH SCHSRTAISDNQVPAFLQVYGE EVRKRAGEVTQAITGFPRYRLF FKMLRCHRSIQVTAST |
| 22688 | 53056 | A | 22816 | 212 | 365 | RCRSGPAPRSAPGARPASPPA AGTCR*RPAGHCPAGAAGLLSL CPRCST |
| 22689 | 53057 | A | 22817 | 293 | 618 | QQNPTNCLPPASR*SKT*RARST AGPTRPHLHHPAAPAGSPACA GEGRLQR/HSPNPLYFNWKKQR FAAKPHFRPQSSLNPQQWLLA GLLQEESLGTDTAPLHSLG |
| 22690 | 53058 | A | 22818 | 3 | 1129 | FCLDDLSSAINEHLSARGRRRS IVKVSHPAVIGLKSFLKKPD QLRKLFIIGLSFETTDESLRSHF EQ\WGTLTDCVVMRDPNTKRS RG\FGFVTYATVEEVDAAMNA RPHKVD\GRV\VEPKRAVSREDS QRPGA\HLTV\KKIFVGGIKEDT EEHHLRDYFEEIILNSMGKLEV VEIH*LDR\GQWPRKRGFVFT FDGHDSVDKIVIQKYHTVNG\H NCEVRKALSKQEMASASS\SQR G\RVGSGNFWCGRT\NGFGGND NFG\RGGNFWSVVAFGG\SRG GVWIWVAVGDGYNGFG\NDGS HFG\GGGSY\NDFGDFH\NQSSK FWTP*RGGNLGGQKLWPPMGG GG\QYFAKPTKPKVAYGRFPAA ASSYGKWPEDFN |
| 22691 | 53059 | A | 22819 | 1 | 568 | MGKMSPGHVRDFHGSCHHNRP GGPGGKSGFMGQALGPG/GCV QPRDLVLCVSATPAMAERGQC GAQAVASEGGSPRPWQLPCGV EPADFRRYMETPGCPGRNL/PA GAGPL*RTSAGAVWKGNVRS SP/PQSLYWGTSAGAVRRGPPSS RNQNGRSTDSLHCMPGKDTQP NP*KQPGGRLHPAKPQGRSCP |
| 22692 | 53060 | A | 22820 | 232 | 389 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22693 | 53061 | A | 22821 | 3 | 401 | VGVCEKRGAPG\PP LAPGPARG PVAAAVPP/GPGASRAP*DAA AAAGGRGPPEQ*T*KAWGLHP GTGSL/RGHPAPM*PLLRAFPRS PLHPLPPPPLPRRAA\SNPGTS KCRTAAGTRQWGGRQSQLQRC QCLR |
| 22694 | 53062 | A | 22822 | 1 | 410 | MGKMSPGHVRDFHGRPSHHRP RGPGGKSGFVGKVQGP HAVCS LGTWCLVSQPLHP\G*KGPMYS SG\VASEGGSPKPWQLPRGVEP MGAQKS RTEVWEPLPRFQKIY GNTWMPRIPMCCARDPGGAKG GCSNPSQRR |
| 22695 | 53063 | A | 22823 | 264 | 979 | GPRHADPANFSARNLSRP*DAP GRVQDPRPQAPQL\PPGLGAPSR VRRPPRRPVDRTLPGGPRPPA AAA\GPTGGRGS\PRAGGTAAA TGPRAGPGARGAAGSAPFLTDP NM\GRPPPPATTPPGAATAPGP REEAPGKFRVSPGPSGAGGPP TRASPTPTAAGGGGGDSEGE GP ILLVADAG\PDSARSPPGLPGCV LSAAPRSRRDPDAVGGLAASA AARRLNTTWKLPQLGASTL |
| 22696 | 53064 | A | 22824 | 271 | 426 | |
| 22697 | 53065 | A | 22825 | 546 | 1296 | KMVDCLANSEANTRRISIVENC FGAAGQPLTIPGRVLIGEVLT KL\CRKKPKARQFFLRNDIVV* GNIVIQKKKYIKQHIIPLENTID SIKDEGDLRNGWVIKTPTKSFA VYAATA TEKSEWMNHINKCVT DLLSKSGKTPSNEHAAVWVPD SEATVCMRCQKAKFTPVNRRH HCRKCGFVVCGPCSEKRFLPS QSSKPVRICDFCYDLLSAGDMA TCQPARSDSYSQSLKSPLNDMS DDDDDDDMQ |
| 22698 | 53066 | A | 22826 | 1219 | 2370 | |
| 22699 | 53067 | A | 22827 | 164 | 601 | DRTNIMVGYHQTNQKTD TGKT PTRRPVLVDHNRLPEGSRGRL AVAVAGDHPAAVQVTMTLVN DTGFDPVFSGSIAESWGQHSGT PSYC*DWEAATMLRAFPLAKK GETKDLRQFPNIDNAYMELGT NRADAVLHDTPNILYFMQF |
| 22700 | 53068 | A | 22828 | 2 | 91 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22701 | 53069 | A | 22829 | 1 | 1188 | MGAEPSLLTSLGTLWSGERFQC MRAKIWERSRKGRFSTDVISP TKDSFAGPFQPISTLVQHQRİY GLKVCVLPDPCKIRILKPNPQC VGKWEEEVAENEIQVFGGERF DINKYSKSPPPPTPQPLYLTAGF ASCRNHRKSEELREGKGESPGK SKPFHLQANFTVALVTTLQGDK HSQEAFIRPVAKAKTTCTYLSN VCEMKDFKRINCPDPFHKMAP KAKKEA\PAPP\KAEAKAKGFK GPRRQVLK\GVHNHKKRKRKK ERSRTFTHLSRRPGRPLR\RRQP \KYPSGRAAPRRNKLD\HYAIIK FPLT\TESA\MKKIEDNNTL\VF\I VELLKATTKNQIKQGC*RSLYD IDVGQGSTPWISAWMGEKKGI CSD LAPDLPIAFGMFANKIWGFI |
| 22702 | 53070 | A | 22830 | 1413 | 2197 | RVEWRWYNVLPCLDVHSGPVD RRSHVMTAAEKPPFCPAWGQA VSQQSCALEPRTGEEGKGIGQ PASGLFPTGEEISVVPNRWLDA SLSPVILGVQG\GSQCLSCGVGQ EPTLTLEVRLGASSLGTQPQML SLLKPGSPQPWCCGTP*QDSVD GSFASSLRILAKALLCGPGFCPS LTLPSFCRKPVTIME\LYLGAKE S\KSFTFYRRDMG\LTSSFESAA\ YPGWFLCTEPE\ADQPVRLTQL PENGGWNAIPITDFYFQQ\CD |
| 22703 | 53071 | A | 22831 | 100 | 177 | KRDHF*SRLQQVSRSVRWSSA TDSR |
| 22704 | 53072 | A | 22832 | 610 | 1080 | |
| 22705 | 53073 | A | 22833 | 1169 | 1308 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|---|
| 22706 | 53074 | A | 22834 | 1 | 1889 | ACRRRAGTWTTPRPRGSGSRA MAGNCGARGALSAHTLLFDLP PALLGELCAVLDS CDGALGWR GLAERLSSSWLDVRHIEKYVDQ GKSGTRELLWSWAQKNKTIGD LLQVLQEMGHRRAIHLITNYGA VLSPSEKSYQEGGFPNILFKETA NVTVDNVLIPHEHNEKGVLLKSS ISFQNIIE\GTRNFHKDFLIGERG E/IFGGYQEGKIQTLYAVKLFFK QEKKMQCKKHWKRFLSELEV LLFHHPNILELAAYFTET\EKFC LIYPYMRNGTLFDR LQCVGDT APLPWHIRIGILIGISKTIHYLHN VQPCSVICGSISSANILL\DDQFH PKLTDFSMAHFRSP\LEHQSCCI NMPSS\SRKHLWY\MPEEYIRQ GKLSIKTDVYSFGIVIMEVLTGC RVVLD DPKHIQLRDLRELMEK RGLDSCLSFLDKKVP PCPRNFS AKLFCLAGRCAATRAKL RPSM DE\ V*RALESTQASLYF\AGDPP TSLKALRGPSPLF\LEKVT\SIPV \EDDEAKPNNNLLPS**KALRMK RWPQK\TPF\ECSQP\EVWFLSLE QKAREARENEEACNMPSSS\CE ESWFPKYIVPS\QDLRPL*GK*K ILSSQAISGHSCARTKPVESSCSS KFSWDEYEQYKKE |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22707 | 53075 | A | 22835 | 1 | 1560 | RWERGGKRFRAADPMSALRRS GYGPSDGPSTYGRYYGPGGGDV PVHPPPPLYPLRPEPPQPISWR VRGGGPAETTLGEGGGGGDG YYPSGGAWPEPGRAGGSHQEQ PPYPSYNSNYWNSTARSRAPYP STYPVRPE\LQGQSLNSYTNGA YGPTYPPPGANTASYSGAYY APGYTQTSYSTEV PSTYRSSGN SPTPVSRGIYPQQDCQTEAPPLR GQVPGYPPSQNPGMTLPHY PY GDGNRSVPQSGPTVRPQEDAW ASPGAYGMGGRYWPSSAPSA PPGNLYMTESTSPWPSSGSPQSP PSPPVQQPKDSSYPYSQSDQSM NRHNFP/CASVHQYESLGDQ*T MDDSRILLDSPSPSIVPEPSACM GNAHPVTHP\NNQDQSSSLPEE CVPSDESTPPSIKKIHHVLEKVQ YLEQEVEEFVGKKTDKAYWLL EEMLTKELELDSVETGGQDSV RQARKEAVCKIQAILEKLEKKR IMKGFITKWKPVNTLTKEHLIW LITLFLKCLLMTRSNTFQLFL |
| 22708 | 53076 | A | 22836 | 8 | 207 | TPVPRALRSPAGLEGSHLSSIST MMPAVMSVGKVTENGGSPPQGI KSPSKPPGPNRIG*RNQVSVHT |
| 22709 | 53077 | A | 22837 | 459 | 5520 | RQVRPAGLEGSDLSSINTMMSA VMSVGKVTENGGSPPQGIKSPSK PPGPNRIGRRNQETKEEKSSYN CPLCEKICTTQHQLTMHIRQHN TDTGGADHSCSICGKSLSSASSL DRHMLVHSGERPYKCTVCGQS FTTNGNMHRHMKIHEKDPTSA TATAPGRGDFASAKSSKRKLSH DAESEREDPAPAKKMVEDGQS GDLEKKADEVFHCPCVCFKEFV CKYGLETHMETHSDNPLRCDIC CVTFRTHRGLLRHNL |
| 22710 | 53078 | A | 22838 | 164 | 434 | |
| 22711 | 53079 | A | 22839 | 23 | 242 | |
| 22712 | 53080 | A | 22840 | 187 | 325 | |
| 22713 | 53081 | A | 22841 | 1 | 130 | NCPMCWPGQSPRPVST*GRRNP PPKRRSVSAES*RHWQSPSP |
| 22714 | 53082 | A | 22842 | 614 | 774 | QEPMRMCTMLANSSPSSSQATP PGL*SWNQPSL PARTLSRHEWT SCLGSSANL |
| 22715 | 53083 | A | 22843 | 396 | 560 | LFPHDGIKHKGKENP/PKGPPPP THPQTTPRPADAPLVATKSTLD QAWALLAVATS |
| 22716 | 53084 | B | 22844 | 124 | 205 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22717 | 53085 | A | 22845 | 1 | 2355 | MVGSRRISGVIPLPFTRRAGIFS DPRANMQPLWAPVPPATFVPTS LPPVPTARPPTSASCHCQQVPC AGLEVALPGNRTICWLSLWPS WQLDEDAQSPALESSSIRQFPT APRSGYPGTLCPSFLFGPRPRTC EYHSPVLCAPSSRASPSATT STRTLWGPAGSHPFVHNTR LSPDLCPGKIVLRALKESGAGM PEQHKDPRVQENPDDQRTVPE VTGDARSAFWPLRDNGGSPSPFV PRPGPLQTDLHAQSSEIRYNHTS QTSWTSSSTKRNAISSYSSTGG LPGLKQRRGPASSRCQLTSLYS KTVSEDRPQAVSLGHTRCEKG ADTAPGQTIAPTASRPHINTSLH VEDKAISDCRPSRPSHTLSSLAT GASGGPPVSKAPTMDAQQDRP KSQDCLGLVAPLASAAEVPAT APVSGKKHRPPGPLFSSSDPLPA NSSHSRDSAQVTSMIPAPFTAA SRDAGMRRTSAPAAAAAAPP PSTLNPTSGSLLNIEWMEAPHIS WPQPQLQHVPRGQ/NVRYNQR SQTSTRS/CPQTKCQLQLPQLY GRPPGSKAEEGPASSHCQLALS SSNTVSEDGPQAVSSGHRCENK AGTAPGQTLAPRGGSRSQASR PHINTALHVEDKAISDCRPSRPS HTLSSLATGASGGPPVSKAPTM DAQQDRPKSQDSLGLLAPLASA AEVPSTAPVSGKKHRPPGPLFSS |
| 22718 | 53086 | A | 22846 | 1 | 1200 | MPEQDKDPRVQENPDDQRRVP EVTGDARSAFRPLRDNGGLS/PP FVPGPGPLQTDLHTQR/LGYRV TVEDLDREKEAAFQIRINSALQV EDKAISDCRLSRPSHTLSSLATG TSGLPAVSKAPSMDAQQERHK SQDCLGLLAPLASAAEVPSTAP MSGKKHRPPGPLFSSSDPLPAT SHSQDSAQVTSLIPAPFPAASM DAGMRRTSPGTSAPAAAAAAPP STLNPTLGSLLIEWIEALHISGPQ PQLQQVPRGQNQRSQTSRTSSC PKRK/CHLQLQLYGRPPGTKA EEGPASSHCQLTSSSNTVSED GPQAVSSGHTHCEKTADTAPG QTLAPRGGFPRSQASRPCRHKF PLLPRRRGEPLMLPPPLELGYR VTAEDLDREKEVAFQRIKSALQ VEDKAI |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22719 | 53087 | A | 22847 | 2 | 1762 | YHSPVLCAPSSRASPSATTLS TRTLWGPGAGSHPFVHNTRL SPDLCPGKIVLRALKESGAGMP EQHKDPRVQENPDDQRTVPEV TGDARSAFWPLRDNGGPPFVP RPGPLQTDLHAQSSEIRYNHTS QTSWTSSSTKRNAISSYSSTGG LPGLKQRRGPASSRCQLTSLYS KTVSEDRPQAVSLGHTRCEKG ADTAPGQTIAPTASRPHINTSLH VEDKAISDCRPSRPSHTLSSLAT GASGGPPVSKAPTMDAQQDRP KSQDCLGLVAPLASAAEVPAT APVSGKKHRPPGPLFSSSDPLPA NSSHSRDSAQVTSMIPAPFTAA SRDAGMRRTSAPAAAAAAPP PSTLNPTSGSLLNEWMEAPHIS WPQPQLQHVPARGQ/NVRYNQR SQTSRTRS/CPQTKCQLQLPQLY GRPPGSKAEEG/PASSHCQLALS SSNTVSEDGPQAVSSGHRCEK AGTAPGQTLAPRGGSPRSQASR PHINTALHVEDKAISDCRPSRPS HTLSSLATGASGGPPVSKAPTM DAQQDRPKSQDSLGLLAPLASA AEVPSTAPVSGKKHRPPGPLFSS SDPLPATSYHSRDTAQ |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22720 | 53088 | A | 22848 | 292 | 2053 | GSVAWSPFSPSPSSLCLWDLPV APTLWGPAGSHPFVHNTRL SPDLCPGKIVLRALKESGAGMP EQDKDLRVQENPDDQRRVPEV TGDARSA/FLAPAGQWSPLSLC AQSRASADIPPCPEVRNQI*PDIP DHLDELMHQPCKHLQLQLCG RLAGAKVEEGASGAKEQGRDA *AGQGTPEQQNPDDQRTVPEV TGDARSTVKPLRDSGGLSPFVP RPGPLQTDLHAQSSEIRYNQTS QTSWTSSSTKRNAISSSYSSSTGG LLGLKQRRGPASSRCQLTSLYS KTVSEDRPQAVSSGHTRCEKA ADTAPGQTLAPRGGSPRSQGSR PRRRKIALLPHR*GELQVEDKAI LDCRPSWPSHTLSSLATGASGE PPVSKAPTMDAQQDRPKSQDC LGLVAPLASAAEIPSTAPVSGK KHRPPGPLFSSSDPLPATSSHSR DSAQVTSLIPAAFTAASMDVG MRRTRPGTSAPAAAAAAPPST LNPTSGSLLNEWMEALHISGPQ PQLQQVPRGQ/NVRYNQRSQTS RTRS/CPQTKCQLELPQLYGRPP GTKGCRHEKNVLC SKLFEGFGF IFVGFFFFAYMGILQLLII |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22721 | 53089 | A | 22849 | 146 | 1789 | RQPSTSGSSRSCPCARRSWWAR TARSGWWWELLGARRSPQTLH CPQATLITLPCPRPSSTTSGSAM T*RGPWRSFGCTTSFCPTSR/PV ERNIDQTDLHAQRSEIRYNQTS QISWTSSCTNRNAISSYSSTGG LPGLKRRRGPASSHCQLTLSSS KTVNSDKFDANDPILKDQTQE WSGSATFTSDGKIRLFYTDYSG KHYGKQSLTTAQVNVSKSDDT LKINGVEDHKTFDGDGKTYQN VQQFIDEGNYTSGDNHTLRDPH YVEDKGGHXYLVFEANTGTENG YQGEESLFNKAYYGGGTNFFR KESQKLQQSAKKRDAELANGA LGIIELNNDYTLKKVMKPLITR GSSRPSIREDENGRSQKPVHPEG DMTMNIKKIVNQATVLTFTTAL LAGGATQAFKENNQKAYKET YGVSHITRDMLQIPKQQQNEK YQVPQFDQSTIKNIESAKGLDV WDSWPLQNADGTVAEYNGYH VVFALAGSPKDADDTSIYMFY QKVGDNISIDSWKNAGRVFKDS DKFDANDPILKDQTQEWRGEA |
| 22722 | 53090 | A | 22850 | 500 | 1034 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22723 | 53091 | A | 22851 | 1 | 2396 | MDKYLLHGPPRPPPAIASRCLA RVPGCAYSSIMVALSLVPLCAH MPTPSGLEVALPGNRTICWLSL WPSWQLDEDAQSPALESSSIRQ FPTAPRSGISPLCAPHSCLGQGR GPASHPTSTQTLDISGVKTTPRR FSVILQDLCSILGDSCLQFHLHR VPQQVSAVLLRVSGASPSATT LSTRTLWGPAGCSHPFGVHNT RLSPDLCPGKIVLRALKESRAG MPEQDKDPRVQENPDDQRTVP EVTGDARSAFWPLRDNGGSPSP VPRPGPLQTDLHAQSSEIRYNH TSQTSWTSSNTKRNAISSYSST GGLPGLKQRRGPASSRCQLTSL YSKTVSEDRPQAVSSGHTRCEK GADTSPGQTIAPTGGSPRSQDS RPRRRKIPLLPRRRGEPLMLPPP LELGYRVTAEDLHLEKETAFQR INSALHVEDKAIPDCRPSQPSHT LSSLATGASGGPPVSKAHTMD AQQHRPKSQDCLGLLAPLASA AEVPSTAPVSGKKHRPPGPLFSS SDPLPATSYHSRDSAQVTSIPA PFTAASSDAGMRRTRPGTSAPA AAAAAPPSTLNPTSGSLLNEW MEAPHISWPQPQLQHVSRGQ/N VRYNQRSQTSRTRS/CPPRKCQL QLPQLYGRPPATKAEEG/PASSH CQLAHSSSNTVSEDGPQAVSSG HTRCEKKAGAS/RWASRF*STH YGCTAGQTQVPRLPGPTGPPSI |
| 22724 | 53092 | A | 22852 | 1 | 3392 | MDKYLLHDPPRPPPAIASRCLA RVPGCAYSSIMVALSLVPLCAH MPTPSGLEVALPGNRTICWLSL WPSWQLDEDAQSPALESSSIRQ FPTAPRSGYPGTLCPSFLFGPRP RTCEYHSKPVLCAPSSRASPSA TTLSTRTLWGPAGSHPFVHNT TRLSPDLCPGKIVLRALKESGA GMPEQDKDPRVQENPDDQRTV PEVTGDARSAFWPLRDNGGSPSP FVPRPGPLQTDLHAQSSEIRYN HTSQTSWTSSST |
| 22725 | 53093 | A | 22853 | 40 | 409 | WKMRRHETRYNVLVSRGVGCH RLFFLNGVFEHLGRAFVQRRKV DTEHQLLRAAVPANQEHRGLT QSQHVDGHSLLLLTLNPSFLCQI QEPSLGSGSGALSGNVRIQPQA QEAPPEPSVLTLLW |
| 22726 | 53094 | A | 22857 | 3 | 220 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22727 | 53095 | A | 22858 | 1 | 356 | MAGPVKDREAFQRLNFVYQVS LRQGPBGDGGARRPRVTAPLPQ AAHCVLAQDPENQALARFYLAH TERTIAKRLVLRDPSVKEELL CRGCSSLLVPGLTCTPAPRDRC RGQRWTGTDLP |
| 22728 | 53096 | A | 22859 | 2 | 270 | |
| 22729 | 53097 | A | 22860 | 2 | 364 | IFSALPAPRRKVGLNLAPVTEPR DQPWAMIIDVFISRYSGSRGQPR QTLTKGELKVLMEKELPG\FL QSGKDKDAVDKLLKDPGRPM GDAQGGTFSEVHPCSVAAITSA CHK\YFEKAGLK |
| 22730 | 53098 | A | 22861 | 282 | 469 | DCGSELQAPPPSLPGPLCPSIM PA/PPYASPPMMPMMGPPFRGM MPVGLAPGPMMLLQYNTCS |
| 22731 | 53099 | A | 22862 | 7 | 522 | SVWWNSNGLQSNMPKFYCDY CDTYLTHDPSVRKTHCSGRK HKENVKDYYQKWMEEQASLI DKTTAAFQQGKIPPTPFSAPPPA GAMIPPPSLPGPPRPGMMPAP HMGGPPMMPMMGPPPPGMMP VGPAPGMRPPMGGHMPMMPG PPMMRPPARPMMPVTRPGMTR PDR |
| 22732 | 53100 | A | 22863 | 3 | 455 | WFLIHDRTHTEKPYKCNECV KAFHRSTCLHAHKRTHTEKP YECNQ*GKAFNSSHSFQIHRT HTGEKPYECKECKGKAFKGPSSV RRHERTHSTKKPYECKHCGKA LSYLTSTFHNHLMHTGEISHTC KICGKAFYSPSV\IQTHE*THT |
| 22733 | 53101 | A | 22864 | 1 | 1665 | |
| 22734 | 53102 | A | 22865 | 1 | 2650 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22735 | 53103 | A | 22866 | 107 | 2384 | MFGVHGTFLGIESRPPLLSLSPS LLYTCEMFQDPVACEDVAVNF TQEEWALLDISQRKLYREVML ETFRNLTSIGKKWSDQNIEY QNPRRSFRSLIEKKVNEIKDDSH CGETFTQVPDDRNLNFQEKKASP EVKSCDSFVCAEVGIGNSSFN SIRGDTGHKAYEYQEYGP KCQPKNKKAFRYRPSIRTQER DHTGEKPYACEKCGKTFISHG IRRHMVMHSGDGPYKCKFCGK AVHCLRLYLHERHTHTGEKPYE CKQCGKSFTYSATHRIHERHT GEKPYECQCGKAFHSSSSFQA HKRTHHTGGKPYECKQCGKSFS WCHSFQIHERHTHTGEKPCECSK CNKAFRSYRSLRHKRSHTGEK PYQCKEKRKAFTYPSSLRRHER THSAKKPYE/CSFQYHERHTHTG EKPYECKQCGKAFRCAPHLRR HGRTH/S/AEKPYECKEKGKAFR SASHLQIHERHTHTIRHISGERP YKCKTCGKGFYSPKSFQRHEKT HTAEKPYECKQCGKAFSSSSSF PYHERHTHTGEKPYECKQCGKA FRSASILQMHAGTHPEEKPYEC KQCGKAFRSAPHLRIHGRHTHTG EKPYECKEKGKAFRSANLRIH ERTQTHVRMHsverpykckic GKGFYSKSFQIHEKSYTGKGP YECGLQLPRTAESVDSEKLQG PGKQETHVQLLSLYCLRRVLD |
| 22736 | 53104 | A | 22867 | 1 | 391 | MKEHIERNPVTIKNVVKPSINT VPLEDMKAHTGEKPYERQKCE LNQRLRDYAFQYHESNSGVVS ADSETKSGHSGCLIKEMKNATK THNGITGGIIFNANHWRNTIY TRIH/GEKSCDYKKCGKAFNQ YSSLRRHESHTGEKPYERQKC ELNQRLRDYAFQYHESNSGVV SADSETKSGHSGCLIKEMKNAT KTHNGITGGIIFNANHWRNTI YTRIHINKQEYQATHVSYAAN |
| 22737 | 53105 | C | 22868 | 179 | 289 | |
| 22738 | 53106 | A | 22869 | 3 | 206 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22739 | 53107 | A | 22870 | 1 | 855 | MPRAEPRATLGEQEKAGLPLG AWRLYLLRHFRKQTELRSSGSR DVTGALLVAAAVASEAVGSLR VAEGGPNTLLLQVLRISWPWC NKLKTMEEKVKRRSPKSFSA HCTQVVNVQKKMSIPVSK\STG FSNPASQVNFTSRPKVKKEVM K\EKTKPQGLEEGQRHSSQLPIQ HSFLT\DVSRCSRKMERGLLSL\ LNDFHSWKTFKHFGN\ECSE\EQ MEHVSSELQEKLARLNLELYG ELEELPEDKRKTASDSNLDRL SDLEELNSSIQKLHLA\DAQDVP |
| 22740 | 53108 | A | 22871 | 67 | 598 | SIRRHCGQRCLVRIRIWPLKLPP RLAVREGLRCGTLRDVMPPSM SGVVVGPPGPAPPGPCGDTTSGP APGTFGQASAPVSPRRGHGEY LCSSPTPVFFPGLWQPPRAGFTA PERSWSCRGPRWQLRAAWAGR LSSSPVSALLTFKVHILSTGLLFG PLGGWKILSSLPEIFANLAT |
| 22741 | 53109 | A | 22872 | 1 | 372 | |
| 22742 | 53110 | A | 22873 | 1 | 3961 | FALAPEAGFYSLGQQPSTRISGS GCVHPVRVWPFSIEPAIGTLNV GESMQLEVEFEPQSVGDHSGRL IVCYDTGEKVFSLYGAAIDMN IRLDKNSLTIEKTYISLANQRTIT IHNRSNIIAHFLWKVFATQQEE DREKYSKVTAVFSIAASSNSRF ALYESSYNSQRSPSEWACDDLI KEEKDETFEEECITDPLLREH LSVLSRTFANQRRLVQGD SKLF FNNVFTVEPLGWSERKEMAEIR DVQKKDTKV |
| 22743 | 53111 | A | 22874 | 1248 | 1716 | WYAEQSAHEATAQLSTPMAIR RAVVMPEQRNRTKKEY/SLRI PFGLPGDRMCFFTHRND/PTG NEVTPPSLAADLGQQFGGDAT DRQPWMIHQMLIHQGSEQLCF VEHGINMLRLGEILHLAATRHE AHFLAFRQFFNHQRSCFALNLA RQDRITDF |
| 22744 | 53112 | A | 22875 | 478 | 663 | |
| 22745 | 53113 | A | 22876 | 508 | 884 | RQRHPDQRPGRSLFHGHGMCP TTPLQQQVDSQHNGDNNSESA P*QRRADSIHRSSLHIKKRPPSE DVSRCFLCIDLAFRQGFTFNKK GIRVRIPFGLPGDRMCFFTHR DDRPAKMLLPFAGNKV |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22746 | 53114 | A | 22877 | 1 | 506 | AFCRFSILVGSFISETDMCLLC PFIGKAISVRLQYFKHETKQSI CLGNQKSPLVCPFFGEQGLDSS SSLDLPSSNPAPTLCPCVQPPR GPVSVSPVSVSMGSRAPLLSA *LFVSVILGRMVILKNPGVLGQ RQAGPSPGAPGLPSPSVRAPLG HKCSERSPSAT |
| 22747 | 53115 | A | 22878 | 621 | 877 | RRRRRRKQRRKQPWSSPARGA *PGPRRPSLRAAGTRRRRKRRA SWTRCSNTCPGRCRTC SRNQA SCPSLLHLLLLLFGSFFSFY |
| 22748 | 53116 | A | 22879 | 1 | 1339 | MPSYKGCGETQRHATNGTAAP PRRSSCRGDAIKLPHAEKKEGR PPASTSYPLRLGTRSARSSSHC WCTSWEDPPEATAGEEK RHPK SPAVCCGEGTVLTASTVTWRA EPARGEIWARLCPRDRPGSRAA AVIWERPCCDRLIADRTGPPNSS EPHCRAATIPLPTWPLPEGQTLT LKALAKMAAPALLLLALLLPV GAWPGLPRRPCVHCCRPAPW/L WTLCPEGKEGAGVRGRAGRS KEGAA\GCPGPAGPQSARRGSV GPPGAACRRAYAAFSVGRREG LHSSDHFQAVPFDTELVNLDGA FDLAAGRFLCTVPGVYFLSLNV HTWNYKETYLHIMLNR/QAA/V VLYAQPSERSVMQAQSLMLLL\ RRATPVWSVPEELPAVLPGQDE LGSLQLHAHHPLADGLVRHEL QPGLAGSSRTGHLVFRTDHGLR QHASHGCPVGPLHVP |
| 22749 | 53117 | A | 22880 | 532 | 783 | VGSTRGIVEGLIFILGEGGECYY PRSLFTVANFTVGKRVKTLNC PSTDKWINKMCHIHTVEYYSDI KRNEIPMRATCRQTLKA |
| 22750 | 53118 | A | 22881 | 275 | 720 | TPIHNCFKENKIPRNPTYKEHEG PLQGELQTTSQGNKRGYKQME EHSMLMG\GRINIMKMAILPKVI YRFTIPIKLPMTFFTELEKTTSKF IWNQKRARIAKSILSRKNKAG/ AHHAT*LQTLQGYSNQNSMVL VPKQRYRPMEQSPQK |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22751 | 53119 | A | 22882 | 1 | 609 | MGRNQSRKAENSKNQSSASTP KDHSASPATEQSWMGNDFDEL TELGFRKSVMTNFSQLKEDVRT HHKEAKNLEKRLDKWLTRINSI EETLNDLMELKTMARELRDTC TSFSSRFDQVEEGEIQTIREYY EHL YANKLENLEEMDKFLDTY TLPRLNQEEVESLNRPTGSEIE AIINSLPTKKIPGPDFRFTA*RRP* MT*WS*KPWHENYVTHAQASV ADSIKWKKGKYK\HHQRIL*TP LRK*TRKSRRNG*IPGHIHSPKT KPGRS*IPE*TNNRF*N*GNN**P TNQKNSRARQIHSQILPEVQRG |
| 22752 | 53120 | A | 22883 | 191 | 564 | PNARKLRTLKGDHSPD**RRKL RKIK*MQ*KMIKGISQSRSHRNT NYHQRTL*TPLHK*TGKSRRNG *IPGHIHPPKSKPGRSQIPEYTN KI*N*GSN**PINQKKSRTGRIHS QILPEVQGA |
| 22753 | 53121 | A | 22884 | 337 | 589 | TRRSRRNG*IPGHIHPPKTKPGR SRIPE*TNNRL*N*GSS**PTNQK KPRTRETD SRILPEVQRGAGTIP SETIPNNRKRGTTP |
| 22754 | 53122 | A | 22885 | 162 | 539 | TRKSRRNG*IPGHIHPSKTKPGR S*IPEETNNKF*N*GSN**PTNQK KPRTRQVHSRILPEPISHGMGKS WKQSL*KPAQDKAVPSLIAPIQ HIIGSSGQGNQARERNKGYSNR KRGSIQVSVCR |
| 22755 | 53123 | A | 22886 | 329 | 459 | NDDTFRKPHRLSPKSP*AADKQ LQQSLRIQNQCAKLRSIPIHH |
| 22756 | 53124 | A | 22887 | 58 | 440 | GLSRQFSPHSVNKAAGEVPTGR GPPQLSKANVARLPLSIPPLWA GHLWKKGGSPSQGIIDKTLISLG QST*GKGQLWVQLQRT*AFLPA GSEESSGSPSTA\PNSAKGQTPS SSGSLTRASSSSLYLW |
| 22757 | 53125 | A | 22888 | 219 | 332 | NEGKNLKGSRERNTNYHQRT Q*TPLHK*TRKSRRNG |
| 22758 | 53126 | A | 22889 | 1295 | 1435 | QNQRQKPHDYLNRCRK/W/HFD KIQQPSMLKTLNKLGN DGTYL RIIRDI |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22759 | 53127 | A | 22890 | 2 | 648 | YRFSGPTIRSIQNHTTHNQGRK WHKKGIKKPRAQRYESLKGPE V*PSGQGVTCLLRADWLSPLL SGTY\VGPKFLRNTRFAKKHNK KGLKKMQANN\AKAMSARAE AIKALVKPKEVKPKIPKGC/RR KLRFDFA\IAHPKLWGRRCFVA RFCQGASGCSGPKGKAKVPKA KVKVS/PKAKAKAKAKDQTKA QAAAPALV\PAQAPKRTQAPTK ASE |
| 22760 | 53128 | A | 22891 | 3 | 370 | QMYCVFNRNEDACRY/GS/AIG VLAFLASAFFLVVDAYFPQISN ATDRKYL\VIGDLLFSG\VLASLA YQRYKAGVDDFIQNYVDPTPD PNTAYASYPGASVDNYQQPPFT QNAETTEGYQPPPVY |
| 22761 | 53129 | A | 22892 | 1 | 297 | |
| 22762 | 53130 | A | 22893 | 3 | 713 | GGGSGDGDMEGAYGAAGA GGSFNLRRFLTQPQV\VARAVV L\VFALIVFSCIYGEYSNAHES KQMYCVFNRNEDACRYGSA\IG VLAFLA\SA\FFLVVDAYFPQISN ATDRKYL\VIGDLLF\SALWTF WFR/VGFCFLTQWAVTK\PKT VLVGADSVRAAITFSFISFSWG VLASLG\YQRYKAGVDDFIQNY VDPTPDNTAYASYPGASVDN YQQPPF\TQNAETTEGYQPPPV |
| 22763 | 53131 | A | 22894 | 3 | 219 | |
| 22764 | 53132 | A | 22895 | 1445 | 1777 | PVHLGSTCHQCRQKTIDTKTNC RNPRLGA/CRGQFCGPCLQNR YGEEVRDALLDPNWHCP\HCR GICNCSFCRQRDGRCATGVLVY LAKYHGFGNVHAYLKSLEKQEF EMQA |
| 22765 | 53133 | A | 22896 | 3 | 337 | |
| 22766 | 53134 | A | 22897 | 425 | 1209 | TMSSTQFNKGPSYQLFAEIKNQ LLFKCDPQKQAALCSWIEGLTR LSFSPDFQKSLKEGIVLCTLMN KLGSVPKI/NRLMQNWHQLENL SNFIKAMVGYDMNPMDLFEAN DLFESRNMTQNRIL/P/PLDHSTI SLQMGANKRSSQ/VGMTAPGTP QHIYNTKLGAHKCDNSSMSLH MGDTQSANHSVQGGFGLGQQIY YPKYCPQ/GPAASGAPLDAGNC PGPGEAPEDPPCSQEEATTEAPE HAGSLHHRPVVWVGIFLYFRL SFFFL |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22767 | 53135 | A | 22898 | 156 | 559 | QHIRETPGAQVHSCGK WNPQA LWRTAWQLLT/DTKHTLGKPPS /MPHLVIYPLEISC\HTKTCTRML IASFFIITKTWKRPRCPSVDKWK NKPWCIIHTGLLSSTVPPGEPGC PIPELSGLLMGLQTTSSRCSVRQ VW |
| 22768 | 53136 | A | 22899 | 161 | 359 | |
| 22769 | 53137 | A | 22900 | 151 | 383 | |
| 22770 | 53138 | A | 22901 | 238 | 546 | PQEHIMEHLEGVINKPRGRRCR PQELQLHYLQKCMDYDGNLL DGFRTLPPQSTHVHKEEGSEQ APLMSEDELINIIDGVLRDDDK NNDGYIDYAEFAKSLQ |
| 22771 | 53139 | A | 22902 | 1 | 819 | MAAEDKLLLPQLPELFETSKQL LDDVEVVTEPAGSRIVQKKVFK GLDLLEKAAEMLSQL/DLVAEL ELPKTKNSAE\NHTANFSMAYP SLIAMASQRQAKRERHKQKEL EHRLSAIKSAVETGQADDERVR EYYLLHLQSLEEIESIDQEIKILR ERDSSREASTSNSSRQERPPVKP FILTRNMAQVKVFGAGYPSLAT MTVSDWYKQHWKYGALPDQG IAKATPEEFRKAAQQQEGQEEK EEEDDEQTLYRVREWDWKG HPRDYGSQQSMG |
| 22772 | 53140 | B | 22903 | 238 | 410 | |
| 22773 | 53141 | A | 22904 | 1 | 638 | VAEELPKTKNSAE\NHTANFS MAYPSLIAMASQRQAKRERHK QKELEHRLSAIKSAVETGQADD ERVREYLLHLQSLEEIESIDQE IKILRERDSSREASTSNSSRQERP PVKPFILTRNMAQVKVFGAGYP SLATMTVSDWYKQHWKYGAL PDQGIKATPEEFRKAAQQQEG QEEKEEEDDEQTLYRVREWD WKGHPRDYGSQQSMG |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22774 | 53142 | A | 22905 | 3 | 1083 | RGNSRLRYSHDELQLPRLPEL F\ETGRQLLDEVEVA\TDPAGFR IVQEK\VFKG\LDLLE\RAAEML SQSTLFGRECRFWKDLSPTHLI TFWGP\AFQGA\PLKQVNPSKR LRILQR\AREHF\INYL\TQCHC YHVGQSFEL\PKT\MNNSAENH TANSSMAYPMLGAM\ASQRQA KIQRKQKKELEHRLSAMKSA VESGQADDERVREYLLHLQR W\VDISLEEIESIDQEIKILRERDS SREASTSNSSRQERPPAKPFILT RNMAQAKVFGAGYPSLP/TLW TVSDWYEQHRKYGSITGFRGIA KSAPEGISGKAAQQQEEQEEKE EEDDEPNNFHRAREWDDWKD TPSLGAYGNRQNMG |
| 22775 | 53143 | A | 22906 | 30 | 457 | |
| 22776 | 53144 | A | 22907 | 401 | 1509 | MWKMNCSSLQSKQMCNQLPP GSTRDGSWKFRQDPRLGKNA/C DCDSCIASEFGVRGYPTIKLLKG DLAYNYRGPRTKDDIIEFAHRV SGALIRPLPSQQMFEHMQKRHR VFFVYVGGESPLKYVTLKEMP AVLVFKDETYFVYDEYEDGDL SSWINRERFQNYLAMDGFLLYE LGDTDLNASSLRERKLILPEDIP LYVGKLVALAVIDEKNTSVEHT SELTVPVVVLTNSNQYFLLD RQIKNVEDMVQFINNILDGTVE AQGGDSILQRLKRIVFDAKSTIV SIFKSSPLMGCFLFGLPLGVISIM CYGIYTADTDGGYIEERYEVSK SENNQEIEESKEQQEPSSGGS VVPTVQEPKDVLEKKKD |
| 22777 | 53145 | A | 22908 | 53 | 543 | LPISSLRTQTLFSSPLFPQHFEHY LALVSVLPFQLGRGRTAPAKKG GEK/RKGHSAINEVVIQEYTINI HKRIHGVRFKKRAPRALREIPK FAIKEVETLSVRIDSRFNKALCA KGIRNVPIRIRVQLSRKRNEDE DSPNKRYTLVTYVPVSTFKNVQ TVHVHEN |
| 22778 | 53146 | A | 22909 | 106 | 491 | IGKGTNELMYGEK/RKGHSAIN EVVIQEYTINIIHKRIHGVRFKKR APRALREIPKFAIKEVETLSVRI DSRFNKAALCAKGIRNVPIRIRV QLSRKRNEDEDSPNKRYTLVTY VPVSTFKNVQTVHVHEN |
| 22779 | 53147 | A | 22910 | 1 | 321 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22780 | 53148 | A | 22911 | 313 | 402 | R*GGEKKKGRSAINEVVTREY TINIHKRIHGVGFKKRAPRALKEI RKFAMKEMGTPDVRIDTRLNK AVWAKGIRNVYPYRVRVLSRKR NEDEDSPNKLYTLVTYVPVTTF KNLQTVNVN |
| 22781 | 53149 | A | 22912 | 1 | 3801 | |
| 22782 | 53150 | A | 22913 | 2 | 535 | GGGMADTVLFEFLHTEMVAEL WAHDPDPGPGVSAGLRGEEAG ATKGQKMSLSVLEGMGFRVGQ ALGERLPRETLAFREELDVLF LCKDLWVAVFQKQMDSLRTN HQGTYYVLQDNSFPLLLPMGSG LQV/YLEEAPKFLAFTCGLLSA LYTLGIESVVTASVAALPVCKF QVVIPKS |
| 22783 | 53151 | A | 22914 | 1 | 201 | GDLPWEINPLSSCSLLHEKDPPT TSGPQT/DQPKKHHTNFKSGPT GNRTVQLTWQPLPEPLELWPK AL |
| 22784 | 53152 | B | 22915 | 226 | 522 | |
| 22785 | 53153 | C | 22916 | 1 | 705 | |
| 22786 | 53154 | C | 22917 | 1 | 462 | |
| 22787 | 53155 | C | 22918 | 1 | 505 | |
| 22788 | 53156 | B | 22919 | 1 | 1059 | |
| 22789 | 53157 | C | 22920 | 1 | 411 | |
| 22790 | 53158 | A | 22921 | 1 | 212 | LTSFLHCCLSHHYHGAQIHPRH FLHLICRCHCHQYCHHAYLDPC PQDSHHLHWCWQPLPEPLELRP RLSD |
| 22791 | 53159 | B | 22922 | 1 | 864 | |
| 22792 | 53160 | B | 22923 | 1 | 635 | |
| 22793 | 53161 | B | 22924 | 1 | 874 | |
| 22794 | 53162 | A | 22925 | 1 | 566 | MPSVRTGDPIILHAHTLNPAVW LA WAVEGEGSLTLNIWICPWQI EPLRHLAYTPGSDATSLTVPTR VISPLCVDSWLFTDPLMKTHAP ERTFLSFPAAAKRQAHLCLVAS NCDKPMYVKLVKAHCAEHQIN LIKGDDNKKLGEWEGPCTIDRE GKPCVVGCSCAVVKDY/GKE SQAQDVIEQYFKCKK |
| 22795 | 53163 | A | 22926 | 59 | 602 | PTAMVEEGIAAGGVMDVNTAV QEVLTALIHDLARGIREAAK ALDKYVYQSQYCGFLQPEQNC HPREEGMEFMVLAQKF*MASV LPET*EK/RQAHLCLVLANCDEP MYVKLVEALCAEHQINLIKVD DNKKLGEWVGLACKIDREGKPR KVVGCSVVVKDYGKESQAK DVIEEYFKCKK |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22796 | 53164 | C | 22927 | 135 | 293 | |
| 22797 | 53165 | B | 22928 | 20 | 325 | |
| 22798 | 53166 | A | 22929 | 677 | 1031 | TPTMCLRSHPLPLALVSVILSFP QPSFSSSLINSSWSSPRSSLSSSSS RSPSSGRVNLHPPQTPSSH*SHL SSRSCCSAPLLTYHSSSLLLVCS VPFPFFPGFPGENPLFVLSGSAP |
| 22799 | 53167 | A | 22930 | 1 | 1011 | MCLRVIFTIGAVSVILSFLSLFFII LDQLQLVIPQSSLSSSSNLEDPY SESYAAARRPDSASTEPPAG KSSAEYRAHFLAVSTEAEIRIRA DLVLRARPLGPAHPTLWPTPP AGPFCRMVAHNQVAADNAVS TAAEPRRRPEP/SPSSSSSPAAT ARPRPCPAVPAPAGDTHFRTF RSHADYRRITRASALLDA\LG YWGPLSVHGAHEPLRAEPVGT FPVRDS\RQRNCFALSVKMAS GPTSIRVHFQAGRFHLDG\SRES FDCLFELLEHYRGGSRADLLGA TLRQRRVRPLQELCRQRI RPP VG\REN\LARIPLNPVLRDY\LSS FPFQI |
| 22800 | 53168 | B | 22931 | 180 | 1466 | |
| 22801 | 53169 | A | 22932 | 1 | 207 | |
| 22802 | 53170 | A | 22933 | 408 | 3758 | CLQQGPGGNQHCSHREEAPAV AACQEPPGHSEPVLP LGAPP SEEDGRQQVGSSRLRHIMAEMI ATEREYIRCLGYVIDNYFPEME RMDLPQGLRGKHHVIFGNLEK LHDFHQHFLRELERCQHCPLA VGRSFLRHLIGQKQFPESP GER PGLTSSHAPCPWMPHYLPEGPA CPVLRIPCEAFNWKHVECTDPV VSPPKQSPLLFQEEQFGMYVIY SKNKPQSDALLSSHGNAFFKVI PLGPPPTACPALS |
| 22803 | 53171 | A | 22934 | 3 | 355 | EAAELDAMCTATRQWSRAGQ GVTGRPCQGR LPRCGLRSTITP KPIPGGHRKKPLLGA\GKHTLS YVERWHWEGHSGI*TRDRQNF ERRLTVPPSRQPFAPTDETRCG DDRISFCNYV |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22804 | 53172 | A | 22935 | 1928 | 5312 | CLQQGPGGNQHCSHREEAPAV AACQEPGHSPEVSLPLGAPP SEEDGRQQVGSSRLRHIMAEMI ATEREYIRCLGYVIDNYFP RMDLPQGLRGKHHVIFGNLEK LHDFHQHFLRELERCQHCPLA VGRSFLRHLIGQKQPESPSGER PGLTSSHAPCPWMPHYLPEGPA CPVLRIPCEAFNWKHVECTDPV VSPPKQSPLLFQEEQFGMYVIY SKNKPQSDALLSSHGNAFFKDK QRELGDKMDLASY |
| 22805 | 53173 | A | 22936 | 3 | 306 | |
| 22806 | 53174 | A | 22937 | 3 | 460 | LQRQRQHPAAAPAVPVRCFTFC FTDIVIMPKRKSPENTEGKDGS KVTKEPTRRSARLSAKPAPPK PEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENG ETKAEIHIHRSSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN |
| 22807 | 53175 | A | 22938 | 3 | 285 | SSCPAREQLQRQRQHPAAAPAV PVRCFTFCFTDIVIMPKRKSPEN TEGKDGSKVTKEPTRRSARLS /AVFV*FKLSLQKPAPPKPEPKP RK TSA |
| 22808 | 53176 | A | 22939 | 1 | 413 | |
| 22809 | 53177 | A | 22940 | 2 | 454 | AEVQVEEAGLRRALRVSSCSGR GSIQRRFYAVPVRCFTFCFTDIV IMPKRKSPENTEGIDGS\KVTKE PTRRSARLSAKPAPPNPEPQPR KTSAKKEPGAKISRGA KGKKE EKQEAGK\EGTAPAENDET KAE EAQKTESVDNEGRMNCP |
| 22810 | 53178 | B | 22941 | 55 | 186 | |
| 22811 | 53179 | A | 22942 | 2 | 397 | |
| 22812 | 53180 | B | 22943 | 339 | 470 | |
| 22813 | 53181 | A | 22944 | 1 | 139 | |
| 22814 | 53182 | A | 22945 | 1 | 416 | MPLLYHL SRCAYVQQCNFANP VVSALCTCLVKPVVEKCTPYA VLLEALALRNVRQLEDLVIEAV YADVLRGSMQQRNQRLEVDYS IGRDIQRQDL SAIARTLQEWG/C HQHLLSLRSAASQRQQCGYHK LHDKQRLLRG |
| 22815 | 53183 | A | 22946 | 315 | 570 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22816 | 53184 | A | 22947 | 933 | 1841 | RPAEPDPGSGHPEPKSPTLSAV MSAEVKVTGRNQEQLLLAKS A\KGAVLATLIHQVLE\APGVY VFGELLDMPNVRELAESDFAST FRLLTVFAYGTYADYLA EARN LPPLTEA\QKNKLSDTFSVV\TL AAKVKCIPYAVLLEALAL\RNV RQLEDLVIEAVYADVLRGSLDQ RNKRL\EV\DYSIGRDIQRQDLS AIARTLQEWCVGCEVVLSGIEE QVSRANQHKEQQL\GLKHQIES EVANLKKTIKVTTAAA\AAATS QDPEQHLTELREPAPGVTNRQ PSKKASKGKGLRGS AKIW\SKS |
| 22817 | 53185 | A | 22948 | 1 | 1319 | |
| 22818 | 53186 | A | 22949 | 365 | 1331 | RAGGGAPWRFTGT FATVAPET AADLSLHRHLLSRTTSAWGTA CITVPIEPPTWPTWAVPIQWGG SATCIQEDKLRQGILYGYSQQV NQAMDSGLRP\VVDSVN AIRVP QDYVTQSVPLREMNGSLGVLA QQLQNAKLQADAAHSALKQSD DLKPVFDQAFTKVVTTPADAL QPLIPAAQTFTQQLVMVGDYIA QQGTQECGKTF SRASYLVQHS RIHIGKKPYECKECGKA FSSGS YLVQHQRHTGEKPYECNKCG KAFTVYGQLIGHQS VHTGEKPF ECKECGKA FRLNSFLTEHQ RVH TGEKPFKCKCKGKTFRYSSAP |
| 22819 | 53187 | A | 22950 | 2 | 206 | GGGQGATSFGRPESGFIRHQPPP PCRRSSTPTRSKLYTL\SAPE*RS VPTSAPGPQDRPPGSVSKSW |
| 22820 | 53188 | A | 22951 | 571 | 1102 | MGSVSLGNPQGPQFTRLPLAN VIHPTFFWETGPRGADSLGAKG RKWQPTFTSRCNLKVYLGRAG SQAATGGPSPSLPNLHVKKLRP RKAEAWPGRRTGKVS GR/LA ALRAPYGESFARAAGPRDAPS/ QQPRPQPEHAPT LISLGSNFGG MVEESWCRMNPDSGRPK EVAP WPPSTK |
| 22821 | 53189 | A | 22952 | 1 | 591 | MGPHWKDFKEIDVKKYIDALSI HTYTHTHTHADITDGDHGG GALLELEINSHLKVQFRELNITA AKETEDGGGGKAIIFVFPQLK SFQKIQVWLRRILPKPTRKSCT\ QNMHWPPRSRTLKAMRDSIPE DLVFPSEIMCMRIHVKLDGSRL IKAHLDKAQYHVERNAETFS GVYMKLTGKDINVEFPEFQL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22822 | 53190 | A | 22953 | 2 | 508 | APPFELPRAAGIRHEGKFSQEK AMFSSSAKIVKPNGEKPDEFES GISQALLELEMNSDLKAQLREL NITAAKEIEVGGGRKAIIFVVPV QLKSFQKIQVRLVRELEKKFSG KHVVVIAHRRILPKPTRKSRTK NKQK\RP RSRTLTA VHDAIPEDL VFPSEIVGKRNR |
| 22823 | 53191 | A | 22954 | 145 | 395 | |
| 22824 | 53192 | A | 22955 | 536 | 717 | |
| 22825 | 53193 | A | 22956 | 1 | 729 | |
| 22826 | 53194 | A | 22957 | 1 | 1158 | |
| 22827 | 53195 | A | 22958 | 1 | 2869 | MAHLRSCCSSLYQPGHLLPPHN PIQDHPLTAPSLTHLTRRAYFTD EKTGGQSAYAVSLLRECVKL RPSDPTVPLMAAKVCIGSLRW MAAKHLAGVLLHSLSEECYWS PLSHPLPEFMGKEESSFATQAL RKPHLYEGDNLYCPKDNIIEAL LLLLISESMLANKLLLLLEMERV QSPGVESGVDRQLSPYSDTNVN AQNAQIVPVAAKSAQNEVPGY PEETEKSRVQSNLLTQFQDLRL LLAAPECLPPRMSPPS |
| 22828 | 53196 | B | 22959 | 28 | 139 | |
| 22829 | 53197 | A | 22960 | 60 | 812 | LASFPVPLHRC SAGSQPPGPVP EGLIRIYSMRFCPYSHRTRLVLK AKDIRHEVVNINLRNKPEWYY TKHPFG\HIPVLKTSKCQLIYES VIACEYLDDAYP\GRKLFYDP YERVRQKM LLELFGKVPHLPK EFPGSVEDVGENAPNLKAALR\ QEF SNLEEILEYQNTTFFG GTCI SMIDYLPL/WPWFERL\ECMGY WNCVSHTPALRLWISAMKWD PTVCALLMDKEHF\QGFLNPYF QNNPNAFDGLC |
| 22830 | 53198 | A | 22961 | 2 | 251 | ILLDFKPWDDETDMAQLEACV CSIQLEELV*GASKLVPMGYGI RKLQIQCVVEDDKVGTDLLEEI TKFEEHVQSV DIAAFNKI |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22831 | 53199 | A | 22962 | 353 | 1071 | APLWPRAERKFYKQMNGPVAS ASRQSSAPG/NDHSELVLQIASL EVENQSLRGVVQELQQAVSNL EAWLN\IRREKSSPGH/RSTVP QTQHVSPMRQVERPSRPPYYD PGQEAEDNEDDDIDLNDKEED KEARRLREERLRLYAKKAKNP SLVAKSSILLDIKPWDNKTDMT QLEACVRSIQLDGLVSGASKLA SVGYGIRKMQIQCVVEDDKVG TDLLEEEITKFEHVQSVDIAAL |
| 22832 | 53200 | A | 22963 | 3 | 482 | PWANEAPAKK/PATPAEG/DAR DDIDLFGSDNEEVEDKQAGHS CGEER\LR\HYAGEEGPRKPAL/ VWPKSLPSLLDVK\PWDDDDGP WPSLEACVR\SIQLDGLVWGGF PSLVPVG\YGIRK\LQ\IQCV\ED DKVGTDFPWRREIT\KFEEARA RSVDIASFSTRS |
| 22833 | 53201 | A | 22964 | 1 | 2835 | |
| 22834 | 53202 | B | 22965 | 571 | 1337 | |
| 22835 | 53203 | A | 22966 | 1 | 489 | |
| 22836 | 53204 | A | 22967 | 1 | 618 | |
| 22837 | 53205 | A | 22968 | 3 | 5227 | SWSRVRPRTPEGLRQLKMRT GWATPRRPAGLLMLLFWFFDL AEPsGRAVNDPLTIFHGNTGKC IKPGYGWIVADHCDEDEDKLW KWVPQHRLFHLHSQKCLGLDIT KSVNELRMFSCDSSAMLWWKC EHHSLYGAARYRLALKDGHGT AISNASDVWKKGGSEESLCDQP YHEIYTRDGNSYGRPCEFPFLID GTWHHDCILDEDHNGPWCATT LNYEYDRKWGICLKPEGCED NWEKNEQFGRCYQFNTQT |
| 22838 | 53206 | A | 22969 | 3 | 453 | GQSPILVIYHETKRPSGISERFSG STSGNTATLTITGTQAMDEADY YCQAGRDFGGGTKLTVLGQPK AAPSVTLFPPSSEELQANKATL VCLISDFYPGAVTVAWKAHSN PVKAGVETTTPSKQSNKYAA SSYLSLTPEQ*KSHRSYSC |
| 22839 | 53207 | A | 22970 | 2 | 354 | |
| 22840 | 53208 | A | 22971 | 1 | 315 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22841 | 53209 | A | 22972 | 1 | 712 | MAWTLFLTLTQGTGSWAQS ALTQPASVSGSPGQSITISCIGTS SDIGAYYFVSWYQQYPGKAPK LLIFDVSGRPSGSISSRFSGSKSGN TASLTISGLQAEDEADYYCASY ARSSTVVFGGGTSTVTLGQPKA APSVTLAFPPSSEELQANKATLV CLISDFYPGAVKVAWKADGSP VNAGVETTTPSKQSNNKYAAS S\YYLSLTPEQWKSHRSYSCQV THEGSTVEKTVAPTECS |
| 22842 | 53210 | A | 22973 | 1 | 1779 | |
| 22843 | 53211 | A | 22975 | 1 | 2001 | |
| 22844 | 53212 | A | 22976 | 292 | 1497 | TGQLNGFHEAFIEEGTFLFTSES VGEGHP\DK\ICDQIS\DAVLDA HLQQDPDAKVA\CETVAKTGMI LL\AGEITSRAA\VDLPRKVVR SCLNTLEYDDSSKGF*LQRLVN VLVALEQQSPDIAQGVHLDRNE EDIGAGDQGLMFGYATDETEE CMPLTIVLAHKLNAKLAELRRN GTLPLWRPDSKTQVTQYMQD RGAVLPPIRVHTIVISVQHDEEVC LDEMARDALKEKVIKAVVPAKY LDEDTIYHLQPSG/RTFVIGGPQ GDAGLT\GRKII\VDTYGGWGA HGG\GAFSGKDYTEKVDRAAY AARWVAKSLVKGGCLCRRVLV QVSYAIGVSHPLSISIFHYGTSQ KSERELL*IVKKNFDLRPGVIVR DLDLKKPIYQRTAAYGHFGRDS FPWEVPKKLIY |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22845 | 53213 | A | 22977 | 67 | 1579 | FFVRSLSHTDTNMNGQLNGFH EALIEEGTFLFTSKADGEGHPD KICDQISEAVLDAHLHQDPDAK VACETVAKTGMILLAGEITSRA AVDYQKVVREAVKHIGYDDSS KGFDYKTCNVLVALEQQSPDI AQGVHLDRNEEDIGAGDQGLM FGYATDETEECMPLTIVLAHKL NAKLAELRRNGTLPWLRPDSK TQVTVQYMQDRGAVLPVRVHTI VISVQHDEEVCLDEMRDALKE KVIKAVVPAKYLDEDTIYHLQP SG\RFVIGGPQGDAGLTGRIIIVD PYDGWGAHEEGAFSGKDYTKV \SRSAAYGARWVARSLVKGGL CRRVLVQVPGPPKKPDEDLYLE CEPDVLAALTQTLSFQVLMPSG PLPRTSVVPREQQMLPLKDSDL LTQPWYSGNCDRYAVESALLH LQKDGA YTVRPSSGPHGSQPFT LAVLLRGRVFNIPRRLDGGRH YALGREGRNREELFSSVAAMV QHFMWHPLPLVDRHSGSRELT |
| 22846 | 53214 | A | 22978 | 3 | 325 | |
| 22847 | 53215 | A | 22979 | 15 | 1014 | |
| 22848 | 53216 | A | 22980 | 7 | 592 | LLCSGRHSLQGVMGILSFLPVL ATESDWADCKSPQPWGHMMLL WTAVLSLAPVAGTPAAPPKAV LKLEPQWINVLQEDSVTLTCRG THSPESDSIQWFHNGNLIPHTHTQ PSYRFKANNNDSGEYTCQTGQ TSLSDPVHLTVLSGQWRKAPG WTWEGQDG*NLLSGRGLQERG VACLLGSI AVSCLSTYQWLFLP |
| 22849 | 53217 | A | 22981 | 32 | 1150 | EKA VTA VLWAPARLQGV MGIL SFLPV LATESDWADCKSPQPW GHMMLLWTAVLFLAPVAGTPA APPKAVLKL\EPQW\INGGSRED SVTL\TC\RGTHSPESDSIQWFH NG\NL\IPHTHTQPSLQVSRANN\N DSGE\YTCQTGQTSLSDPVHL\T VLSEWLVLQTPHLEFQEGET\IV LRCHS\WRDKP\LVKVTF\HNG KSKKF SRSDPNFSIPQANHSHSG DYH\CTG\NIG\YTLLFIPRLLTIT VQAPSSSPMGIIIVAVVTGTAVA AIVAAVVALIYCRKKRISANPT NPDEADKVGAE\NTITYFTSQW HPGWLWEEPDDQNRILVSIVLA LGIWRRNSEREDLVFPGLKFPL GEDTGRCCQFPKEKVFLPGVIL |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22850 | 53218 | A | 22982 | 1 | 471 | MKSSFQGHNKEKREKKGPSLFS AAYGGGSCLLLSIMAALRPLVK PKIVKKRTKEFIWHQSDQHVKI KCNWRKPRG\QILMPNTGHGSN /KKTkHMLPSGFRKFLVPSVKE LEVLMCNKSPCAEIAHSVSSK\N KTIVERAAQ/LAVRVTPNPARNL RSEENE |
| 22851 | 53219 | A | 22983 | 103 | 564 | GIFRGIMAALRPLVKPKIVKKR TKKFIRHQSDRYVKIKRNWRKP RGIDNRVRRRFKGGQ\ILMPNIGY G\SNKKTk\HMLPKWLSGKFLG SHQRSREL/EKLLA*CCNKFFTC CPRFVSHCFSFQGTGKGLRGER SLPNWAFRVTPNPARNLRSEENE |
| 22852 | 53220 | A | 22984 | 3 | 177 | |
| 22853 | 53221 | A | 22985 | 74 | 735 | RFAGAGAIPEARARPPDVQAAE EEKEMDLPDSASRVF/CGDASS NMGEHRMNVNAIILAQKNML D\RFECTNEMLLNFNNLSSARL ASRLSERFLHHTRTLVEMKRDL \DSIFRRIRTLKGKRLARQHPEAF SHIPEASFLEEED\EDPIPTQAPT TTIATSE\QSTG\SC\DTSPDTV\S PSLEPLASEDLSHVQALASPAI\ NGPQPDQIDEEMTGRIALPARC |
| 22854 | 53222 | A | 22986 | 3 | 275 | MRTVAEKVDAVRIVHIHSVINL RRSDKRKDRVEISPEQLSAAST EAERLAELTGRPMRVVGWYHS HPHITVWPSHVKGKYHGVAMFI VFRN |
| 22855 | 53223 | A | 22987 | 1 | 886 | AKMAVQVVQAVQAVHLESDA FLVCLNHALSTEKEEVMGLCIG ELNDDTRSDSKFAYTGTEMRT VAEKVDAVRIVHIHSVINLRRSD KRKDRVEISPEQLSAASTEAE LAELTGRPMRVVGWYHSHPHI TVWPSHVDVRTQAMYQMMDQ GFVGLIFSCFIEDKNTKTGRVLY TCFQSIQAQKSSEYERIEIPHIHIV PHVTIGKVCLESAVELPKILCP/ QEEQDAYRRIHSLTHLDSVTKI HNGSVFTKNLCSQMSAVSGPLL QWLEDRLQEQHLQEL\HQE KEELMQELSSLE |

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|------------|--------------------------------|---------|-------------------------------|---|---|---|
| 22856 | 53224 | A | 22988 | 10 | 988 | LKAMSWAKMAVQVVQAVQA VHLESDAFLVCLNHALSTEKEE VMGLCIGELNDDTSRSDSKFAY TGTEMRTVAEKVDAVRIVHIHS VILARRSDKRKDQVEISPGQLSA ASTEAEKLAELTGHPMRVVGW YHSHPHITVWPSHVDVRTQAM YQMMDQGFVGLIFSCFIEDKNT RAGRVLTYTCFQSIQAQKSSESL HGPQDFWSSSQHISIEGQKEEER YERIEPIHIVPHVTIGKACLESA VELPKILCQEEQDAYWRIHSLT HLDSVTKIHNGSVFTKNLCSQM SAVSGPLLQWLEDRLEQNQQH LQELQQEKEELMQELSSLE |
| 22857 | 53225 | A | 22989 | 1 | 1362 | |
| 22858 | 53226 | A | 22990 | 284 | 542 | KLFQKKNKKSSCISDNFFFLAI MVNLLQIVRDHW\VH\VLVPM GFVIGCYLDRKSDERLTAFRNK SMLFKSFPHRELQPSEEVTKW |
| 22859 | 53227 | A | 22991 | 272 | 1241 | FPGGAACDICWVKEENGSLMS MKMGWKAKSCLPVTVHPRCL TPYSARLSSTFPL*NSITTGP*QS PACKRPF*LTTC*GGSRRNSNR KAA*GPCSPPPSPPPSPATLPR GPAGLQPPGVPVLPPLRPRKHY APGGLP\PPASLLEDDDDTFCTS QAMQPTAPTKLSPPALLPEKDS FSSALDEIEELCPTSTSTEATA ATDSVKGTSSEAGTQKLDGPQE SRADDSKLMDSLPGNFEITTST GFLTDLTLDDILFADIDTSMYDF DPCTSSSGTASKMAPVSADDLL KTLAPYSSQPVTSPSQPFKMDLT ELDHIMEVLVGS |
| 22860 | 53228 | A | 22992 | 1 | 3234 | MELKCVCLKNRSPSAEEQPSLL PEPSAQESHGGHPRSALYGRER LTGQPPSSPHNPAPWASCPAVI DPVPIYSSVAEAYDSGTEGIPTV PGLRHVESGSLRATAQRLPPER RV/QQRTTAPPPRQPPRRPLRAS LSAAPPEPREPVVAAGPEPGSL QRPARTALPNRPEPQAASPGTL VEKYAAPVATQDLLDENPCTS RLGVVDLQAVLTLRKLENLRS GAQTPLEGGQSGRVGPHALRW NRGEEGERLLC |
| 22861 | 53229 | A | 22993 | 307 | 1906 | |
| 22862 | 53230 | A | 22994 | 1 | 1752 | |
| 22863 | 53231 | A | 22995 | 588 | 704 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22864 | 53232 | A | 22996 | 3219 | 3407 | DQVVWTKRLQDAILVLV*EFRL HSPALRLCVMKQVGMSQGELE WGQFLKLSSRNKRKRSGERI |
| 22865 | 53233 | A | 22997 | 1 | 588 | |
| 22866 | 53234 | A | 22998 | 1 | 917 | |
| 22867 | 53235 | A | 22999 | 1 | 1692 | |
| 22868 | 53236 | A | 23000 | 1 | 2266 | MKRIRDYYERSHANNLDNLEE MDELLETHNLPGLNHEETENLN KPITTSLSPLAGVSSTKKNTKNE LSIVLPFTGSILPVGFA TRPRGL ASSNPILLH MVAF LFANGTEEL PVPLMTPTTRQKKVIPLIPLMVG LGVSASTIALGTGITGISTSVTTF RSLSNDFSASITDISQTL SVLQA LVDSSAAVVLQGQLRGLDLLT AEKGGLCIFLNEECFYLNQSG LVYDNIKKLDRAQKLANQAR QNLD SMLHGTGMKSDSDQKKS ENGVT LAPEDTL PFLKCYCSGH CPDDAINNTCITNGHCFAIIEED DQGETTLASGCMK YEGSDFQC KDSPKAHV RRTIECCRTNLCNQ YLQPTLPPV VIGPFDGSIRWLV LLISMAVCIIA\MISSSCFCYKH YCKSISSRRRYNRDLEQDEAFIP VGESLKD LIDQSQSSGSGSGLPL LVQRTIAKQIQMV RVGKG RY GEVWMGKWRGEKVAVKVFFT TEEASWFRETEIYQTVLMRHEN ILGFIAADIKGTGSWTQLYLITD YHENGSLYDFLKCATLDTRALL KLAYS AACGLCHLHTEIYGTQG KPAIAHRDLKSKNILIKKNGSCC IADLGLAVKFN\SDTNEVDVPL NTRVGTK\RYMAPEVLDES LNK NHFQPYIMADIYSFGLIIWEMA RRCITGGIVEEYQLPYYNMVP DPSYEDMREVVCVKRLRPVSN |
| 22869 | 53237 | A | 23001 | 68 | 636 | GVTSNPKALLGALIAPAFASLPE GRGKRIQALNMFRPKNSWRLG LKYPSSSEKKTQVPKTLISGLPE RKSTTRVGEKLQSAHKMPLSPG LLLLLFSGATATA/APLPLEGGP TG\RDSEHMQEAAGIRKSSLLTF LAWWF EWTS\QASAGPLIGKEA REVARRQEGAPP\QQSARRDRM PCRNFFWKTFSCK |
| 22870 | 53238 | A | 23002 | 1 | 144 | GIRLPSSADWQKTEAQKRREQL \LLDELVALVNKR DALVRDLDA QEKQ |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22871 | 53239 | A | 23003 | 2 | 667 | RWNSSDPDADRTTLNHADHSS KIVQHRLLSRQEELKERARVLL EQARRDAALKAGNKHNTNTAT PFCNRQLSDQQDEERRRQLRER ARQLIAEARSQVVKMSELPPYG EMAAEKLKERSKASGEQNSKL VDLKLKLLLEVQPQVANSPSSA AQKAVTESSEQDMKSGTEDLR TERLQKTTERFRNPVVFSKDST VRKTQLQSFSQYIENRPEMKRQ RSIQED |
| 22872 | 53240 | A | 23004 | 1 | 1437 | |
| 22873 | 53241 | A | 23005 | 1 | 2009 | MAKPYLYKKYGNQQGVAAIPD VPAAWEAEPSPIPSPVLGRKPN ASQSLLVWCKEVTKNYRGVKI TNFTTSWRNGLSFCAILHHFRP DLIDYKSLNPQDIKENNKKAYD GFASIGISRLLEPSDMVLLAIPD KLTVMTYLYQIRAHFSGQELN VVQIEENSSKSTYKVGNYETDT NSSVDQEKFYAELSDLKREPEL QQPISGAVDFLSQDDSVFVNDS GVGESESEHQTDPDDHLSPTAS PYCRRTKSDTEPQKSQQSSGRT SGSDDPGICSNTDSTQAQVLLG KKRLLKAETLELSDLVSDKK KDMSPPFICEETDEQKLQTLDIG SNLEKEKLENSRSLECRSDPESP IKKTSLSPTSKLGYSYSRDLDA KKKHASLRQTESDPDADRTTL NHADHSSKIVQQDEERRRQLR ERARQLIAEARSQVVKMSELPSY GEMAAEKLKERSKASGDENDN IEIDTNEEIEPGFVVGGGDELTN LENDLDTPEQNSKLVDLKLKKL LEVQPQVANSPSSAAQKAVTES SEQDMKSGTEDLRTERLQKTTE RFRNPVVFSKDSTVRKTQLQSF SQYIENRPEMKRQRSIQEDTKK GNEEKAAITETQRKPSEDEKGF KDTSQYVVGELAALENEQKQI DTRAALVEKRLRYLMDTGQNL |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22874 | 53242 | A | 23006 | 145 | 3217 | LDEYEARLTLANLDDFEEDNED DDENRVNQEEKAAKITELINKL NFLDEAEKDLATVNSNPFDDPD AAELNPFPGDPDSEEPITETASPR\K TEDSFYNNSYNPFKE\VQTPQ YLNPFDEPEAFVTIKDSPQSTK RKNIRPVDMSKYLADSSKTEE EELDESNPFYEPKSTPPPNLVN PVQELETERRVKRKAPAPPVLS PKTGVLNENTVSAGKDLSTSPK PSPIPSVLGRKPNASQSLLVWC KEVTKNYR |
| 22875 | 53243 | A | 23007 | 1 | 165 | RPAAPRHERRPAADHGHHRPEP GRGTGQKACSELPSEACS/GIA IG*SLLCSACSVRSRKRW |
| 22876 | 53244 | B | 23008 | 26 | 625 | |
| 22877 | 53245 | A | 23009 | 325 | 526 | |
| 22878 | 53246 | A | 23010 | 1946 | 2224 | LLQWRHGLLNPNINSPYNSPILPV QKPKDPYRLVQHLCLIYQIVLP HPMVPNPYTLSSIPFTTHYSVL DLKHAFFTIPLYSSQPLFAFTW TDPDTHQAQQITLAVLPQCFIDS PHYFSQAQISSSSVTYLGILMK THIGLGAVEQGVVLVGEARAA QEPMEWVGSGMVGCRSRALP RGKAAKARREIERSAVTIVPVL DFNPAFHIPDTPDHHDCISLIH LTFTFPFHISFFPVPHLEHTWFID GSSTR |
| 22879 | 53247 | A | 23011 | 1 | 1479 | MEENFIRVFFTTTMTLLIALIK QGELCESFDGKSLDGRDERVVI CFDAAAGLHRACSIRGEQQNL GTHYFTWQRLFAEVIKLGGLM KPKARNASSLWKEKTKNGFFS LETPEERQTSDLHKYQLAFRLF FIKYKNPAQFMAHLATTLRHFT ALDPESHNFQNLFSSSHLMHIL SAPRLLRLYSRFVESPTVTIVPG PDFNPASNIIPDTPDPHDCISLI HLAFTFPFYISFFPVPHPDHTWF IDGSSTRPNCHTPAKAGYAIVSS TSIIEATALPPSTTSRQELIALT QALTAKGLRINIYTD/SHILHH HAVLWA/E/RGFLTMQGSSIINA SLIKTLLQAALLPKEAEVIHCKG HOKASDPITQGNAYADKVPSL AHAPTLTLAPVLQCPLREVAGT EDDNGKAVLEIPSNIRKSAHVP VQTWKGWDPTNLLGGWFSNL GGFKTLVGTVIFIIGFLLFLPCVI PRIIKAIKTLVETTVSRQIIQTILL |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22880 | 53248 | A | 23012 | 854 | 1777 | |
| 22881 | 53249 | A | 23013 | 27 | 496 | |
| 22882 | 53250 | A | 23014 | 117 | 210 | |
| 22883 | 53251 | A | 23015 | 124 | 414 | |
| 22884 | 53252 | A | 23016 | 3 | 627 | |
| 22885 | 53253 | A | 23017 | 1 | 567 | |
| 22886 | 53254 | A | 23018 | 44 | 551 | GGGRRSAPLQLGFMSRQAKDD FLRHYTVSDPRTHPKGYTEYKV TAQFISKKDPEDVKEVVVWKR YSD\FRK\LHGD\LAYTHRNLFR RLEEFPAFP\RAQ\VFGRF\EASV DSRER\RKGAEDLLRFTVHIPAL NNSPQLKEFFRGGEVTRPPEVS RDLHILPPPLIPTPPPG |
| 22887 | 53255 | A | 23019 | 25 | 488 | |
| 22888 | 53256 | C | 23020 | 9 | 119 | |
| 22889 | 53257 | A | 23021 | 52 | 241 | |
| 22890 | 53258 | B | 23022 | 4 | 402 | |
| 22891 | 53259 | A | 23023 | 249 | 984 | GSTMYKMNICNKPSNKTAPEK SVWTAPAQPSGSPSELQGQSR RNGWSWPPHPLQIVAWLLYLF FAVIGFGLVPLLPHHWVPAGY AVSLGKRRAGPWNPFSLVSAET ILPQCMGAIFAGHLVVHLTAVS IDPADANVRDKSYAGPLPIFNR SQHAHVIEDLHCNLCNVDVSA RSKHCSACNKCVCDFDHHCKW LNNCVGERNYRFLHLSVASALL GVLLLV/LGGHICLRGVLCQPH ASAHQPTL |
| 22892 | 53260 | A | 23024 | 2 | 224 | |
| 22893 | 53261 | A | 23025 | 111 | 1368 | QQPSGSGALARGSGLPPRPGR PARSPVQKRKGGWPKGKKNRP PRDLAV\RVPTTGymIFLNEQRS QLRATHPDLPFTEIMKMLAVQ WAQLSQDKKGRKYAGKALGV TPPPSALTPVALIEEPKQLDIQSL PFQPILDRLKIKDKRQLVPSYLG GMHTVTEGLAGRQVLLQQVQ GGAWEAFLTCPWAMAAAAP GPTLTMLQPSISAVGFSQMAMG PHVQGRASKLSIYVNPRRQLST TTAMGDELNDLYCGTSRQLFSS LCNKKEPAAKAAPAAPLSSPGP PALGHAGHGRQLLLERSLTFLH LYELLKYPRASPGLWPPRVWM PHSLTCGTFWVPMIMMRFAH VASGLLRPPFNQVFAHLSPAQG RHPGENGIIVLTSRAAVRIRCSS CSRSLTGNLKKILPRTQSTWSL WRKRDK |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22894 | 53262 | A | 23026 | 2 | 405 | |
| 22895 | 53263 | A | 23027 | 1 | 391 | |
| 22896 | 53264 | A | 23028 | 3 | 463 | |
| 22897 | 53265 | A | 23029 | 74 | 466 | FAFNMPEPAKSAPAPKKGSKK AVTKAQKKDGKKRKRSRKESY SVYVYKVLKQVHPDTGISSKA MGIMNSFVNDIFERIAGEASRL AHYNKRSTITSREIQTAVRLLLP GEL\AKHAVSEGTK\AVTKYHQ |
| 22898 | 53266 | A | 23030 | 168 | 597 | KEETDFLFWFCHYCFIMPELAK SAPAPKKGSKKAVTKAQKKDG KKRKRSRKESYSVYVYKVLKQ VHPDTGISSKAMGIMNSFVTTT FE\RIAGEASRLAHYNKRSTITS REIQTAVRLLLPGELAKHA\VSE GTNA\VTKYTSSK |
| 22899 | 53267 | A | 23031 | 18 | 321 | FTATWLNQEVGIVGKYRTRYG VSLQKMVKKIEISQYAKYICSFL WQNSKMKRR\AVGIWCCG/SCM KTVKVSSSRNHIVWTYNTTSAV TVKSTIRRLKQLKDQ |
| 22900 | 53268 | A | 23032 | 12 | 445 | FTCRSHVSEVEERCVEAPGLLG SRSITGFSLSKQAKRTKKVGIV \GKYGNPLWGPSLR\KMKVKK\IE ISQHAQVHFALFCGKTKMKRR AVGIWHCGSCMKTV\AGGAWT \YNTTSAVTVKSAIRRLKEFERP SRTLLYSLRTSLGL |
| 22901 | 53269 | A | 23033 | 3 | 175 | |
| 22902 | 53270 | C | 23034 | 378 | 434 | |
| 22903 | 53271 | A | 23035 | 1 | 578 | MVRCVRLVEAGSVVRYLSTSIC RPVVDAGSRALCLQEWADSQQ VKEKQYSSRDVQRAALNIYRI PPSSRKPALCPTPRDRLEYDEDR LEHIAVVRARELHTLEVTGLET VAQSKAHVASLEGLIPEDKVVL LAGSPLQNEATLGQCGVEALTT LEVVGRRLGASL/HTSASKHTM VRALTYCSSREETFTAI |
| 22904 | 53272 | C | 23037 | 236 | 379 | |
| 22905 | 53273 | A | 23038 | 178 | 534 | VVQKTEPRLCFAVSPPFSCSLPL PSLFPHSPLLGRPKRQAKPAAD EGFWDCSVCTFRNSAEAFKCSI CDVRKGTSTRYLKICVTWVVV VI*QVFIEHTAICALGVQWYKD RPGPCSYGA |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22906 | 53274 | A | 23039 | 44 | 1012 | VGGGGVQPSMTMGDKKSPTRP KRQAKPAADEGFWDCSVCTFR NSAEAFKCSICD\VRKGTSTRKP RINSQLVAQQVAQQYATPPPPK KEKKEKVEKAGQKRKPEKRPR KFSP/SVVTKKNTNKKTKPKSD\ ILKDPPS\EANSIQSANATTKTSE TNHT\SRPRLEKRGTTGGIAQQFG QLTVG\NVTVIITDFK\EKTRSS\ TSSSTVTS\SAGS\EQQNQRLR GFRGATDKGSLPVPPNPKGRPC QAVNDESFLKLAHGNCGLWN SGVWKFNLPAPHACLHPWEN LSCGTSTSLVDCQDNFLLCHG HSWPPRDFRHPDDYSGHF |
| 22907 | 53275 | A | 23040 | 1 | 626 | MAGCRNPCKAESHRSKSLSEA ESLFREAESQHDRGSKNAGHR DESVEVWLSLLSSSQTRAEIER QSRGKQWLRHLLRDTEGPKET VRPELATRAAMDVAEVEFLAE KELVTIIPNFSLDKSYLIGVDNIP KADEIRTLVKDIWDTRIAKLRV SADSFVRQQEAHAKPDNLTL EINPSGTFLTQALNHTYK/LRTN LQPSESTQSQDF |
| 22908 | 53276 | A | 23041 | 1 | 951 | MDAAEVEFLAEKELVTIIPNFSL DKIYLIGTWELKYREIRWLSQG PHGKPHADPGSSILQNSSGPGS VRTNGKSKPWEPFVAEEFAHQ FHESVLQSTQKALQKHKGSA VLSAEQNHKVDTSVHYNIPELQ SSSRAPPQHNGQQEPPTARKG PPTQELDRDSEQEEDDEDGE DEEEVPKRKWQGIEAVFEAYQ EHIEERTLERNRSSTAADKAQL LAANRQGHGQPTDPASDNIPKA DEIRTLVKDMWDTRIAKLRVS ADSFVRQQEAHAKL\DNLT\LM EIHTSGTFLTQALNHMYKLRT NLQPLESTQSQDF |
| 22909 | 53277 | A | 23042 | 1 | 626 | MAGCRNPCKAESHRSKSLSEA ESLFREAESQHDRGSKNAGHR DESVEVWLSLLSSSQTRAEIER QSRGKQWLRHLLRDTEGPKET VRPELATRAAMDVAEVEFLAE KELVTIIPNFSLDKSYLIGVDNIP KADEIRTLVKDIWDTRIAKLRV SADSFVRQQEAHAKPDNLTL EINPSGTFLTQALNHTYK/LRTN LQPSESTQSQDF |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22910 | 53278 | A | 23043 | 2 | 642 | RPRLLRDAEGPEETVRLWPAA RAAMDAAEVEFLAEKELVTIIP NFSLDKIYLIGGDLGPFNPGLPV EVPLWLAINLKQRQKCRLLPPE WMDVEKLEKMRDHEARKETTF TPMPKPFTTLELTAKLLLNHASD NIPKQDEIRTLVKDMWDTRIAK LRVSADSF\VRQQEAHAKLADN LTLMEIHTSG\TFLTQALNHMY KLRTNLQPLESTQSQDF |
| 22911 | 53279 | A | 23044 | 3 | 1038 | TSSMAAGCSEAPRPAAGSDGS LVGQAGVLPCELPTAAACA LVNSRYSLVAGPHQRHIALSP RYLNRKRTGIREQLDAELLRYS ESLLGVPIAYDNIKVVGELGDIY DDQGHILNIEADVFVFCPEPGQ KLMGIVNKVSSSHIGCLVHGCF NASIPKPE\QLSAEQWQTMEIN MGDELEFEVFRLDSDAAGVFCI RGKLNITSLQFKRSEVSEVTEN GTEEAACKPKKKKKKKDPETY EVDSGTTKLADDADDTPEES ALQNTNNANGIWEEPKKKKK KKKH\QEVSRQTQDPCFSQGQLT S\SGYQSDHKKKKKKRKHSEEA EFTPPLKCSPKRKGSNFL |
| 22912 | 53280 | B | 23045 | 82 | 323 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22913 | 53281 | A | 23046 | 3 | 1624 | QLEIRAPTAD EIHVTVG EARNLI PMDP NGLSDPYVKLKLIPDPRN LTKQKTRTVKATLNPVWNETF VFNLKPGDVERRLSVEVWDWD RTSRNDFMGAMSGVSELLKA PVDGWYKLLNQEEGEYYNVPV ADADNCSLLQKFEACNYPLEL YERVRMGPSSSIPSPSPSPDTPK RCFFGASPGRLHISDFSFLMVLG KGSFGKVMLAERRGSDELYAI KILKKDVIVQDDVDCTLVEKR VLALGGRGPGGRPHFLTQLHST FQTPDRLYFVMEYVTGGDLMY HIQQLGKFKEPHAAFYAAEIAI GLFFLHNQGHYRDLKLDNVML DAEGHIKITDFGMCKENVFPGT TTRTFCGTPDYIAPEIIAYQPYG KSVDWWSFGVLLYEMLAGQPP FDGEDEEELFQAIMEQTVTPK SLSREAVAICKGFLTKHPGEAP GASGP*WGNLTIRAHGFFPLGF DWERLERLEIPASFSRPRPCGRS GENFDKFFTRAAPALTPPDRLV LASIDQADFQGYVNPDFVHP DARSPTSPVPVPM |
| 22914 | 53282 | A | 23047 | 1 | 1522 | MLRAPRQATRDHHFAHIDIVQV TCFRYLRRSALAPAMPSPVR VDRGSFPPVAGGNHTRRRGGTP QEGVTREALAFFDVVATTGAE MMWSNFFLQEENRRRGAAGR RAHGQGRSGLTPEREGKVCLA LLLAAWAPRWCCPWAPSSG WTQHLQGQRQRRVRSRGPTWG CGRRAPSGCGRRTCPWTGTPA APRSCPEASERNSEHPALICTLP QPHMLKRRARRAPGSMAPPLP RPPQAASVPVFPDWEPLSRA RSKSPLHSQHRPAQETGRHSRP RTSTRKRQQKHSTEKATHTPER APKPQTRENNPKGRAQGSAPR DHNPA SRHQKTSNDKRSTHDT HKTRKDSQTRRKTRNNEKQQ PDR/IGPQIIAYQP/YGKSVDWW SFGVLLYE/MLAGQPP/FDGEDE EELFQAIMEQ/TVTPKSLSREA VAIC/KGCGRSGENFDK/FFTRA APALTPPDRLV/LASIDQADFQ FTYVNP/DFVHPDARSPTSPVP PASSPTRPQLLENKFGC |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22915 | 53283 | A | 23048 | 505 | 2345 | SIWGMVMMNPTPSSITLRRMM SLFPASLTTKYGGFYINSGTLQF RQASESEDDFIKEKKKKSPKKR KLKEGGEKIKKKKKDDTYDKE KKSCKSKFSKAGFTALNASKEK KKKKYSGALSVKEMLKKFQKE KEAQKKREEEHKPVAVPSAEA QGLRELEGASDPLLSLFGSTSD NDLLQAATAMDSLTDLDLEHL LSESPEGSPFRDMDDGSDSLGV GLDQEFRQPSSLPEGLPAPLEKR VKELAQAARAAEGESRQKFFT QDINGILLDIEAQTRELSSQVRS GVYAYLASFLPCSKDALLKRA RKLHLYEQGGRLKEPLQKLKE AIGRAMPEQMAKYQDECQAHT QAKVAKMLEEEKDKEQRDRIC SDEEEDEEKGGRRIMGPRKKFQ WNDEIRELLCQVVKIKLESQDL ERNNKAQAWEDCVKGFLDAE VKPLWPRGWMQARTLFKESRR GHGHLTSILAKKKVMAPSKIKV KESSTKPKDKKVSVP SGQIGGPIA LPSDHQTGGLSIGASSRELPSQA SGGLANPPPVNLEDSDLDEDLIR NPASSVEAVSKELAALNSRAAG NSEFTLPAPSKAPAELVGGVLC TEEKRNFAPSPSAPPPASSLQS |
| 22916 | 53284 | A | 23049 | 1 | 379 | A YRNFTSASDVWSYGIVMWEV MSYGERPYWDMSNQDAPNTAL LDPASPEFSAVVSVGDWLQAIK MDRYKDNFTAAGYTTLEAVVH VNQEDLARIGITAITHQNKILSS VQAMRTQMQQMHGRMVPV |
| 22917 | 53285 | A | 23050 | 1 | 123 | |
| 22918 | 53286 | A | 23051 | 3 | 221 | |
| 22919 | 53287 | C | 23052 | 80 | 379 | |
| 22920 | 53288 | A | 23053 | 71 | 924 | AFSVNSSNSWEKA*SQKCLQV NYLSLSSASYLP/CMTCPPSAPL NLISNVNETSVNLEWSSPQNTG GRQDISYNVCKKCGAGDPSK CRPCGSGVHYTPQQNGLKTTK VSITDLLAHTNYTFEIVAVNGV SKYNPNPDQSVSVTVTTNQAAP SSIALVQAKEVTRYVALAWLE PDRPNGVILEYEVKYYEKDQNE RSYRIVRTAARNTDIKGLNPLTS YVFHVRARTAAGYGDFSEPLE VTTNTGNKDHPDSVTSEAIFIIQ LNPITVKSKELSVIFGSADILLQ |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22921 | 53289 | A | 23054 | 1 | 1102 | MRWLLKWERKYTLYSSGVLK HKNLLESLLGQFLGPPAQRFD AGGVRPKNDGRFTVIQLVGML RGIGSGMKYLSMSYVHRDLA ARNILVNSNLVCKVSDFGMSR VLEDDPEAAAYTTRGGKIPRWT APEAIAIRKFTSA/SDVWSYGIV MWEVMSYGERPYWDMSNQD VIKAIIEGYRLPPPMDCPIALHQ LMLDCWQKERSDRPKFGQIVN MLDKLIRNPNSLKRTGTESSRP NTALLDPSSPEFSAVVSVGDWL QAIKMDRYKDNFTAAGYTTL AVVHVNQ/EVSTQRCNTKGDL ARIGITAITHQNKILSVQAMR TQMQQ\MHGRMVPRLSTVLNK LKTLEISLPHPCTLIEELHFFNFV |
| 22922 | 53290 | A | 23055 | 148 | 3229 | NAFRFHLLNPAGESHDLQDLL SAVRSPTKRQEQRWHRRTMAG IFYFALFSCFLGICDAVTGSRVY PANEVTLLDSRSVQELGWIAS PLEGGWEEVSIMDEKNTPIRTY QVCNVMESQNNWLRTDWITR EGAQRVYIEIKFTLRDCNSLPG VMGTCKETFNLYYESDNDKE RFIRENQFVKIDTIAADESFTQV DIGDRIMKLNTEIRDVGPLSKK GFYLAHQDVGACIALVSVRVFY KKCPLTVRNLAQFP |
| 22923 | 53291 | A | 23056 | 57 | 450 | VGDCLTSRGMSWVQATLLAR/ ALCRAWGGT/CRGALTGTSISQ VPR LAPRGLHCSA/ASVSSEQS LVSPPEPRQR/PPGGERDKASF LQTVQKFADTSVVD SGHIDFIY LALRKMREYGVERDLAVYNQL LNIFP |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22924 | 53292 | A | 23057 | 89 | 1502 | VGDCLTSRGMSWVQATLLARG LCRAWGGTTCGAAL/SQEPPSLR SLASLPRGLHCSAAHSSEQVL VPSPPEPRQEGPPRLLVPFEGPV LGQAGLGERGQGRAFL/LDGC RNLRTTSVRKRGPV/VDLFYLA LRKMRE\YGVVERG/DLAVYNQL LNIFPKEVFRPRNIIQRIFVHYPR QQECGIAVLEQMENHGVMPNK ETEFLLIQIFGRKSYPMKLVLRL KLWFPFRFMNVNPFVPRDLPQD PVELAMFGLRHMEPDLSARVTI YQVPLPKDSTGASKIPPKPHIVG HRACMSPHQESKSRSSKAAL\ ARHNPS\RPV\FVEGPFSLWLRN K\CVYY\HILRA\DLLPPEEEGK WKRTPEEWE\LYP\RQLDLEY VRSG\WDNYEFDINEVEEGPVF AMCMAGAHDQ\ATM\VKWI\Q GPAGDQPQTLAQNPWSFRLRR VQPGELPDILLQGWRSR/HPAR GPPRKKTTTCKRQQQGPELV |
| 22925 | 53293 | A | 23058 | 1 | 2517 | |
| 22926 | 53294 | A | 23059 | 1 | 927 | IIVVEFVSRGLARAPSGPAVFSH LAMARLPLRGVRWGCLLTAVH PEPPTACREKQYLINSQCCSLCQ PGQKLVS DCTEFTETECLPCGE SEFLDTWNRETHCHQHKYCDP NLGLRVQKGTSETDTICTCEE GWHCTSEACESCVLHRSCSPGF GVKQIATGVSDTICEPCPVGFFS NVSSAFEKCHPWTSCETKDLV VQQAGTNKTDVVCQPQDRLRA L\VVPIIFGILFAILL\VLVFIKKV AKKPTNKAPHPK\QEPQEINFP DDLPG/SSNTAAPVAGRIFTWG GQPV\TQEDGQRESHFSCRERQ |
| 22927 | 53295 | B | 23060 | 24 | 439 | |
| 22928 | 53296 | A | 23061 | 1 | 582 | |
| 22929 | 53297 | C | 23062 | 1 | 2607 | |
| 22930 | 53298 | A | 23063 | 248 | 430 | ATNYTREQDSMWNCVR*GRTT ATTHSVTQRTDERQRRADTAL TLADYRNTSVTGVFAGLF |
| 22931 | 53299 | A | 23064 | 776 | 1426 | |
| 22932 | 53300 | A | 23065 | 284 | 598 | VFRLLRGQKSEPGKSRPKAL*N KPANTPVQSHISLYAAGINS KVR*SCRQSSARQSGSYL*TS SPQNRQQTGEITATVIAFGRT TAPDITPHPASAR |
| 22933 | 53301 | A | 23066 | 3139 | 3792 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22934 | 53302 | A | 23067 | 2 | 830 | GVPNMAAPQDVHVRICNQEIV KFDLEV KALIQDIRDCSGPLSAL TELNTKVKEKFQQLRHRIQPVL YQRAFIWTASTFFFKLTYSLTDF SSTQHDFNSPTTPVTFSDL\AEQL AKEQDKESENQLLLQEVENHK KQMLSNQASWRKANLTCKIAI DNLEKAELLQGGDLLRQRKTT KESLAQTSSTITESLMGISRMM AQQVQQSEAMQSLVTSSRTIL DANEEFKSMSTIQLGRKLITK YNR\RELTDKLLIFLALRLFLAT VLYIVKKRLFPFL |
| 22935 | 53303 | A | 23068 | 1231 | 1458 | |
| 22936 | 53304 | B | 23069 | 1 | 2133 | |
| 22937 | 53305 | A | 23070 | 722 | 957 | VFRLLRGQKSEPGQKQAKSTLE QTSEYPSNRGPIIRQSECSIRTPL PFVRLALRD*VRGCGCAPLSSVD SFFCCTEAL |
| 22938 | 53306 | A | 23071 | 2 | 1137 | VPNMAAPQDVHVRICNQEIVKF DL\EVKAPIQDIRD\CSGPLS\AL TELNPKVKEKFQQLRHRTGP/ VEQLAKEQDKESKQLLLQ\EV ENHKKIQMLQQFRPSWEGKLN SSPGKICNSDNLEKAELLQGGD LLRQRKTTKE\SLAQTSSITES LMG/ISGRMMAQQVQQSEAM QSLVTSSRTILDANEEFKSMST IQLGRKLITKYNRRELTDKLLIF LALALFLATVLYIVKKRLFPF VRFPKVPVLAPFNSLFSGICPWF PEAPRLPKAEHTPLRFAPQLP CRLGWEHQCPPLFLQSSWLVK GEQSPWEEGPGIGMPPLGTYP PPSHHCALWEAAAAWSTLKSE PPRTRMPLLSPAIVPLNARSGG GKREER |
| 22939 | 53307 | A | 23072 | 64 | 665 | RVRGGAEELAMAAAEEL\SGAP NVPNRRERGGAGRPKTPFECNIC LETAREAVVSVCGHLYCWPC LHQLWLETR\PERQECV\CKAGIS REKVVP\LYGRGSQEAPRIPELK TPPPPPRGQR\PAPESTRGGF\QPF GDTGGFHFSFGVGAFPF\GFFT TVFNAHEPFRRGTGVDLG\QG HPSLQLGKEFPLPGFSAIFFLFW |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22940 | 53308 | A | 23073 | 1 | 416 | MQRRRRRLLLLPPRRQTDRAL PPPPSPGSMPPPLPPPP/PPARGG GLRPGDGLYPK/PSPARRGSGA RTSWCTMCAPPSTSAPRASRRP RPSSCATRPPTSKPPPA\GHAPH PPPRDLGGGLDSGVQSDGVVLQ HLQRPQH |
| 22941 | 53309 | A | 23074 | 1 | 1713 | |
| 22942 | 53310 | A | 23075 | 1305 | 1538 | LKVVRNCTSS*SPTIGHD*QSNL SLPPSDFAKPPFPFSLLRCSKFR KLKAA YRKRKKGHKSSLSLSV KINKTAAANK |
| 22943 | 53311 | A | 23076 | 49 | 355 | |
| 22944 | 53312 | B | 23077 | 253 | 471 | |
| 22945 | 53313 | A | 23078 | 1267 | 1497 | LKVVRNCTSS*SPTIGHD*QSNL SLPPSDFAKPPFPFSLLRCSKFR KLKAA YRKRKKGHKSSLSLSV KINKTAAANK |
| 22946 | 53314 | A | 23079 | 3 | 1237 | HEVAGAVPGAIMDEDDYYGSAA EWGDEADGGQQEDDSGEGED DAEVQQECLHKFSTRDYIMEPS IFNTLKRYFQAGGSPENVQLLS ENYTAVAQ\AVNLLAE\WLIQT GVEPVQVQDTVEYHLKSLLIKH FDPRIADSMFTEEGETPAWLE\Q MIAHTTWRLDFYKLAEAHPC LMLNFTVKLISDAGYQGEITSV STACQQLEVFSRVLRTSLATILD GGEENLEKNLPEFAKMVCHGE HTYLFAQAMMSVLAQEEQGGG AVRRIDQEVQRFAQEKTVLTQE AIITVKGVSLSYLEGLMASTIS SNASKTIVAAMSNLVPPVELAN PENQFRVDYILSMNVDPDFDP PEFYEHAKALWEDEGVACYE RSNEYQLIDCAQYIFVLEMQVP CCEEAQSHPGQHGGVQVGRN |
| 22947 | 53315 | A | 23080 | 1358 | 1589 | LKVVRNCTSS*SPTIGHD*QSNL SLPPSDFAKPPFPFSLLRCSKFR KLKAA YRKRKKGHKSSLSLSV KINKTAAANK |
| 22948 | 53316 | A | 23081 | 33 | 458 | GITGSTDASGVTMKFNPVFSD RRKNRKRHVNPASHVRRKIMS SPLSKELRQKYNVRSMPIRKDD EVQVVRGHHYKGGQIGKVHV YRKKYVIYIERVQREKANG/DK DRKKILERKAKSRQVGKEKGY YKEELIGKMQEYIEP |
| 22949 | 53317 | A | 23082 | 1 | 576 | |
| 22950 | 53318 | B | 23083 | 37 | 276 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22951 | 53319 | A | 23084 | 124 | 549 | NNSLSSPVQADVYFRLIVPFCG HIKGGMRPGKKVGVMGIVDLN PKSFAINLTCDSEDPADGAIE LKAVFTDRQLLRNSCISGERGE EQVSNPLLSIHSTTMPFRVEILC EH\HCFR\VFVDGHQLDFYHPH SNRYLAI |
| 22952 | 53320 | A | 23085 | 1 | 215 | QGFIPPLKEENFTLPPGKFGP PKGSLNSPPS/PSSP*SPGGGILL VYYLYRALFQKGCKEAAWLEY PLT |
| 22953 | 53321 | A | 23086 | 533 | 983 | PWGPGCNKRWPCLAKDPPPTP QSSGVGQPFGGAEPAGAYIRTG PHLGPPPPPPDSSTNLHSPNPS DDGADTPLAQSDDEEERGDGG AEP\GPAASSGPLAYRPDPAGY SPTSRRPGPSPEPLG/AEDPDSLL ASRAPRGGNGWWDCGTL |
| 22954 | 53322 | A | 23087 | 1422 | 1670 | NRYIDKTGWAWWLTPVIRHFR RPRWVDCLRLGVREQPGQHSKI KSLQKNAK\ISQAWWHAPVDP ATWKADAGGSLEPGSLRLQ |
| 22955 | 53323 | A | 23088 | 2 | 663 | VLLDERSAALDGAKRDLAL AAGALCREARAAQVFLKGGY EAFSASCPELCSKQ/INVSANCP NHFEGHYQYKSILCGMTTHKA DISSWFNEAIDFIDSIKNAGGRV FVHCQAGISRSATICLAYLMRT NRVKLDEAFEFVKQRRSIISPNF SFMGQLLQLESQVLAPHCSAEA GSPAMAVLDRGTSTTTVFNFV SIPDHSTNSALSYLQSLITTSSHC |
| 22956 | 53324 | A | 23089 | 3 | 206 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22957 | 53325 | A | 23090 | 982 | 2252 | LFLEKRRPALGPENRQRAPOGR STLGALRPAMVMEVGTLDAG GLRAL\GERAAQLPACLDERS FF\AFNAGHIAGSVNVRFSIVR\ RRAKG\AIGALE\HIVPNAELR\ RLLAGAYHAVVLLDERSAG\LD GAKRDGTLALAAGRA/LCREA RAAQVFF/LSKGGYEA\FSASCP\ ELCSKQSTPMGLS\LSLSTSVPD SAESGC\SSCSTP\LYD\QGGPVE ILPFLYLGSAYHASRKD\MLDA LGHRLPWINVLSQIVPNHF\EGH \YQYKSIPVEDNHKADISFWFN\ EAIDFIDSIKNAGGRV\FVHCQA GISRSAT\ICLAYLMRTNRVKLD EA\FEFVKQRRSIISP\NFQLHGA SLLQFEFPRMLGPALFRAEAGK PRQMAVL\DRGT\STTTVFNFVP SIPVHSTNSALSVFPRAPLTDLS QLVERPTGR |
| 22958 | 53326 | A | 23091 | 13 | 287 | |
| 22959 | 53327 | A | 23092 | 1 | 492 | |
| 22960 | 53328 | A | 23093 | 1 | 636 | |
| 22961 | 53329 | A | 23094 | 1 | 506 | PTRTWTRGRIPRLSAQPSRGAR GTMADPRVRQIKIKTG\VKRL \KEKVL\YEKEPKQ\QEEKIEKM RAEDGENYDIKKQAEIL\QES\ MMIPD\CQRR\LEAAYLDLQRI LENEKDL/EKEAEYKEAR\LVL DSVKLESCLKFSYGVVFALKPR GPILQSIIFDHVLCVQV |
| 22962 | 53330 | A | 23095 | 1 | 786 | |
| 22963 | 53331 | A | 23096 | 183 | 1059 | VLGAFIWQGLDPSPETAFTDHR ATEWGTNDQSLCLNSP*\DAPS AKHEYQASVSGSVSSKPEIDLQ LYDEV RDQDVPVKRNFARIVV NVSDTNDHAPWFTASSYKGRV YESAAVGSVVLQVTALDKDKG KNAEVL\YSIESGSHPPYKTAAD VLLKAPPPGWRPTNTKPVHSTE AQPTQNQRTQQKH\NQGASRSP RHSFATSTRAGAGICGCKTRRW MTRWMEESRGS\QTLPSTRLEP GSSAAWLDPEEQAQSLQFSSQE APFLGEGGENHIKGVPHGTKES QQQPLNHRSSL |
| 22964 | 53332 | A | 23097 | 1 | 1224 | |
| 22965 | 53333 | A | 23098 | 1 | 660 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|---|
| 22966 | 53334 | A | 23099 | 129 | 595 | LFPRLLSCLTTPPHCSFSICFVIC SRTLILKGSSLMYVFCLPNTAIV MALSPRGWRSKFGMPWHKPT WIMTL*FPLEKTGALSLSLSDTS MFTVVVLTGGLPLSEA*T/GG NYDSHFDVDKGTGTHIVAKPLD AEQKSNNLTVEATDGTTTILT |
| 22967 | 53335 | A | 23100 | 1 | 1782 | MAARIEVIHELISIRLLLMKTDL DAATAALLNVQPAKSGDNTSG APFPGKISQTLLKDPHNGYHV FALAGSPKDADDTSIYMFYQK VGDNISDSWKNAGR VF KD SDK FDANDPILKDQTQEWSGSATFT SDGKIRLFYTDYSGKH YG KQSL TTAQVNVS KSDDTLKINGVED HKTIFDGDGKTYQNVQQFIDEG NYTSGDNHTLRDPHYVEDKGH KYL VFEANTGTENGYQGEESLF NKAYYGGGTNFFRKESQKLQQ SAKKRDAELANGALGIIELNND YTFEKSNEAADHFKHGGGATIK GRVADNGKPQLSSLTYIDIRVIE ESIYPPAILPLEIFITASGEEYSGG VIGKIHATDQDVYDTLTYSLDP QMDNLFVSVSSTGGKLI AHKKLD IGQYLLNVSVTDGKFTTVADIT VHIRQVTQEMLNHTIAIRFANL TPEEFVGDYWRNFQRALR\NIL GVR RNDIQIVSLQSSEPHPLDV LLFVEKPGSAQISTKQLLHKINS SVTDIEEIIIGVRILNVFQKLCAG LDCPWKFCDEKVSVD SVMST HSTARLSFVTPRHRAARQQ\R GPPLHNPADT*TTARKYNCDKR |
| 22968 | 53336 | A | 23101 | 184 | 13958 | AMGRHLALLLLLLLLLFQHF GDS DGSQRLEQTPLQFTHLEYNVTV QENSAAKTYVGHPVKMGVYIT HPAWEVRYKIVSGDSENLFKAE EYILGDFCFLRIRTKGGNTAILN REVKDHYTLIVKALEKNTNVE ARTKVRVQVLDTNDLRPLFSPT SYSVSLPENTAIRTSIARVSATD ADIGTNGEFYYSFKDR TDMFAI HPTSGVIVLTGR LDYLET KLYE MEILAADRGMKLYGSSGISSMA KLT VHIEQANECA |
| 22969 | 53337 | C | 23102 | 56 | 331 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22970 | 53338 | A | 23103 | 2249 | 2680 | GEFLKTREFSIYFLEKYTTFPGE NLEHGFWDSSSTPPVLLHPGIPA SRJ/PVSSIFTKVPPKKSATKP/PV SIWGAPPLGPPGFWGCCPTGEQ RGVCHPSEPHPPVVD FRKKPPF LCVSLSLINIFKSNKFLLTTCNL VIFYTCSL |
| 22971 | 53339 | A | 23104 | 739 | 1672 | CQEAASEFGGPLHTPAMFLRRL GGWLPRPWGRRKPMRPDPYP EPRRVDSSENSGSDWDSAPET MEDVGHPKTKDSGALRVSRRA SEPSKEEPQVEQLGSKRMDSLK WDQPISSTQESGRLEAGGASPK LRWDHVDSSGGTRRPGVSPEGG L\GVPGPGAPLEKPGRREKLLG WLRGEPGAPSRYLGGPEECLQI STNLTLLHLELLASALLALCSRP LRAALDTLGLRGPLGLWLHGL LSFLAALHGLHAVLSLLTAHPL HFACLFGLLQALVLA VSLREPN GDEAATDWESEGLEREGEEQR GDPGKGL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22972 | 53340 | A | 23105 | 122 | 2437 | RLELKLPLWTMRFTMELLGH LSIFKITGKQKQLTRTAPGPSGQ LRNQTGNSLEPSGQPRSSQTT GNSLEPSGQPRSSQTTGNSLEPS GQPRSSQTTGNSLEPSGQPRSSQ TTGNSLEPSGQPRSSQTTGNSLE PSGQPRSSQTTGDSLEPSGQLRS NQTTGDSVQPNNREQPGTVRS APLQPNNREQPGTVRSAPLQPN NRGQRPTKQQTWTNRQVSSA PTKQQTAR\PSGQPRSNQTTG NSLEPSSQLRSNQTTGDSVQPN NREQPGTVRSAPLQPNNRGQR TKQQTAR\PSGQPCSNQTTGN SLEPSSQLRSNQTTGDSVQPN REQPGTIRAPLQPNNRGQRWD RQVSSAPTKQGTALGPSGASSAP TKQGTALPSSQLRSNQTTGN SLEPSGQPRSNQTTGNSREPSSQ LCSNQTTIGNSQDRQVSSAP/IQT TGNSQDRQVSPAPTKQQTAG NRQVSSST/PIQTGNSVQPNNREQ PGTVSGAM/VWVATPVKGP VETSAHKVSAAGLPKKKT/QPG VTGGAPRLTLNTVLPKHSRTPS RHEAGSTQALYHNGQAQYALS FPHEAAPMAAFYVVTGIEVTTA LTLEEAPCTVEITTALTEEPPC TVFWNKTERNRTLVDKGSN TKGFVQTATCCFRADCKASRPS PHPPSPHREWTSDLRHKQVSKF PGAHLRPGHPELPIQEAWDRGE |
| 22973 | 53341 | A | 23106 | 605 | 813 | LFVFINFRENALLRWAYAR\TI NVYP\NFRPTPKNSLMGALCGF GPLIFIYYIIKTERVSIQTRCLVF |
| 22974 | 53342 | A | 23108 | 273 | 936 | AYSNKVPSWNQKA\PSPTKPAG TLIFDFPAVKTVRNKFVFFINYP VSGYTEDLKKFLKPYTLEEQKN LTVCPDGALFEQKGPVYVACQ SPISLLQACRGMNDLDFGYSQR NPCILVKMNRIIGLKSEGVPRID CVSKNEDIPNAVAVPHNGIIDL KYFPYYGEKLVHGYLQPLVAV QVSFAPNDTGKEVTVECKIDGS ANLKSQDDRDKFLGRVMFKIT |
| 22975 | 53343 | A | 23109 | 104 | 478 | ETEVGGLVEASMSHNCTTALQ PGQHSQKENLQNKPIPGREKY* VSIEFELIYFP/YYCQVGYLQPL VAVQVSFAPNNTGKEVTVECKI \DGSANLKSQ\DDRDKFLG\RV MFQNHSTVHMSRVSSTE |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22976 | 53344 | A | 23110 | 3 | 903 | LLSPVRAHTMTKNEKKS LNQSL AE\WKLFIYNPTTGEFLGR TAAS WGLILLFYLVFYGFL\AALFSFT MWV MLQTLNDEV PKYRDQIPS PGLMVFPK P\VTALEYTF SRSDP TSYAGYIEDLKKFLKPYTLEE Q KNLTV\CPDG\ALFEQKGPVYV ACQFPISLLQACSGMNDP DFG YSQGNPCILVKLNRIIG\LKPEG VPRIDLCFKRMKDIPNVA VYS\ HNGMIDLK YFPYYGKKTAMF/ VGIYQPIGLLVQVSFAP*QPLGK EVTVE/CAKIDGSSQPKKVQDD\ RDKVFGDEFMFQIHSTVH |
| 22977 | 53345 | A | 23111 | 467 | 931 | SRDSRRGTPLAGGRGRDFAGQ MGHRVQGRHGSRGRLP SG DAR VNAERAEPVGAGAGGPGGGSS VRGFCGRSWSEA/RGRRRAGG GVH\IEP\RYRQFP\QLTQIPRCSQ SEF\FSGLMWFWIF\WRF WHDP K\KVLGHFPV/YPDPSQWTD\EE L\GIPPDD |
| 22978 | 53346 | A | 23112 | 1 | 390 | VTIPTSLAELQGLPHIRVFLDNN PWVCDCHMADMVTWLKETEV VQGKDRLTCAYPEKMRNRVLL ELNSADLDCDPILPPSLQTSYVF LGIG*ALIGAIFLHYRNNGPLTIS SEGGLASLLCKDSRGVPLL |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 22979 | 53347 | A | 23113 | 3 | 1653 | PQRIQRGVPTRGEEVAPGRRQE EEREQERGAERPDPCCVLSGGK GRGNRPLREAPGGEGVSQVPA AAPLPRFHERKVFFFQTLPPAR ALRAQPPEPSEAPSPSSGETR AAMPGGCSRGPAAAGDGRRLRLA RLALVLLGWVSSSSPTSSASSFS SSAPFLASAVSAQPPLPDQCPAL /CACRSEAARTVKCV\NRNLTE VPTDLPAYVRNLFLTGNQLAVL PAGAFARRPPLAELAALNLSGS RLDEVRAAGAFEHLPSLRQLDLS HNPLADLSPFAFGSNASVSAPS PLVELILNHIVPPEDERQNRSE GMVVAALLAGRALQGLRRLEL ASNHFLYLPRDVLALQPLSRHL DLSNNSLVSLTYVSFRNLTHLE SLHLEDNALKVLHNGTLAELQ GLPHIRVFLDNNPWVCDCHMA DMVTWLKETEVVQGKDRLTC AYPEKMRNRVLELNSADLDC DPILPSSLQTSYVFLGIVLALIGA IFLLVLYLNRKGKKWMHNIRD ACRDHMEGYHYRYEINADPRL TNLSSNSGCLEEIEDRPTTLH |
| 22980 | 53348 | A | 23114 | 288 | 877 | ASRLSLPTRTSMRSSSSTSPSSSS SSSLCRFLNLSRVTDAAFNFL VWYYCTLTIRESILINNGSRWG RAGPEGGEHGMGCQGPSGKGR EQGAGG*WWVFCSR\KGGW VFHHYVSTFLSGVMLTWPDL MYQKFRNQFLSFSMYQSFVQF LQYYYQSGCLYRLRALGERHT MDLTVGESGVALASGHSPFLPS |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22981 | 53349 | A | 23115 | 1 | 1273 | MAPLHSILGNRVGLCQASVRA CPGATVSSQCRASLRSRLAWRG SELPANRGRTWPGPGGLRLQA APRLAYLGRATLLVLTPLYDLP PNVRFTSMASPHTYFLVLGAPI FLLLRSTWSYYHACRFEYATPN DRNTTYLAISGPTRRTYDVATF AYKDEYEKFKLYLTHILILISFTC RFLNSRVTDAAFNFLLVWYY CTLTIRESILINNGSRPDGLMYQ KFRNQFLSFSMYQSFVQFLAQY YYQSGCLYRLRALG\ERHTM\D LTVEGFQSWMWRLTFLLPFL FLW/YNSGQLFNALTLEKPGPR DPQLQGVGRCLCCGFPFLALFL GNFFTTLRVVHHKFHSQRHGS KKDLRLGLSPCRPRRGFLVPVC FWEGDWEGAPSSVRVSGGLFY SPLGFMGRCGPGKEDPGPSCPQ |
| 22982 | 53350 | A | 23116 | 238 | 398 | |
| 22983 | 53351 | A | 23117 | 1 | 386 | |
| 22984 | 53352 | A | 23118 | 13 | 580 | |
| 22985 | 53353 | B | 23119 | 39 | 1171 | |
| 22986 | 53354 | A | 23120 | 381 | 795 | PPSSKAPSSKGPACIVCIYWALI LQSNEVTITDKFNLIKAAAV TVEPFWPSFFAKALASVNIGSLL CNAGVG/SMAPA ACTAQAGGP ATSTTAASASFRNHNPRAPKFR GVLAHEQYLSE RATWVWAPNP NPKSLF |
| 22987 | 53355 | A | 23121 | 1 | 960 | |
| 22988 | 53356 | A | 23122 | 2 | 3952 | |
| 22989 | 53357 | A | 23123 | 1058 | 1494 | KSVRLVVN/YLRTQKAVVRVSP EVPLQNILPVICAKCEVSPEHV LLRDNIAGEELELSKSLNELGIK ELYAWDNRRVPSAVPMQGPWP AEHFLQVNEQPPAGSPSPCPSS SSSSGLRGGMQTANGPACALTP TCAQTDCPCPTSH |
| 22990 | 53358 | A | 23124 | 195 | 398 | TDSSSALQPQHRGRP ALRQRTP PRRSP/SPGLSPPRGASPAS\SGA PARGVAFGGDEPPIGAEAMYSK P |
| 22991 | 53359 | A | 23125 | 2 | 155 | |
| 22992 | 53360 | A | 23126 | 1 | 339 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22993 | 53361 | A | 23127 | 150 | 1017 | LGRWRQDQVPHGLECRSQSEW SCTDSRQHSSSYSDSRREQIGK MRYVSVRDFKGVLDIREYW MDLKRLPRKPRTGEAGSGSLSS PGADTPVEAAVTWRLGLGSVD VGSFRAWQRGKSAAVGHTVSP RWPRWQGGDSSALSMASLSTL TCSWGLRYSALSPTTSAQREEG SALYRHLSPPSLRFYPTVKWAT LAITRPRPPAPRSHSHHPQPRAL CPVWVLFQHPKTHGENLGDRW KEGSALVSSKGTPAKLSSGRIR NALQNTLGEVSVARIQTHRGIF VETTEARL |
| 22994 | 53362 | A | 23128 | 1 | 584 | APIECGGIPSLPVLQCQRANDQE GVRLLPESEAMPKSKELVSSSSS GSDSDSEVDKKLKRKKASLL/P ENPVKK\QKTGETS\RALSSF*TE PASSRDDNMFQIGKMRYVSV\ RDFKGSKA*FDIREYWMDPEGE MKPERKGISLNP\QQWEPSSLKE QISGPLIDASKKTCKISEPILIKPC TVPVVLICLVTVAVCF |
| 22995 | 53363 | A | 23129 | 186 | 687 | LLWARGLGRAKSAVPTVSTML GLPWKGGLSWALLLLLLGSQIL LIYAWHFHEQRDCDEHNVMAR YLPATVEFAVHTFNQQSKDYY AYRLGHIFNSWKEQVESKTV\F SMELLGRTRVWEYLKTTIDNC HFQESTELNNTFTCFFTISTRPW MTQFSLLNKTCLGEGH |
| 22996 | 53364 | A | 23130 | 232 | 402 | LFKAWECCFLIFLQVVITRLKLD KDRKKILERKAKSRQVGKEKG KYKEETNEKMQE |
| 22997 | 53365 | A | 23131 | 637 | 758 | NVEEKNRKKILERKAKSCQIK KEKGEYKEETIGTMRECGL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 22998 | 53366 | A | 23132 | 1 | 1095 | IVFLLYLETCLEVMDDKPNPEA LSDSSERLFSFGVIADVQFADLE DGFNFQGTTRRRYYRHSLHLQ GAIEDWNNNESSMPCCVLQLGDI IDGYNAQYNASKKSLELVWQ FKRRKGPVHHTWGNHEFYNFS REYLTHSKLNTKFLEDQIVHHP ETMPSEDDYYAHFVFPKFWFI LLDAYDLS/ALGAWDQSSPKYG GSVWKILEGSHNP\NTGNWNSS SRDFSEA/RSLFQFNGRVSAQE LNWLNEVLTFSDTNQEKVVIVS HLPALYPGPPFDNVCLAWNYRD ALAVIWSHECV\GVSLLGHTHD GGYSEDPFGVYHG\NLEGVIET APDSQRFGTVHVYPDKMMLKG RGRVPDRIYELQGKEEPHC |
| 22999 | 53367 | C | 23133 | 235 | 382 | |
| 23000 | 53368 | B | 23134 | 63 | 293 | |
| 23001 | 53369 | A | 23135 | 160 | 330 | |
| 23002 | 53370 | B | 23136 | 1 | 870 | |
| 23003 | 53371 | A | 23137 | 2 | 1013 | |
| 23004 | 53372 | A | 23138 | 1 | 1552 | |
| 23005 | 53373 | B | 23139 | 120 | 1034 | |
| 23006 | 53374 | A | 23140 | 1 | 584 | RTRGRRSLAFLLLAERGAAAA VLWSGCRRFRARLGCLPGGLR VLVQTGHRSLTSCIDPSMGLNE EQKEFQNAAFDFAAREMAPNM AEWDQKELFPVDVMRKAAQL GFGGVYIQTDVGGSGHVRLDT SVIFEALA/TGCTSTTAY\IRHPQ CPQSQHSFVQEGGTHYKAGHL CCRQWGPRACLPPGRPCHRG |
| 23007 | 53375 | A | 23141 | 2 | 412 | |
| 23008 | 53376 | A | 23142 | 47 | 487 | |
| 23009 | 53377 | A | 23143 | 77 | 459 | GWKGIEHTLGRCLAEAGGVINY RMLLSWRRWLVAHPVF*SFSCE VGPVGQS*RTMMLHCRHSDPV AKRLSCRRGDFASVVVLCPPQ RLRTLKHFLFFGGGLPLSIDFVMT VDFCCHLHLTDFSSNFGF |
| 23010 | 53378 | A | 23144 | 1 | 304 | KVAGSPSPTPAGQQVLDVNSCL DSSVLDSSFLTFSGLHAE/AEGS TGGPAALAYLGLKTLCTSQQAF AGQMKSDLFLDDSKSDLEEW ELRKEGAPRSRDRE |
| 23011 | 53379 | A | 23145 | 1 | 207 | |
| 23012 | 53380 | A | 23146 | 1 | 3009 | |
| 23013 | 53381 | A | 23147 | 3 | 298 | |
| 23014 | 53382 | A | 23148 | 1 | 636 | |
| 23015 | 53383 | A | 23149 | 1 | 795 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23016 | 53384 | A | 23150 | 125 | 1527 | SSPRQQTQLARVHP/DGRAQ/LA PSCLPGLGLCPLPVCPPVCNCPA CPCHEHCGEAP*GVA\AKRGAL RVHHPHSCGGPRAMTVTLHGQ DVLMLPGDLVGLQHDAGPGAL LHCSPAPGHGPGQAPYLSANAS SWLPHLPAQLKGTWACPACAL RLLAATEQLTVLLGLRPNLGLR LPGRYEVRAEVANGVSRHNLS CSFDVVSPPVAGLRVIYPAPRDG RLYVPTNGSALVLQVDSGANA TATARWPGGSVSARFENVCPA LVATFVPGCPWETNDTLFSVVA LPWLSEGEHVVDVVVENSASR ANLSLRVTAEEPICGLRATPSPE ARVLQGVLVVLLAGSSGYLVG FKFLESHGSDSGSANSFHCLISQ NEFKTLLPDLTRAPRYSPVVEA GSDMVFRWTINDKQSLTFQNV VFNVIIQSAAVFKLSLSADSAP RPRWRLQSPRVGRSLSPDPGFFG SPGPCQPRLQAFLI |
| 23017 | 53385 | A | 23151 | 648 | 1387 | ASTQSLLAWCPA WLSIPSTWPS SFSSGCPG/CKAQPVEVSRSSY VYLEGRCLNCSSGSKRGGYTFT LTVLGRSGEEEGCASIPLSPNRP PLGGSCRLFPLGAVHALTTKVH FECMGWHDADAGAPLVYAL LLQRCRQGHCEEFCVYKGSLSG YGAVLPPGFRPQFEVGLAVVV QDQLGAAVVALNRS LAITLPEP NGSAMGLTVWLHGLTASVLP LLRQADPQLVIEYSLALVTVLN ETYTESL |
| 23018 | 53386 | A | 23152 | 2 | 654 | DKHIWLSIWDRPPRSCFTRIQRA TCCVLLICLFLGANAVWYGAV GDSAYSTGHVSRLSPLSVDTV AVGLVSSVVVYPVYLAILFLFW MSRSKVAGSPSPTPAGQQVLDI DSCLDSSVLDSSFLTFSGLHAEV INTLADHQHRTDFGGSPSVLII TVSLRSYKFAISLCTTYLVVINT LADHRHRTDFGGSPWLLIITV FLRSYKFAISLCTTYLC |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23019 | 53387 | A | 23153 | 2 | 4072 | SRDPAGSYHLNLSSHFRWSALQ VSVGLYTSQCQYFSEEDMVWR TEGLLPLEETSPRQAVCLTRHL TAFGASLFVPPSHVRFVFEPTA DVNYIVMLTCAVCLVTYMM AAILHKLDQLDASRGRAIPFCG QRGRFKYEILVKTGWGRSGT TAHVGMILYGVDSRSGHRHLD GDRAFHRLNSLDIFRIATPHSLG SVWKIRV\WHDNKGLSLALGFL Q\HVIVRDLQTA\QSTFFLVNDW LSVETEANGGLVEKE |
| 23020 | 53388 | A | 23154 | 1 | 10922 | MPPAAPARLALALGLGLWLGA LAGGPGRGCGPCEPPCLCGPAP GAACRVNCSGRGLRTLGPALRI PADATALTAMAKADGDVKKY GSKRGALALTHGHSLLRDVSH NLLRALDVGLLANLSALAELDI SNNKISTLEEGIFANLNLSEINL SGNPFECDCGLAWLPRWAEQ QVRVVQPEAATCAGPGSLAGQ PLLGIPLLDSGCATLVGPHGPL ASGQLAAFHIAAPLVTATRWD FGDGSAEVDAAAGPAAS |
| 23021 | 53389 | A | 23155 | 3887 | 14184 | HVLCWVVTYMMVMAAILHKLD QLDASRGCAIPFCGQRGRFKYE ILVKTGWGRSGTTAHVGIHA VWGGQPERPPAPGTATEPSTAT VWDIFQIRHPAQPGVACWKIRV FGTTTKGSALPRFPCSTSSSGTC RRHAAPSSWSMTGFRWRRRPT GAWWRRRCWPRVRPRSVFPLR HAALLRFRLLGAELQRGFFDK HIWLSIWDRPPRSYFTHIQRATC CVLLICLFLGANAVWYGAVGD SAYSTGRVSRLNPLSVY |
| 23022 | 53390 | A | 23156 | 1 | 442 | GGASGMGGITASTVNQ\SLLS LVLEVDP\NIQAVRTQEKEQIK\ TLNNKFASFIDKVRFLEQQNKM LETKWSLLQQKTARSNMDN MFESYINNLRRLQETLGQEKLK LEAEFTTWGPPLPMPPATKQFN CFFFLVQNKTSASSANVK |
| 23023 | 53391 | A | 23157 | 1 | 497 | |
| 23024 | 53392 | C | 23158 | 208 | 422 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23025 | 53393 | A | 23159 | 81 | 1339 | ELSSPRSSFSAPSRISAWFGPPAS TPASTMSIRGTQKSYKGSTSGP RAFKQAAS*QRSGPGFRISSSSF SRVGSSNFRGGLG\GGYGGASG \MGGITAVTVNQ/SRALLSPLVL EVDPNIAVVRTQEKEQIKTLNN KFAS\FI\DEVGFLQNNKMLGT KWSLLDQKTA\RSNM\DNMF\ ESYINNLRRLQLETLAQEKLKLE AELGNMQGLVEDFKNNYED\EI NKSTETENEFLIKKDVDEAYI NELYEEEIRELQSQISDTSVVLISI DNSRSLDTSIIAEVKTEISEMN RNISWLQAETEGKGGRLSLEA GIADAEQRRELVIKDANAKLSE LEAALQQTKKLLE\MENMSIHT KTTSGYAGGVSLAYGGLTGSG LSYGLSSSSRSGAGSSSFRTSSST RAMVVKKIKTRDGKLLTSLR |
| 23026 | 53394 | A | 23160 | 1 | 651 | MTAFNSGKVDIVAINDPFIDLN YVMVFLYDSTHGKFHGTVK AENGLVINGNPITIFQDQDPS KIKWAP/LAKVIHDNFGIIEGFM TTVHTITATQTINGPSGKLSRDG CRALQDIIPVSTGAAPVGVKVIP ELNGKLTGMAFHVPTANVSVA DLTCRLEKPA/KYDDIKK\NTHS STFDAGAAIVLKDHSVKLISWY DNEFGYSNRVVHLMAHNASKE |
| 23027 | 53395 | B | 23161 | 1 | 382 | |
| 23028 | 53396 | A | 23162 | 3 | 1151 | ASAHASAVRQSAAIFFCVASRA HIAETPLGKVKVGNGFGRIGR LVTRAAFNKGKVDIVAINDPFID LNYMVYMFQYDSTHGKFHGT\ VKAENGKLVINGNPITIFQE\RD PSKIKWG\DAGAEYRRGSPLGV FNQPWRKAGGSICKGGSQKGSS ISAPSAECPPCFVMGCEPMKKY DKQAFK\ISN\ASCTNQLL*HPL AKG*FHDNFGNSLEGLHDHKS MAITANPRKTVD\GPSRGKLWP LMGRGAL\QNIIPASTG\AAKAV GKVIPELNGKLTGMAFRVPTAN VSVVDLTCRLEKPAKYDDIKK VVKQASEGPLKGILGYTEHQV VSSDFNSDTHSSTFDAGA\GIAL\ NDHFVKLISWY\DNEFGYSNRV VDLMAHMGFQGS |
| 23029 | 53397 | A | 23163 | 160 | 236 | |
| 23030 | 53398 | A | 23164 | 931 | 1124 | |
| 23031 | 53399 | A | 23165 | 132 | 303 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23032 | 53400 | A | 23166 | 20 | 171 | |
| 23033 | 53401 | A | 23167 | 1008 | 1262 | HELQCSLLPVRHATAGHTNGQ NRLHWGHVAHSNYGAALKTN GVEVR*FTAAIARCDGNPYESF RKDVRADFQTRIDAIVRCLPK |
| 23034 | 53402 | A | 23168 | 732 | 1162 | RCHEKGRKGHQAPTGSTRPDG TLSACRSCQQGQGMASAGVP ARQMGSTGNLPHLV*PYFLGLS SKAQHTG*LHKKR |
| 23035 | 53403 | A | 23169 | 2 | 1093 | |
| 23036 | 53404 | A | 23170 | 236 | 496 | |
| 23037 | 53405 | B | 23171 | 22 | 3084 | |
| 23038 | 53406 | A | 23172 | 305 | 522 | LRDGRGSMSSSSPNSASGSAICP ASSVMPETVSVSRVMPNVTKP A/MTAKQTRIRNQMVAITIES DAWNRSYQ |
| 23039 | 53407 | A | 23173 | 177 | 386 | |
| 23040 | 53408 | A | 23174 | 3 | 200 | GAVAPMHPLAHPVPGAAAQPP PA*QPATPCHQPA*GQPAPPDV PGEPSAGRSLHHAHICLAPNEQ |
| 23041 | 53409 | A | 23175 | 171 | 535 | |
| 23042 | 53410 | A | 23176 | 190 | 505 | VPTDRIRTRLTSVCKRRCEVHQ LEDRPFVEYQVA/PRRD*SFETS VWNHMRKQ/PPLDVRQLAS*N VLHRQLDIMDSAVASMYSIHLS IKMGIGFSGVTTVVKGTPK |
| 23043 | 53411 | A | 23177 | 349 | 1272 | |
| 23044 | 53412 | A | 23178 | 518 | 1451 | VSSSIIMFGPLSQFPRQQVGSSV KRPSNVVCPGLMFSFFSSAA*IP **PLI*QPGV |
| 23045 | 53413 | A | 23179 | 2436 | 2894 | TSPDVLRAGRVPSVQGTSPSQ SCPGQRPHGPNASKAYGR/LSVM AQYYCNVIPVLE/VPPSAFTPPP KVDSAVV/RLVPHATMPHPVK DVRVLSRITTEAFNQRRKTIRNS LGNLFSVEVLTGMGIDPAMRA ENISVAQYQCMANYLAENAPL |
| 23046 | 53414 | A | 23180 | 1846 | 2557 | IPVSERQGSDFRFFSVYVVNKA GGLIYQLDSYAPTGLRLEKTFIS YPLDLLLKLHDERVLVAFGQR GRHPEWGHAVLAINGMDVNG RYTADGKKVLEYLGVPANYP VSYLFAQPR\TSNDKMLAL MFHSLFAIGSQACLPEQGKPPQ IENAWKTDTFKLHCYQTLTGI KFVVLADPRQAGIDSLRKIYEI YSDFALKNPFFSLEMPIRCELF QNLKLALEVAEKAGTFGPGS |
| 23047 | 53415 | C | 23181 | 34 | 225 | |
| 23048 | 53416 | B | 23182 | 105 | 381 | |
| 23049 | 53417 | A | 23183 | 1 | 837 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23050 | 53418 | A | 23184 | 3 | 744 | HEASCRSERRRRQMADFDTYDD RAYSSFGGGRGSRGS\AGGHGS RSQKELPTEPPYTAYVGNLPF\N TVQGDIDAIFKDLIRSVR\LVR DKVTGKFK\GFCYVEFDEV\DSL K\EALTYD\GALLGDRSL\RVDF AKGRKTKIRVAFGF\RKGGPDD R\GFRDDF\LGGRGGS\RPGD\RR TGPPMGSR\FRD\GPPLRG\SN\MM DFREPTEEERAQRPRIQ\LKPRT VWRPLNQVANPNSAIFGGARPR EEVVQKEQE |
| 23051 | 53419 | C | 23185 | 1 | 1038 | |
| 23052 | 53420 | A | 23186 | 1 | 1486 | MGRNQSRKAENSKHESTYSP KDHSSSQAMEQSWTENGFEKL GFRRKEALYYLDLTASCQSQEL FQLYAGMSVVGTSMPVQAVCP YCGNRIITVTTFPVPGALTWLLC TTLFLFGYVLGCCFLAFCIRSLM DVKHSCPVCQRELFFYYHRLRQ MELASSARTVVAPSRPCAGREG RGDANGKNSSPTAGSAMSSEPP PPPQPPTHQA\GVGLLDTPRSRE RSPSP\LRGNVVP\SP\LPTRRT FS\ATVR\ASQGPVYKGV\CKCF CRSKG/HIGFNYPAGWAGPDIF PGTSLDVGRGSY\VPSGKGDEV TLLKCAPIPTPKNEKLAGPWEV VHHSPWHPGT\KHET\WSG\HVI SFLGGLVESTPLSLCFVGDFA RRQQTLEDDILPHETGLQRGNG PSQVSPGGKGYGGAGVGCVF PAISTAYGPLQQLHHLKSIKSH LKRRGAHWWLSGGSNPIPGSGS RVGISSQLAQTHGLNPQNPS SSWSWRPQIPRSGPLAA |
| 23053 | 53421 | A | 23187 | 2 | 617 | |
| 23054 | 53422 | A | 23188 | 1 | 993 | |
| 23055 | 53423 | A | 23189 | 779 | 1210 | AAAGSEAGRRRGADPTRGPHV LPGSRQRRP/PIFPSLDLSGFFLF CSEFCPEIKSTNPGISIGDVAKE KKKLGEWNSLNDSEKQPYFT KAAKLKEKYEKDVADYKSKG KFDGAKGPAKVARKKVEEED EQQEEEEEEEEEEEEDE |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23056 | 53424 | A | 23190 | 116 | 522 | KAPYSTNSLSLPPFPILFMGSGY RKGPTFQEPKPLPGAAARGPGC DPTQPPRHSAPRDHGPP\SPRCS PRPARPRASPAWLPPRAPTPPSP PAPAAAPRSCRGHARASSGRSG TTATPRRRRGGLWNQSPMDIK G |
| 23057 | 53425 | A | 23191 | 1 | 152 | |
| 23058 | 53426 | A | 23192 | 1 | 676 | MWSAGRGGAAWPVLLGLLLA LLVPGGGAAKTGAELVTCGSV LKLLNTHHRVRLHS\HDITYGS GSGQQ\SVTGVEASDDANSYW RIRGGSEGCGPRGSPVRCGQAV RLTHVLTGKNLHTHHFPSPLSN NQE\VSAFGE\EGEGDDPGTLW TVRCSGTA/HWEREAAVRFQH VGTFVFLSVTGEQYGSPIRGQH EVHGMPQCQ\QHNTWKAMEGI FIKPSVEPSAGHDEL |
| 23059 | 53427 | A | 23193 | 1 | 1044 | |
| 23060 | 53428 | A | 23194 | 1 | 1083 | MTATLAAAADIATMVSGSSGL AAARLLSR\SFLLPHNGIRHCAY TA\SLRQHLYVDKNTKIICQGFT GKQG/TPFHSQQALEYGTKLVG GTPGKGGQTHLGLPVFNTVK EAKEQTGATG\SVIYVPPPFAAA AINEAIE\AEIPLVVC\YPRGIPQP GLGHSSSHKTCGPGKDKAYWG PNCPGV\INPGECKIGIMPG/HIF HKKGRIGIVSTSGTLTYEAGH/Q TTQKLGLGQSLCVGIGDPAFN GTDID\CLEILFERFLPQEGII G\EIGGNA\EENAAEILEPLYSGS KF/ARPVVS\FIAGLTAPPGRRN GVMPGAIISGREKVGAKRERSS ALQSAGVVV\SMSPCTAGEPRF YKEFEKREDRL |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23061 | 53429 | A | 23195 | 1173 | 2110 | FFTELEETILKFIWNQKRACISK ARVNTNDKSGGITLPDFKLYNE AIVAKTTWYWKSRHIDQEK REEKKE*KKDPSVPETLKKKQR NFTELKIQCLSKKFAQKMLQTA RRKLIYEKVKHCHKEYRKMYR TEIRMARMATKAGNFYVPAEP KLAFFVIRJRGINGVSPKVRKVLQ LFLLYQIFNGAFVKLNKASINM LRIVEPYIA/WRYPNLKSVNELI YKCGYGKINKK*IALTDNALTA RSLGKYGIICREDLIHEIYTVGK CFKEANNFLWPF/K/LSSPRGGM KKKTTHFVEGGDAGKREVQIN RLIRRMN |
| 23062 | 53430 | A | 23196 | 3 | 571 | GTMEGVEEKKKEVPAVPETLK KKRRNFAELKIKRLRKKFAQK MLRKARRKLIYEKAKHYHKEY RQMYRTIIRMARMARKAGN FYVPARTQIWRVFVIRGINGS EPQRFKVLQLLRPFVKIFNG/T PFVKLQQGFRFNMLRDCRSHIL AWGYPNLKSVNELIYKRGYG QNQFDLHFPTEKRSHPGSQ |
| 23063 | 53431 | A | 23197 | 2 | 340 | PRVRPRVRDSKMASVGEVSGP QYPVKDKKLL\EVQTGGSFPSW VLMRGPPSPSGIFG\AFQRGLLR GTYNKYINVKKGSDLGGFTMV LACYVLFYSYSFSYKHLKHER\ LRKYH |
| 23064 | 53432 | A | 23198 | 2 | 48 | PRVRLRC*MVDEYCGCEW GK* LNGGRVLWM |
| 23065 | 53433 | A | 23199 | 123 | 693 | QACIMREYKLVLGSGGVGKS ALTVQFVQGIFVEKYDPTIEDS YRKQVEVDAQQCMLLEIDTAG TEQFTAMRDLYMKNQGQFALV YSITAQSTFNDLQDLREQILRV KDTDDVPMILVGNKCDLEDER VVGKEQGQNLARQWNNCAFL ESSAKSKIYVNEIFYDLVRQINR KTPVPG\KAPQKSPSCQLL |
| 23066 | 53434 | A | 23200 | 461 | 1422 | SPHGEPLLQQRREMVGWSLH TESPLGQWGSQILKLQNDLL |
| 23067 | 53435 | A | 23201 | 232 | 331 | TPL*KWLRGVMATVTVTPQTG IIAIPDPHHEWGSGTGYPRLPA |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23068 | 53436 | A | 23202 | 5 | 1223 | GLDSGPESGLRAQPGLLAGKRK MSVLRRMMRVSNRSLAFIFFF SLSSSCLYFIYVAPGIANTYLFM VQARGIMLRENVKTIGHMIRLY TNKNSTLNGTDYPEGNNSSDYL VQTTTYLPENFTYSPYLPCEKL PYMRGFLNVNVSEVSFDEIHL FSKDLIDIEPGGHWRPKDCKPR WKVAVLIPFRNRHEHLPIFFLHL IPMLQKQRLEFAFYVVEQTGTQ PFNRAMLFNVGFEAMKDSV WDCVIFHDVDHLPENDRNYYG CGEMPRHFAAKLDKMYILPY KEFFGGVSGLTVEQFRKINGFP NAFWG\WGGEDDLWNRVH YAGY\NV\TRPEGDLGKYKSIPH HHRGEVQFLGRYKLLRYSKER QYIDGLNNLIYRPKILVDRLYT NISVNLMPELAPIEDY |
| 23069 | 53437 | A | 23203 | 78 | 495 | CTFEKAPPFQLGRGRMVPAKK GGEKKTGR\AINEVVTREYTINI HKRIHGVGFKKRAPWALKEIR KFAMKEMGTPDVRIDTRLNKA VWAKGIRNVLYRIHVRLSRKR NEDESPNKLYTLVTYVTVTTF KNLQTVNVNVDEN |
| 23070 | 53438 | A | 23204 | 138 | 360 | KNQKRQLSGGHCADQTSVLVA RLAPLFPPTMSDKPDMAEIEKF DKSKLKKTTETQKNPLPSKETT EQEKQAGKS |
| 23071 | 53439 | A | 23205 | 145 | 728 | KRQPTSAMKDPSRSSTSPSINE DVIINGHSHEDDNPF\A\EYMW GKMEGRNFNR\QIGRRELWGR KD\FLNRCFPKE\MLGEEGKEG ALNWWLFPSEILPHQTMGPNP RTSFNDPCLSSDGSFSWEDLVV KS\NLNPNAKEFVPGGEVRKYL SRRGPLLDVAQFPHCEGSIRR LNCKSSLGHCVTLYAIAQSFC |
| 23072 | 53440 | A | 23206 | 530 | 707 | |
| 23073 | 53441 | A | 23207 | 1 | 515 | MDFSKVPPHAAFRAQPPPALT WGLAKGSGRGAGEGGERPDRR R\PAARTGTPAWRPAGRRRLPP RSPPPAPVPVRPALPHVVRPGKE TGKTRRRRHYSRGRPLRGAAA AAAAA\VAQTASPSWAEGGRS GAGGSAESP\AFSSPALPCPEGLL CPSAVPVPSKQSVSEVLAIF |
| 23074 | 53442 | A | 23208 | 3 | 713 | |
| 23075 | 53443 | A | 23209 | 1 | 704 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23076 | 53444 | A | 23210 | 2 | 1631 | GLPRRPTRPPTRSGVSPWP GPH SGVLFPLLHCTGSLSQAVLTQ PSSLSASPG\ASVKLTCTLRSDIN VGSPFIYWYQQKPGSPQFLLR YKSDSDNQQSGVPSRFSGSKD ASANAGILLISGLQSEIVRDDYY CQAWDSSTAHS DTGRCGIVGRP PVRQCWPLLLLGLAMVAHGLL RPMVAPQSGDPDPGASVGSSRS SLRSLWGRLLLQSPQRADPRC WPRGFWSEPQSLCYVFGTGTK VTVLGQPKANPTVTLFPPSSEEL QANKATLVCLISDFYPGAVTVA WKADGSPVKAGVETTKPSKQS NNKYAASSYLSLTPEQWKSHR SYSCQLQWGLGLGASQGGFLY EPVSQCVVFGGGTKLTVLGQP KAAPSVTLFPPSSEELQANKAT LVCLISDFYPGAVTVAWKADSS PVKAGVETTTPSKQSNNKYAA SSYLSLTPEQWKSHRSYSCQKP NHASHGTSRMPVSAPVSGLK CWSGTGDRSALGQMPGPCHGI PDPMQQASDSGQPKAAPLGSL CSKPSSEELSGQQGPHWCVS |
| 23077 | 53445 | A | 23211 | 1 | 959 | VFLLLYL VAMPDPAKSAPAPK KGSKKA VTKAQKKDGKKRRR SRKESYSVYVYKVLKQVHPDT GISSKAMGIMNSFVNDIFERIA GEASRLAHYNKRSTITSREIQT VRLLLP GELAKHAVFIENLLNY RKYL VKSSEKDRNYPCLPGLK SKVDICTPYCLLLPQPRHYPG KDTKEETEDFPNSPPPINREEDK RYTTVMGPCLRQA ALEGELLA CPVMEDQQANWVHEPITFNTF KEIRKSIRENGPASPFTRGLIEVI ADSSDLVASTQKLTPKETPSA PYNDISDLTNQDSWFIGFPPIWN AGETDLSNNKTT |
| 23078 | 53446 | A | 23212 | 3 | 463 | |
| 23079 | 53447 | A | 23213 | 74 | 464 | |
| 23080 | 53448 | A | 23214 | 41 | 490 | |
| 23081 | 53449 | A | 23215 | 2 | 369 | PDPAANAPAAAKPAAAKALPV FLLLLSGGAGPAHPMRAPGC*G ELGYTEQLFQFLQATAQEEGIF EYTDPKLAISAVWTFRDLGVLQ QTPSPAGPRLHLSPTFASLDNQE KLEQFIRQFICS |
| 23082 | 53450 | A | 23216 | 124 | 301 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23083 | 53451 | A | 23217 | 3 | 2426 | PGVLSTATFRESGLSPCSKCLKHP GPRGRLQYSPPTAGQGRLNG AGHPQSTGPVATLSVAEYGTQ GGASGPARIPIGSRGCLLAGRA EASLWSSGFGMKLEAVTPFLG KYRPFVGRCCQTCTPKSWESLF HRSITDLGFCNVILVKEENTRLF SWALLRVLKLLFLNVQLHKGQ MKMVQKAAQQVGQVGTSLWL SPEQGLPLVLLSTHKTLLDGILL PFMLLSQGLGVLRVAWDSRAC SPALRALLRKLGGFLPPEASLS LDSSEGLLARAVVQAVIEQLLV SGQPLLIFLEPPGALGPRLSAL GQAWVGFVVQAVQVGIVPDAL LVPVAVTYDLVPDAPCDIDHAS APLGLWTGALAVLRSLWSRWG CSHRICSRVHLAQPFSLQEYIVS ARSCWGGRTLEQLLQPIVLGQ CTAVPDTEKEQEWTPITGPLLA LKEEDQLLVRRLSCHVLSASVG SSAVMSTAIMATLLLFKHQKG VFLSLLGEFSWLTEEILVRGFD VGFSQQLRSLQLHSLSLRAHV ALLRIRQGDLLVVPQPGPGLTH LAQLSAELLPVFLSEAVGACAV RGLLAGRVPPQGPWELQGILL SQNELYRQILLMLHLLPQDLLL LKPCQSSYCYCQEVLDRLIQCG LLVAEETPGSRPACDTGRQRLS RKLLWKPSGDFTDSDSDDFGE ADGRYFRLSQSHCPDFFLFLC |
| 23084 | 53452 | A | 23218 | 169 | 955 | ASSQLPCSMACCATWAPLKM RWLCSTAWSTSSLSLPPSWSSL QASQPSCCHATSLAPPCAGQCL ARAWPVLSFLCTCALGLLASIA MTFATQGKALLAACTFGSSELL ALAPYCPFDPTRIYSSSLCLWGI ALRCSAWAENVFAVRCAQLTH QLELRP\WWGKKQPTHMMRE NPVELVEG\RDLLSCT\SSE\PLTL CRDDVLPRP\DGQLRTLQATLL CDPGPGLGAGLRGLKWTLLGG P\SGAFQPSSPTTPAHLHLKIETL F |
| 23085 | 53453 | A | 23219 | 1 | 344 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23086 | 53454 | A | 23220 | 214 | 1355 | FCSSWLRLSLADSSLSWKMFVLG LTGGIASGKSSVIQVFQQLGCA VIDVDVTARHVVPQGYPAHRR VEVFGTEVLLLENGDINRKVLGD LIFNQPDRES\LNATHPEIRKE MMKETFKYFLRGYRYVILDIPL LFETKKLLKYMKHTVVVYCDR DTQLARLMRRNSLNRKDAEAR INAQLSLTDKARMARHVDNS GEWSVTKRQVILLHTELESL YLPLRFGVLTGLAAIASLLYLLT HYLLPYAYTASAIPPSGAASRG PGARCSAIRKRAPARPTSAVSP GAPRSPARGLRADRAAGTRNL NATLPPPGPPAPPSPPSPSSITL HVFHQLQPDITRGREGTDFQWE KFPGRVLVADSRRLRCLAPAP TWLV |
| 23087 | 53455 | A | 23221 | 2 | 1231 | TPLFLRKGTADGSARTTVIHLG FTKGKQRCVETQAAAVAGDVG RTAAGGRVGKESGVISDDRPG LPVGQSQPEGGEQEATDTVSVH ATTSSQAWPGGADSKELSSKAE ERETGKDQQTELPLCLPLRDFP DSAPVMSSDSGHATESLHLASS DSKPPMPTPNEGPGSTVGHAGP PRTVKADLCTEPQLALRGLQVS LPLRLHLVGVIYAEHQASGLEGC GHAGSCSPDGSPRAPGATLCLS KPLSFRTKRCLPCWLPASAPVGI PGAPVHIPGAPVCIPGAPACISN APVHIPGAPVGIPGAPVCIPGAA VCVPNTPMCIPSAPMCIPNTPVC IPNTPVCIPNTPVCIPGAAVCILG A/PRAHPWCSSCVHPGAPECYL GCGLTQADRLEPAVLDAQLQE PLFALCGQALPS |
| 23088 | 53456 | A | 23222 | 2 | 408 | |
| 23089 | 53457 | A | 23223 | 62 | 251 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23090 | 53458 | A | 23224 | 2111 | 3003 | TQKAICMCLGLCKKIHLLSLQ CLISQIKMIMGAGWQ/SSGFTDE KETSKIKADPEKLKKLQESLLE EDSEEEGDLCRICQIAGGSPSNP LLEPCGCVGSLQFVHQECLKK WLKVKITSGADLGAVKTCMC KQGLLVDLGDFNMIEFYQKHQ QSQIKTEATVVEHKDIYNVTET QLVPEARSVLLVGAGQMLLTG ANRALNSDYSSMRPKVKAQNE LMNSGLYLVLHLLHLYEQRFAEL MRLNHNQVERERVVRVTRVLGG LSPNVSCGVVSGVGSFQWVRG LTDLKNEASDLHAQIPAE |
| 23091 | 53459 | A | 23225 | 1 | 594 | MIAAFNPGKVDVTVTNGPFIDL NYMVYMFHYDPTHGKFHDVP MFVMGMNHHKHNKLTVISNAS CTTNCLDPLAKVIHDNFGIREG LMTTVHSHIATQKTVDGPSRKL WHDHGAQNTIPASTGAAKI KKVVRQA/SQGPKGILGYTEH QVVPLEFKSNTRPSTFEAGAGI AVNDHFVKLISWYGNEFAYSN KVIKPM |
| 23092 | 53460 | A | 23226 | 3 | 232 | |
| 23093 | 53461 | A | 23227 | 1078 | 2221 | QQTLOPAALPCFPPTHPPEVL PTAMNTTSSAAPSLGVEFISLL AIILLSVALAVGLPGNSFVWSI LKRMQKRSVTALMVNLALAD LAVLLTAPFFLHFLAQTWSFG LAGCRLCHYVCGVSMYASVLL ITAMSLDRSLAVARPFVSQKLR TKAMARRVLGIWVLSFLLAT PVLAYRTVVPWKTNMSLCFPR YPSEGHRAFHLIFEAVTGFLLPF LAVVASYSDIGRRLQARRFRS RRTGRLVVLIIITFAAFWLPYH VVNLAEAGRALAGQAAGLGLV GKRLSLARNVLIALAFLSSSVNP VLAYACAGGGLLRSAGVGFFVA KLLEG\TGSEASSTP\RGGS LGQ TV\KSGPAALEPGPSES LTASSP LKL\NELN |
| 23094 | 53462 | A | 23228 | 6125 | 6319 | ASVVPVTSALAMCSPKSGIGDG FAVLRVEDVAQK***KAALGV ASSPAWQQTREREHVQGNSPL |
| 23095 | 53463 | A | 23229 | 1 | 1347 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23096 | 53464 | A | 23230 | 1 | 1124 | MRECISIHVGQAGVQIGNACWE LYCLEHGIQPDGQMPSDKTIGG GDDSFNTFFSETGAGKHVPRAV FVDLEPTVVDEVRTGTYRQLFH PEQLITGKEDAASNYARGHYTI GKEIVDLVLDIRKLFGGGTGS GFASLLMERLSVDYSKSKLEF AIYPAPQVSTAVVEPYNSILTT HTTLEHSDCAFMDNEAIYDIC RRNLDIERPTYTNLNLRLIGQIVS SITASLRFDGALNVDLTEFQTN LVPYPRIHFPLATYAPVISAEGA YHEQLSVAEITNACFEPANQMV KCDPRHGYMACCMLYRQDGV VPKDVNAAIATIKTKRTIQFVD WCPTGFKV*LGDMFAFQQAAD AQNTGTGLEGPHPLGRSLFLHGL |
| 23097 | 53465 | A | 23231 | 1 | 2918 | MDVYCAHESLRHTKSPEATGQ TSGQRPEALQAFWPAFGSSPVT GSSPVEVTTKGRWSSSRQVL WDRIPAKSRPAISNRQSRTNI PWWESCPILNLEREQPPRFAQP GTYASRWKALEEMEKQREQ VDRNIREAKEKLEAEMEAARH EHQLMLMRQDPGLALVSCMQ QGQSMSRSPKKVFKHLYELNL TKLQSLGSRSLRWKDSFPWGE EAGGKRPLVSLALHRSPSLLL LFVPKHPSKGRPDCTVQRS |
| 23098 | 53466 | A | 23232 | 1 | 158 | |
| 23099 | 53467 | A | 23233 | 1 | 414 | LGGLKGTWGETKPAMAAEEEE DGGPEGPNRERGGAGATKTL YTG NHLFS PQWLETRPERQEC VCKAGISREKVVGESLLTFS HFLRLKTPQICRLPV*LFLPP*GF QPF GDTGGFHFSFGVGAFPF GF FNPSY |
| 23100 | 53468 | A | 23234 | 1 | 663 | |
| 23101 | 53469 | A | 23235 | 2 | 667 | SWAGGGFWFVGACVCVFGGTE GYVGRNKTGHGSSRRRRSGAP NVPNRERGGAGRPKTPFECNIC LETARELVLSVLNLYFWTISH QV\LE\TRPE\RQECPVCKAGISR EKVVPLYGRGSQEAPRIPRLKT PPPPPRGQR\PAPE\SRGGF\QPF GDTGGFH\FSFGVGAFPF GFTTV F\NAHEPFRRGTGVDLG\QGH P A\SSWQD\SLLLFLAIFFF\WLL |
| 23102 | 53470 | A | 23236 | 363 | 476 | |
| 23103 | 53471 | B | 23237 | 224 | 364 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23104 | 53472 | A | 23238 | 1 | 1324 | MRQRRAEELSKDKRVRTDGN KCSPSAIGKRKERTNDWIEGD NNQESQGLNCSDTLNRDLGPN TRGFLYAGLSGLDPPSLPTPD MSSEVLEDNLDTLNLSYSGKDSD SVKLLEEYADSESQASLQGRSR CWQHHPHAPLSYPPAASGSQSL LQGKFPSAKPPLLGGYTCTAQR TQWALTKRSLRATRESVSRQQ GVYGLVGRKRTRHHRGVLGLL GIPSARPERPGTGSEAGPTRLPG AAVARRRPARPVGRGLDPAP TAAQTSGPASLPPPPPSYGGDP HQNGYPDPDPAPSASPDLPAA GDTRGSGGRRKKRRTGTARLN TPGRKA\PKQKAAAGRKGRAH QPAPRTPEPQRRRPIRPPNQTD LRHPHRRAGRGGPPGGAGGTA NPSTGANGGAATARTAGART RGARGASERAGRHGSRPASWL TATPPPGT |
| 23105 | 53473 | A | 23239 | 1 | 433 | PTRPSSPEETDGPWDPEGH PLTDPPNAPVLALPPAIPGLSLS MADGSSDAAREPRPAPAPIRRR SSNYRAYATELQDLRQLHAR VDKVDEERYDIEAK\VTKNITEI ADLTQKIFDLRGKFKRPTLRRV RISADAMMQALL |
| 23106 | 53474 | A | 23240 | 2 | 409 | |
| 23107 | 53475 | A | 23241 | 3 | 490 | SSPEETVGPWDPEGH PPNAPVLALPPAIPGLSLIMADG SSDAVRAAG*GVAGTPRARAR EPRPAPAPIRRRSSNYRAYATEP HAKKKSKISASRKLQKLTLLQ IAKQELEREAEERRGEKGRALS TRCQPLELAGLGFAELQDLRQ LHARVDK |
| 23108 | 53476 | A | 23242 | 149 | 846 | VSAWRNGSSDAAREPRPAPAPI RRRSSNYRAYATEPHAKKKSKI S\ASRKLQKLTLLQIAKQELE REAEERRGREGARSLAPRC\QP LELAG\LGFAADLPGLCCRFHA RVVDKVDEERYDIEAKVSKNITE IAN\LTQKIFDLRSKFKRPTLARR VRISADAMMQALLGARAKESL DLRAHLKQVKKEDPEKENREV GDWRKNIDALSGMEGRMKKW RELSLPAYCPCPEEGH |
| 23109 | 53477 | A | 23243 | 1 | 487 | |
| 23110 | 53478 | A | 23244 | 80 | 511 | |

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|------------|--------------------------------|---------|-------------------------------|---|---|---|
| 23111 | 53479 | A | 23245 | 427 | 1417 | KTMWKVEFGVRFISITRLLLEHQ PKQTMYPILPK/PPLWPEEPKTE APKQTPRAPPKPKTSRPRIPQT QPEETDQSTQEPFTTKIPRTTEL AKTTQGLEMLSLIHNPMMHK DSTNEQIAASLQACYEQLLM YIRVTDVDSVGPNGKEAVTA PQAPTLFWLNHKAQLAKDWA GKDVNITPTFATSKKENKPPNN LQICNVSKIHQRAKVAGKPEIK DKHIQKEMPLDAIEASKINLVKI FNEFLKAWKCRLSFEYRIPENQ GHKGSFYLLVGSSRTSWLLTEK IGSSKRVLRMPPMDILKTTQILL SFLWSINLTPRGKNNHLVAPAH |
| 23112 | 53480 | A | 23246 | 3 | 1011 | |
| 23113 | 53481 | A | 23247 | 2 | 334 | PIQSFFLVKKPPLRKGVYLSSK SLSRWFFKVQAN*RSQPQKAFS RLSCHC |
| 23114 | 53482 | A | 23248 | 1 | 642 | |
| 23115 | 53483 | A | 23249 | 854 | 1150 | KEDTNKWKNI PCSWLGRINIVK MAIMPKVNL*IQCHPHQATNDF SSQNWKKTTLKFIWEPKKEPAL PSQS*AKRAKLGGITLPDFQTIT YKATVTKTA |
| 23116 | 53484 | A | 23250 | 1754 | 2393 | PSNRREFGESWPETQAPGALRP LLPAPGTPRARERPAWPAPRM EVYIPSFYEEEDLERGYTVFKI EVLMMNGRKHVFVEKRYSEFHAL HKKLKKCIKTPEIPSKHVRNWV PKVLEQRRQGLETYLQAVILE NEELPKLFLDFLNVRHLPSPK AESCFSDETESEESSKLSHQPV LLFLRDPYVLPAAADFNPVIE GVLHGIFYPHLQPR |
| 23117 | 53485 | A | 23251 | 1 | 265 | AGNRLRFQLELEFVQCLANPNY LN/WYPQCLHMLELLQYEHFR KELVNAQCAKFIDEQQILHWQ HYSRKRMRLLQQA\AKQQQQN NTSGK |
| 23118 | 53486 | A | 23252 | 1 | 987 | |
| 23119 | 53487 | A | 23253 | 1 | 491 | RGFRNFARVSGLLLCQAGGVL VSSFVMAAAVAMETDDAGNR LRFQLELEFVQCYANHNTLIFLP QR\GYF\KD KAFVNYLKYLLYW \KDPEYAKYLKYPQCLHMLGA APNMEHFRKEAGWNAQC\AKF IGWNRQVSTLGKHYSRKRMR LQQALAEQQQQNNTSGK |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23120 | 53488 | A | 23254 | 73 | 355 | HEGQVHVLLASAHVDVAIVLG AGSMVEGEARPEQAAQHHQGI APLHLDA PGPSWTQSRSPRNRA NQNHTCSEAT*SHPEQLPQTLW ECHAPRSP |
| 23121 | 53489 | B | 23255 | 1 | 441 | |
| 23122 | 53490 | A | 23256 | 528 | 698 | HGQRFLHGVPV/H/HHSHYDN/PH HSLHHHRCLHHCHLHHHRHHL HHHPLHCYHHHPGQNG |
| 23123 | 53491 | A | 23257 | 1 | 403 | |
| 23124 | 53492 | A | 23258 | 509 | 4547 | LYLTTSRREEHLKSLVVETQDL ASPVLRSVSICTKVEEAFRQAH VIVVLDDSTNKEVFTLEDCLRS RVPLCRLYGYLIEKNAHESVRV IVGGRTFVNLKTVLLMRYAPRI AHNIIAVALGVEGEAKAILARK LKTAPSYIKDVIIWGNISGNNYV DLRKTRVYRYESA IWGPLHYSR PVLNLI FDSEWVKREFVAILKN LTTTGRQFGGILAAHSIATTLKY WYHGSPPG EIVSLGILSEGQFGI PKGIVFSMPV |
| 23125 | 53493 | A | 23259 | 56 | 290 | |
| 23126 | 53494 | A | 23260 | 468 | 993 | VLLACFWPGSDFWPRSRRKTY GTAPQSCYSFYVALDCGGVSRL VIFVSWRNPQVAP TSAHQNRPS RNPVSRPPNTQRVARRKHYAL ADGYTERRWTNAPCRAESSFPP NCPSAAPI DSYDK*PSRATLFT SHLTVEAFPVWSYLYPGETPRL HPRAHTRTVPAAIRYPDRQTPN GLRGANTMHSQMDTLNGDGR THLAGQRARSPTARPQRQYRI HTTSDLPGLVRKYASGCCLRW YCCAWIERALSLQVGGGVFGD PLSEGQAEC DHGST |
| 23127 | 53495 | A | 23261 | 1 | 3114 | |
| 23128 | 53496 | A | 23262 | 3 | 401 | TSSL SLSGKSGRYIVFLRRSVGI QSPSAVATVRLLLAGSDRRFAA GSAGCAVLSRAERS*EPGCCYR IRRS AFRLRAGSIGNRDKPVAW PDTGSGDNTEVYFRAHQAGILP DTVLAGPAQRVA VSGGTPVDW |
| 23129 | 53497 | A | 23263 | 2874 | 3062 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23130 | 53498 | A | 23264 | 2766 | 3323 | MPDLVEGREKSDKGAQPQPR QSRARTNGSGVRILHSLWRIIG IPLLLGYSLVCSRVLACFWPG SDFWPRSRRTYGTAPQSCYSF YVALDCGGVSRLVIFVSWRNP QVAPSAHQNRPSRNPVSRPPN TQRVARRKHYALADGYTERR WTDAPCRAESSFPPNCPL*RQY RIHIVDASVCGP |
| 23131 | 53499 | A | 23265 | 968 | 1440 | |
| 23132 | 53500 | A | 23266 | 3 | 640 | LSVVRRIHMGVGVGVGCPVR YRNQDDHELQITHGNKILCGIV CDKGAQPQPRQSRARTNGSG VRILHSLWRIIGIPLLLGYSLVCS RVLLACFWPGSDFWPRSRRTY YGTVPQSCYSFYVALDCGGVS RLVIFVSWRNPQVAPSAHQNR PRRNPVSRPPNTQRVARRKHYA PADGYTERRWTIAPCRAESSFP PNCPSAAPIPDSYDK |
| 23133 | 53501 | A | 23267 | 1 | 3140 | MVYKMRYRSQHPYSIKEKQMK SEVLSVKEKIGYGMGDAASHII FDNVMLYMMFFYTDFGIPAGF VGTMFLVARALDAISDPCMGL LADRTRSRWGKFRPWVLFAL PFGIVCVLAYSTPDLSMNGKMI YAAITYTLLTLLYTVVNIPYCA LGGVITNDPTQRISLQSWRFVL ATAGGMLSTVLMPLVNLIGG DNKPLGFQGDLSPMFSTPEEIA RPGPYENDVHVVGASSLAAGH KTLIPELVRSAEQHMGR |
| 23134 | 53502 | A | 23268 | 750 | 1340 | ILHAPAPPFSASASHEQPEWSD KGAQPQPRQSRARTNGSGVR ILHSLWRIIGIPLLLGYSLVCSR VLLACFWPGSDFWPRSRRTYGT APQSCYSFYVALDCGGVSRLV IFVSWRNPQVAPSAHQNRPSR NPVSRPPNTQRVARRKHYALA DGYTERRWTNAPCRAESSFPPN CPFAAPIPDSYDK*PFRIVS |
| 23135 | 53503 | A | 23269 | 93 | 699 | RASVQQKKLSTDDKGAQPQPR TQSRARTNGSGVRILHSLWRII GIPLLLGYSLVCSRVLACFWP GSDFWPRSRRTYGTAPQSCYS FYVALDCGGVSRVRSYLYPGET PRVAPSAHQNRPSRKPG\TRPP NTQRVARRKHYALADGYTER\ SATNAPCRAESSFPPELPVPQVP NTGFIRQVTFRDCFVNTPQAAA SGFW |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23136 | 53504 | A | 23270 | 1000 | 1530 | QRYSDNPPNDKGAQPQPRTQSR SARTNGSGVRILHSLWRIIGIPL LLGYSLVCSRVLACFWPGSDF WPRSRRKTYGTAPQSCYSFYV ALDCGGVSRLVIFVSWRNPQV AP TSAHQNRPSRNPVSRPPNTQ RVARRKHYALADGYTERRWT NAPCRA/VEFPFPNCPWEAQYRI |
| 23137 | 53505 | A | 23271 | 242 | 711 | LKQKRDKEKDRSSRVSAVLLIK/ HRRPLPLPIGLKACHCSCTAKC LGGCESPRKGGQLLIFEGHVKI DLEIFTKSLWLTRQLIVKKETEK AVKHASNICIMRTGLTFQSHKIE DGLFGLLVIAATEAWSYVCQST NPVDVYPLTAVPACCIISASDVP |
| 23138 | 53506 | A | 23272 | 2 | 459 | CVNSQIGRGHKITTYPFSPRKS RKGMAQSQGWVKRYIKAFCK GFFVAVPVAVTFLDRVACVAR VEGASMQPSLNPGGSQSSDVVL LNHWKVRNFEVHRGDIVSLVS AKNPEQKIIKRVIALEGDIVRFP *DFCMPMPHISC GPQSAGR NW |
| 23139 | 53507 | A | 23273 | 1 | 474 | |
| 23140 | 53508 | A | 23274 | 358 | 948 | PLTPFSPRKSGRKGMAQSQGW VKRYIKAFCKGFFVAVPVAVTL LDRVACVARVEGASMQPSLNP GGEPV/ASDVVLLNHWKVTEF/ SEVHRGDIVFIG\APKNPEQKIIK RVICSLKGDIFQNHRTQKP\DVK VPRGSHLGLEGDHSWDTVFDS NSFGPVSLGLLHAHATHILWPP ERWQKLESVLPPELPGTERRG MTA |
| 23141 | 53509 | A | 23275 | 90 | 664 | NKYRLQSPPRALWDRASDPP APPEDPETAPAMEEDQELERKI SGLKT\SMVEG\ERKTTLELV\Q AAG\TDRP\CVTFVLHEEDHTLG \NFLRY\MIMKNP/EKVEFCGYT YG/HPSFQRAKLNLPHSRFRGYP FPAVEPISREALNELMNVC\QP CAFTSFRASIKDYKESKSKQEM ESTFLVLLWQFYKGGTVL |
| 23142 | 53510 | C | 23276 | 108 | 320 | |
| 23143 | 53511 | B | 23277 | 446 | 625 | |
| 23144 | 53512 | A | 23278 | 1 | 3042 | |
| 23145 | 53513 | A | 23279 | 1 | 3156 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23146 | 53514 | A | 23280 | 518 | 2076 | QQR*MCQNLMT\QNQRSGR SQNDF*RRRKNISERSAVYR*R QLYIRRQPYAERPS\HVEDKGH KYLVEANTGTENGYQGEESLF NKAYYGGGTNFFRKESQKLQQ SAKKRDAELANGALGIIELNND YTLKKVMKPLITSNTVTDEIER ANVFKMNGKWYLF TDSRGSK MTIDGINSNDIYMLGYVSNLT GPYKPLNKTGLVLQMG LDPND VTFTYSHFAVPQAKGNNVVITS YMTNRGFFEDKKATFAPSFLM NIKGNKTSVVKNSILEQQQLTW LQVAKRAGLGGGQSGRTVLRE RVRIEIASTHIALAVECVSVRV WKVPRLPSRQKYAKHASQLVS NQKSEEEYMKTFNISQQDLEL VEVATEKITMLYEDNKHVGA AIRTKTGEIISAVHIEAYIGRVTV CAEAIAIGSAVSNGQKDFDTIV AVRHPYSDEVDRSIRVIPTYGT DEWEQWWNAFNEENLFCSEE MPSSDDEATADSQHSTPPKKKR KYIYVLVIAITMVMRFWQYING |
| 23147 | 53515 | A | 23281 | 299 | 457 | |
| 23148 | 53516 | A | 23282 | 584 | 1185 | QQR*MCQNLMT\QNQRSGR SQNDF*RRRKNISERSAVYR*R QLYIRRQPYAERPS\HVEDKGH KYLVEANTGTENGYQGEESLF NKAYYGGGTNFFRKESQKLQQ SAKKRDAELANGALGIIELNND YTSEKSNEAADHFKHVPQAKG NNVVITSYMTNRGFFEDKKATF APSFLMNIKGNKTSVVKNSILE QQQLTVN |
| 23149 | 53517 | A | 23283 | 1 | 3618 | |
| 23150 | 53518 | A | 23284 | 191 | 819 | VNVTSFGSRPICSTSPVLFSGL* GPVKEFDT*PSM*ISFELIPSIVIF EPRESVNKYHLPFILKTFARSISS VTVFEVISGFIFFNV*SLFNMI PRAPFANSASRFLALC*SFWLSL RKKFVPPP*YALLNKDSSPW/SS VFCSRVGFEYKVFMAFVFNVV RVSQRMVVAGCIAFIDKLLNV LICFSVSVKNRFVIFHSVDFECV |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23151 | 53519 | A | 23285 | 2 | 2556 | WRKIYQAN/GKTKKAGVAILVS DKTDFKPTKIKRDKEGHYIMVK GSIQQEELTILNIYAPNTGAPRFI KQVLSDLQRDLDSYTHMGDFN TPLSTLDRSMRQKVNKNTQEL NSALHQADLIDIYRTLHPKSTEC TFFSAPHHMYSKIDHIVGCKAL LSKFKRTEIITNCLSDHSAIKLEL RIKKLTQNCSTTWKLNLLND YWVHNEMKAEIKMFFETNENK DTTYQNLWDTFKA VCRGKFIA LNAHKRKQERSKIDTLTSQKE LEKQEQTHSKASRRQEITKVRA ELKEIETQKTLQKINEFRSWFFE RINTIDRPLARLIKKKREKNQID AIKNDKGDITDPTETQTTIREY YKHL YANKLENLEEMDKFLDT YTLPRLNQEEVESLNRPI TGSGI VAIINSLPTKKSPGPDGFTAIFY QRYKEELVPFLKLFQSIEEEGI LPNSFYEASIIIPKLGRDIKKE NFRPISLMNIDAKILNKILAHRI QQHIKKLIHHDQVGFIPGMQG WFDIRKSINVIQHINRTKDKNH MIISIDAEKAFDKIQPFMLKTL NKLVLVLEVLVRAIRQEKEIKCIQL GKEEVKLSLFADDMIVYVENPI VSAQNLLKLISNFSKVSQYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASKSIKYLGIQLTRHVKD LFKDNYKPALNEIKEDTNKWK NIPCSWIGRINIVKELEKTTLNFI |
| 23152 | 53520 | A | 23286 | 1 | 3087 | |
| 23153 | 53521 | A | 23287 | 1 | 741 | MLGKKKPVCEVGGDSGVPKKE FQEGRQVLFKLWRGQANKVG DNSIDSWKNAGR VFKDSDKFD ANDPILKDQTQEWSGSATFTSD GKIRLFYTDYSGKH YGKQSLTT AQVKVSKS/V*HTQNQRSGRSQ NDF*RRRNIS*RSAVYR*RQL YIRRQPYAERPS\HVEDKGHKY LVFEANTGTENGYQGEESLFNK AYYGGGTNFFRKESQKLQQA KKRDAELANGALGIIELNNDYT LKKVVKPLITSN |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23154 | 53522 | A | 23288 | 849 | 1688 | QQRR*MCQNLMTHTQNPQSGR SQNDF*RRRKNISSERSAVYR*R QLYIRRPYAERPS\HVEDKGH KYLVEANTGTENG YQGEESLF NKAYYGGGTNFFRKESQKLQQ SAKKRDAELANGALGHIELNND YTLKKVMKPLITSNTVTDEIER ANVFKMNGKWYLF TDSRGSK MTIDGINSNDIYMLGYVSNLT GPYKPLNKTGLVLQMGLDPND VTFTYSHFAVPQAKGNNVVITS YMTNRGFFEDKKATFAPSFLM NIKGNKTSVVKNSILEPGQLAV |
| 23155 | 53523 | A | 23289 | 1 | 3171 | MVKGSIQQEELTILNIYAPNTG APRFIKQVLSLDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRIEITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLNDYWVHNEMKTEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAYKRKEERSKIDTL TSQLKELEKQEQRHSPRRQE ITKMRAELKEIETQ |
| 23156 | 53524 | A | 23290 | 1 | 3255 | |
| 23157 | 53525 | A | 23291 | 1 | 3924 | |
| 23158 | 53526 | A | 23292 | 1 | 3139 | |
| 23159 | 53527 | A | 23293 | 1 | 3210 | MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEITNCLSDHSAIK LELRIKNLTQNRSTTWKLNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTTHSKASRRQEITKIR AELKEIETQ |
| 23160 | 53528 | B | 23294 | 1 | 3127 | |
| 23161 | 53529 | A | 23295 | 1 | 3325 | |
| 23162 | 53530 | A | 23296 | 1 | 3145 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23163 | 53531 | A | 23297 | 191 | 819 | VNVTSGSRPICSTSPVLFSGL* GPVKEFDT*PSM*ISFELIPSIVIF EPRESVNKYHLPFILKTFARSISS VTVFEVISGFITFFNV*SLFNMI PRAPFANSASRFLALC*SFWLSL RKKFVPPP*YALLNKDSSPW/SS VFCSRVGFEYKVFMAFVFNVV RVSQRMVVAGCIIAFIDKLLNV LICFSVSVKNRVFVHFSVDFECV |
| 23164 | 53532 | A | 23298 | 1 | 3352 | |
| 23165 | 53533 | A | 23299 | 1841 | 2679 | QQR*MCQNLMT\QNQRSGR SQNDF*RRRNISERSAVYR*R QLYIRRPYAERPSHVDEKGH KYLVEANTGTENGYQGEESLF NKAYYGGGTNFFRKESQKLQQ SAKKRDAELANGALGIIELNND YTLKKVMKPLITSNTVTDEIER ANVFKMNGKWYLFDSRGSK MTIDGINSNDIYMLGYVNSLT GPYKPLNKTGLVLQMGDPND VTFTYSHFAVPQAKGNNVVITS YMTNRGFFEDKKATFAPSFLM NIKGNKTSVVKNSILEQGQLTV |
| 23166 | 53534 | A | 23300 | 1207 | 1533 | YVHCKPSGWTVRTFDKPRKRFI AFFIAGILFRAIKNHFLPRETLQ CLPYILTGFRRGQSEYFSFSNM DLADTMFL*GAIRFSDLVNEQ IQHTFLIPGETICRLSEVV |
| 23167 | 53535 | A | 23301 | 1 | 3253 | MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQGDLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKWKRTEIITNYLSDH SAIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQKLELEKQEQTHSKASRRQE ITKIRAELEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK |
| 23168 | 53536 | A | 23302 | 1 | 3095 | |
| 23169 | 53537 | A | 23303 | 2 | 2678 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23170 | 53538 | A | 23304 | 1 | 3335 | MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLS DHS AIKLELRINKLNTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNVYKRKQERSKIDTL TSQLKELEKQEQT HSKASRRQE ITKIRAE LKEIETQ |
| 23171 | 53539 | B | 23305 | 1 | 2293 | |
| 23172 | 53540 | A | 23306 | 1 | 3810 | |
| 23173 | 53541 | A | 23307 | 255 | 1215 | CVGQLAAAKR*RNSS*IQLRSR CVCSCGKPERR**HINLHVLSK GRRQLN/QTAGKTRAVSLKTAI SSTPTIRS*KIRRKNGPVLQPLH LTEKSVYSTLTIPTKAINTLYSK PTREQKTDTKAKNLYLTKRTT AAARTSSVKKARSFSRALKNA MLS*RTAPSVS*S*IMITH*KK** SR/CITSNTVTDEIERANVFKMN GKWYLF TDSRGSKMTIDGINSN DINMLGYVSNSLTGPYKPLNKT GLVLQMGLDPNDVTLTNSHFA VPQAKGNNVVITSYMTNRGFF EDKKATFAPSFLMNIKGNKTSV VKNSILEQQQLTVN |
| 23174 | 53542 | A | 23308 | 1 | 4539 | |
| 23175 | 53543 | A | 23309 | 1 | 3229 | |
| 23176 | 53544 | B | 23310 | 1 | 3552 | |
| 23177 | 53545 | A | 23311 | 1 | 3139 | |
| 23178 | 53546 | A | 23312 | 1 | 3057 | |
| 23179 | 53547 | A | 23313 | 1 | 3215 | MGKKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDEL R EEGFRRSNYSELREDIQTGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELREECRSLRSR CDQLEERVSAMEDEMNMKRE GKFREKRIKRNEQSLQEIW DYV KRPNLRLIGVPESDVENGTKLE NTRLRDIQENFPNLRQANVQIQ EIQRT PQRYSSRRATPRHIVRFT KVEMKEKMLRAAREKDRSTRQ KVNKDTQELNSA |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23180 | 53548 | A | 23314 | 1 | 1921 | MVKGSIQQEELTILNTYAAHTG APRLIKQVLSLDLQRDLDSTIIM GDFNTPLSTLDRSTRQKVNKDT QELKSALHQADLTDIYRTLHHK STEYTFSSAPHHIYSKIDHILGSK ALLSKCKRTEITNYLSDHSAIK LELWIKNLTQNHSTTWELNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYHNLWDTFKAVCRGK FIPLNAHKRKQERSKIDTLTSQ KELEKQEQTNIHASKARRQEITK IRAEKKEIETQKTL*KINESRSW FFERINKIDRLRLARLIKKKREKN QIDAIKNDKGDITTDPTIEIQTIR EYCKHLYANKLENLEEMDKFL DTYTLPRLNQEEVESLNRPTG AEIVAIINSLPTKKSPGPDGFTA KFYQRYKEELVPFLLKLFQSIEK EGILPNSFYEASIIILIPKGRDIT KKENFRPISLMNIDAKILNKKL AKRIQQHIKKLIHHDQVGFIPG MQGWFNIRKSINVIQHINRAKD KNHMIISIDAEKAFDKIQPFML KTLNKLGIKYLGIHLTRDVKDL FKENYKPLLKEIKEDTNKWKN PCSWVGRINIVKMAILPKMCL* RRWTPCLLLTAAASLNRE*ERL VQPLLWRQMYCGPRHCRQVPQ HRLNWSPSLRLS |
| 23181 | 53549 | B | 23315 | 1 | 2907 | |
| 23182 | 53550 | A | 23316 | 584 | 1278 | QQR*MCQNLMT\QNQRSGR SQNDF*RRRKNISERSAVYR*R QLYIRRPYAERPS\HVEDKGH KYLVEANTGTENGYQGEESLF NKAYYGGGTNFFRKESQKLQQ SAKKRDAELANGALGIIELNND YTLKKVMKPLITSNTVTDEIER ANVFKMNGKWYLFDTDSRGSK MTIDVPQAKGNNVVITSYMTN RGFFEDKKATFAPSFLMNIKGN KTSVVKNSILEQQQLTVN |
| 23183 | 53551 | A | 23317 | 1 | 3345 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23184 | 53552 | A | 23318 | 2 | 3366 | WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYIMVK GSIQQEELTILNIYAPNTGAPTFI QQVLSDLQRDLDSHTLIIGDFN TPLSTSDRSTRQKVNKDTQELN SALHQADLIDIYRTLHPKSTEYT FFSAPHHTYSKIDHILGSKALLS KCKRTEIITNYLSDHSAIKLELM IKNLTQNHSTIWKLNNLLNDY WVHKEMKAEIKMFFETNENKD TTYQNLWDTFKA VCRGKFIAL NAHKRK\QER |
| 23185 | 53553 | A | 23319 | 1 | 2611 | MGDFNTPLSTLDRSTRQKANK DTQELNSALHQVDLIDIYRTLH PKSTEYTTFFSAPHHTYSTTDHIL GSKALLSKCRRTEIITNYLSDHS AIKLELRIKNLTQNRSTTWKLN NLLLNDYGVHNEMKAEIKMFF ETNENKDTTYQNLWDTFKA VC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTTHSKASRRQE ITKIRAELEKETQKTLQK\INES RSWFFERINKIDRPLARLIKKKR EKNQIDAINDKGDITTDPTIEIQ TTIREYYKHLIYANKLENLEEM DKFLHTYTLPRLNQEEVESLNR PITGSEIVAIINSLPTKKSPGPDG FTAEDQRYKEELVPFLKLQFQ SIEKEGILPNSFYEASIIIRKPGR DTTKKENFRPISLMNTDAKILN KILAKRIQQHIKKLIHHDQVGFI PGMQGWFNHKSINVIQHINRA KDKNHMIISIDAEKAFDKIQQPF MLKTL SKLGIDGTYFKIIRAIYD KPTANIILNGQKLEAFPLKTGTR QGCPLSPLLNFIVLEVLARAIQ EKEIKLISNFSKVSGYKINVQKS QAFLYTNNRQTESQIMSQLPFTI ASKRIKYLGIQLTRDVKDLFKE NYKPLLKEIKEDTNKWKNIPCS WVGRINIMKMAILPKVIYRFNA IPIKLPMFTFFTELEKTTFKFIWN QKRARITKSILSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23186 | 53554 | A | 23320 | 1 | 3099 | MGELITPLSTLDRSTRQKVNKD TQELNSALHQGDLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITNYLSDHSA IKLELRIKNLTQNRSTTWKLNN LLLNDYWIHNEMKAEIKMFFET NENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTTHSKASRRQEI TKIRAELEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK |
| 23187 | 53555 | A | 23321 | 911 | 1539 | VNVTSFGSRPICSTSPVLFSGL* GPVKEFDT*PSM*ISFELIPSIVIF EPRESVNKYHLPFILKTFARSISS VTVFEVISGFITFFNV*SLFNMI PRAPFANSASRFLALC*SFWLSL RKKFVPPP*YALLNKDSSPW/SS VFCSRVGFEYKVFMAFVFNVV RVSQRMVVAGCHAFIDKLLNV LICFSVSVKNRFVIFHSVDFECV |
| 23188 | 53556 | A | 23322 | 191 | 820 | VNVTSFGSRPICSTSPVLFSGL* GPVKEFDT*PSM*ISFELIPSIVIF EPRESVNKYHLPFILKTFARSISS VTVFEVISGFITFFNV*SLFNMI PRAPFANSASRFLALC*SFWLSL RKKFVPPP*YALLNKDSSPW/SS VFCSRVGFEYKVFMAFVFNVV RVSQRMVVAGCHAFIDKLLNV LICFSVSVKNRFVIFHSVDFECV |
| 23189 | 53557 | A | 23323 | 965 | 5050 | TWKGTTSTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDIY RTLHTKSTEY/TFFSAPHHTYSK IDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRIKNLNQSRSTT WKLNNLLLNDYWVHNEMKAE IKMFFETK\ENK\DTTYQNLWD AFKAVCRGKFIALNAHKRKQE RSKIDTLTSQLKELEKQEQTTHS KASRRQEITKIRAELEIETQKT LQKINESRSWFFERINKIDRPLA RLIKKKREENQ |
| 23190 | 53558 | A | 23324 | 1 | 2787 | |
| 23191 | 53559 | A | 23325 | 1 | 902 | |
| 23192 | 53560 | A | 23326 | 1 | 3640 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23193 | 53561 | A | 23327 | 1 | 3686 | MHIVVETALSASWQNKAKPPA RVLLQVVPNVWFLVAVVWEL YPSLDLMDRSIECSSSPATEQS WTENDYDKLREEGFRRSNYSE LQEDIQTKGKDVENFEKNLEEC ITRITNTQKCLKELMELKTKAR ELREECRLSRSCDQLEERVSV MEDEMNMKQEGKFREKRIKR NEQSLQEIWDYVKRPNLRLIGV PESDGENGTKLKNTLQDIIQENF PNLARQAKVQIQEIQRMPQRY LTRATPRHIIVRFTKVE |
| 23194 | 53562 | A | 23328 | 1 | 3433 | MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQNRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTTHSKASRRQE ITKIRAEKIEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDAIKNDK |
| 23195 | 53563 | A | 23329 | 1 | 3070 | MEGEMNMKREGKFREKRIKR NEQSLQEIWDYVKRPNLRLIGV PESDGENGTKLENTLQDIIQENF PNLARQANVQIQEIQRTPQRY SRRATPRHIIVRFTKVEMKEKM LRAAREKDRSTRQKVNKDTQE LNSALHQADLIDIYRTLHLKSTE YTFFSAPHHTYSKIDHILGSKAL LSKCKRTEIITNYLSDHSAIKLE LRIKNLTQNRSTTWKLNLLLNDY WVHNKMKAEIKMFFETNEN KDTTYQNLWDA |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23196 | 53564 | A | 23330 | 3 | 2372 | TTNCLSDHSAIKLELRIKKLTEN HTTTWKLNNLLNDYWVDNE MKAIEKMF FEINEKK\DTTSQNL WDTFKA VCRGKLI ALNAHKRK QERSKIDTLTSQLKK\LEKQEQR NSKASRKQEITKIRAE LKEIETQ KKT LQKINESRSWFF EKINKIDG PLARLIK K KREKNQVDAIKNDK GDIITDPT EMQTTIREYYKYLY ANKLENLEEMDKFLNTYTLQR LNQEGIESLNR PITGSEIEAIINSL PTKKSPGPDGFTAKFYQRYKEE LVYPEPRSESECLSNIREFLRGC GASLRLESIREDRNGRSQKTVH TEGDMNMNIKKIVKQATVLT TTALLAGGATQAF AKENNQKA YKETYGVSHITRHDMLQIPKQQ QNEKYQVPQFDQSTIKNIESAK GLDVWDSWPLQNADGTVAEY NGYHVVFALAGSPKDADDTSI YMFYQKVGDNSIDSWKNAGR VFKDS DKFDANDPILKDQTQE WSGSATFTSDGKIRLFYTDYSG KHYGKQSLTTAQVNVSKSDDT LKINGVEDHKTIFDGDGKTYQN VQQFIDEGNYTSGDNHTLRDPH YVEDKGHKYLVFEANTGTENG YQGEESLFNKAYYGGGTNFFR KESQKLQQSAKKRDAELANGA LGIIELNNDYTLKKVMKPLITSN TVTDEIERANVFKMNGKWYLF TDSRGSKMTIDGINSNDIYMLG |
| 23197 | 53565 | A | 23331 | 2 | 2987 | APRFIKQVLS DLQRDLDSHTIIM GDFNTPLSTLDRSTRQKVHKDT QELNSALHQADLIDIYRTLHPK STEYTCFSAPHHTYSKIDHIVGS KALLSKCKRSEIITNCLSDHSAI KLELRIKKLTQNRSTTWKLNNL LLNDYWVHNEMKAEIRMF FET NENKDTTYQNLWDTFKA VCRG KFIALNAHKRKQERSKIDTLTS QLKELEKQE QTHSKASRRQEIT KIRAE LKEIETQKTL\QKINE\SR SWFFERINK |
| 23198 | 53566 | A | 23332 | 339 | 701 | PDKEGNEIWVDMYTVKPSGWT VRTFDKPRKR FIAFFIAGILFRAI KNHFLPRETLQCLPYILTGFRRG QSEYFSIFSNDLADTVMFL*G AIRFSDLVNEIQHTFLIPGETIC RLSEVV |
| 23199 | 53567 | A | 23333 | 190 | 502 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23200 | 53568 | A | 23334 | 4472 | 8032 | KKSGNNRLMRVHGKKRFLWQ KQGVCEVEIQARESARDGTD REDAESPHA EVT VPRGTRTEILT LWASRDRPASACGVTVPKGST THPGGMDRVCVDTAVLHWM KQVQGISNLEVETGPRRRDMD EAGSRHSQQTNIGTENQTPHVL THKWQLNRNSACDKLHKPHSV PGGVAAGDVGGKTISNPGVCAI EYQVDGSPHIWEDVNKGVYIEE DRAPLMERSSSPAMEQSWMEN DFDELREEGFRRSNYSELRED |
| 23201 | 53569 | A | 23335 | 1 | 2374 | MVSISDLVICPPRHPKVLGLQGP PGLDSISDPSAGAGFLDWGEIG MPGPGRAGHQALCKCDCQCLE KTTTKAPGKMPKSTRSGPVRV RLADGPNRCAGRLECGMPDAG EQCVMTTGTSGRHCGLLGTGL WKG YTDLTIIPPGPGTTPPQERTC QGDYHSGGTWTHSPLETTTRP GSSSPAIRRLPAQM LLLPARPPH PRSSSPEAMDPPPPKAPFPKAE GPSSTPSSAAGPRPRLGRHLLI DAN/GVYPYTYTVQLEEEPRGP PQREAPPGEPPRKGYSCECA RVFASPLRLQSHRVSHSDLKPF TCGACGKAFKRSSHLSRHRATH RARAGPPHTCPLCPRRFQDAAE LAQHSWGT PRG PLLAAACNCE VARGRLESPGERLLHGYGGRE EEGGWGRAAGGLDRVEGFIS KAHHYLLIDTQGV PYTVLVTRS HRGSQGPVGLQARKVLQLPRV LKGLRVHVHLQRHSITHSEVPQ DFAGSLDSFQTPGESLRLVFRA LDTTQSSRISKAEPCLKEEPLSL GDLPYMHTTLCFCRKRASPGP GTLQRGALAWPDWASPRALPV PSLSSTTRSPAAPLFAVPLSGRT TQAMAFDGIIFQQQSQRSAGLT TTSRFLACQRPLRLCAWWASRS PRCTLRPVGLRPGVHPRPRLV YRDLKPENVMASGQPRDRPQP WFAWPPRPTRFCGGCWTLTPK |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23202 | 53570 | A | 23336 | 853 | 1602 | PGAAWSRPDLRGCCTEPQPALR MLVLASPCPQPLAFSSVETMEG PPRRTCRSPEPGPSSSIGSPQASS PPRPNHYLLIDTQGVPIYTVAW LDEESQREPGASGAPGQKKCYS CPVCSRVEFYMSYLQRHHRFSH SEVKPFECDCGK\AFKRSQHL/ SARHHSIHLGGWVGGPACRFG PRRFARDAGELAQHSRVHSGER PVS\STLPSPLYGAETHAETHA VEASHEAGLPGAPGTHRTLQG ALDSCPDTW |
| 23203 | 53571 | A | 23337 | 1 | 1144 | MGHHLMDKLVALGGLYYAIQ RHYATKCSVLKNDQILVIGLFM IQNVIYRKHFANPLSALFLQQGI ELFAAIAEIHITTVAERNHAITQI RLEAQTIFDSLKEWHNAIRKSL DYEALQAFEFVRVGATDRGFPAL SSEALVRVLVLDANDNSPFVLY PLQNGSAPCTELVPRAAEPGYL VTKVVAVDGDSGQNAWLSYQ LLKATEPGLFGVWAHNGEVRT ARLLSERDVAKHRLVVLVKDN GEPPRSATATLQVLLVDGFSQP YLPLPRAAPAQAQADSLTVYL VVALASVSSLFLFSVLLFVAVR\ LCRRSRAAPVGRCSVPECPFG HLVDVSGTGTLSQSYQYEVCLT GGSGANEFKFLKVPINLLSRDS |
| 23204 | 53572 | A | 23338 | 1 | 1260 | MVCYIQENLPFLKPSVENFYIL ITEGALDREIRAENITITVTDL GTPRLKTEHNITVLVSDVNDNA PAFTQTSYTLFVRENNSPALHIG SVSATDRDSGTNAQVTYSLLPP QDPHLPLASLV SINADNGHLFA LRSLDYEALQAFEFVRVGATDRG SPALSREALVRVLVLDANDNL\ PFVLYPLQNGSAPCTELVPRAA EPGYLVTKVVAVDGDSGQNA WLSYQLLKATEPGLFGVWAHN GEVRTARLLSERDAAKHRLVV LVKDNGEPPRSATATLHVLLVD GFSQPYLPLPEAAPAQAQAEAD LLTVYLVVALASVSSLFLLSVL LFVAVRLC\RRSRAASVGRCSM PEGPFPGRLVD\VSGTGTLFQSY QYEVCLTGGSETGEFKFLKPITP HLPPhRGKKEIENSTLPNSFGF |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23205 | 53573 | A | 23339 | 123 | 5794 | SSSDSGSLKGACTEVKMEPAGE RFPEQRQVLILLLEVTLAGW EPRRYSVMEETERGSFVANLAN DLGLGVGELAERGARVVSEDN EQGLQLDLQTGQLILNEKLDRE KLCGPTEPCIMHFQVLLKKPLE VFRAELLVTDINDHSPEFPERE MTLKIPETSSLGTVFPLKKARD LDVGSNNVQNYNISPNSHFHVS TRTRGDGRKYPELVLDTELDRE EQAELRLTLTAVDGGSPPRSGT VQILILVLDANDNA |
| 23206 | 53574 | C | 23340 | 20 | 313 | |
| 23207 | 53575 | A | 23341 | 119 | 247 | RSRCISASPRRPASFRKSIPEEED ESLNI*KGQVSILFFYIK |
| 23208 | 53576 | B | 23342 | 55 | 288 | |
| 23209 | 53577 | A | 23343 | 1 | 3576 | MAFLFEFSDLVSLLSIGTMLAY SLVAFSVLVLRYPDENFSKNE KPKEEVVEMNSVPKAESPACVP EASSTPASLWSPVSTIPTPRWGR IVYGCAFLLVLLSMLCLVLAH WPKRLFSGELIYIAAAVLLLVI VGFTFTVWRQPQSNTPLYFKPP HISTSQNLSLPEHPMEYLLRTGI EPDVRGVLTVNALPAGPPVACS PLVSISAHVYLMQMMTTETWA QCGVWMLIALECPNLKCLKPP WLHMLPLAMTMYA |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23210 | 53578 | A | 23344 | 3 | 1762 | SVRPGPGHVRVRRFFSLSPPLR PWPLCPAARRTMGSLSRRIAG VEDIDIQANSAYRYPPKSGNYF ASHFFMGGEKFDTPHPEGHLFG ENMDLNLFLGSRPSQFPYVTPAP HEPVKTLRSLVNIRKDSLRLVR YKDDADSPTEDGDKPRVLYSL EFTFDADARVAITIYCQASEEFL NGRAVYSPKSPSLQSETVHYKR GVSQQVSLPSFKIDFSEWKDDE LNFDLDRGVFPVVIQAVVDEG/ DSVVEVTGHAHVLLAGFEKHM DGSFSVKPLKQKQIVDRVSYLL QEIYGIENKNNQETKPSDDENS DNSNECVVCLSDLRDTLILPCR HLCLCTSCADTLRYQANNCPI RLPFRALLQIRAVRKKPGALSP VSFSPVLAQSLEHDEHSCPFKK SKPHPASLASKKPKRETNDSV PPGYEPISLLEALNGLRAVSPAI PSAPLYEEITYSGISDGLSQASC PLAAIDHILDSSRQKGRPQSKAP DSTLRSPSSIHEEDEEKLSE DAPPLGGAELALRESSSPESFI TEEVDESSSPQOGTRAASIENVL QDSSPEHCGRGPPADIYLPALG |
| 23211 | 53579 | A | 23345 | 35 | 3134 | RPREGPTWPQLPGSSPRRLFPW SPGSSSRGLFPWSPGSSSRGLFP WSPGSSSRGLFPWSPGSSSRGLF PWSPGSSSRGLFPWSPGSSSRGL FPWSPGSSSRGLFPWSPGGSSR GSSRGHPGPPPGSSRGHPGPPP GALPVVTRVLLPGLFPWSPGSS SRGLFPWSPGSSSRGLFPWSPGS SSRGLFPWSPGSSSRGSSRGHPG PPPGALPVVTRVLLPGLFPWSP GSSSR/RTLPPVTRLLLSGTLPV VTRVLL |
| 23212 | 53580 | A | 23346 | 3 | 91 | |
| 23213 | 53581 | A | 23347 | 3 | 174 | |
| 23214 | 53582 | A | 23348 | 3 | 360 | |
| 23215 | 53583 | B | 23349 | 158 | 368 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23216 | 53584 | A | 23350 | 3786 | 4928 | PPPARTRPCASLTPEKAKWWRS KPLGLTRAPARCGLSSPQTGSCS APASAG*VSGNSRSGTRRGLRP TRG*GPCGPSSRARAISSPRAS/L RMSQRELGLWDPNNFEFPVAL QEMDTSNGLVLLPFYDPDSSIVY LCGKVLTAGQGEQGTGWRCG GPCPGAPLNRLILQGDSSIRYFEI TDEPPFVHYLNTFSSKEPQRGM GFMPKRGLDVSKEIARFYKLH ERKCEPIIMTVPRKSDLFQDDL YPDTPGPEPALEADEWLSGQD AEPVLISLRDGYVPPKHREL RV TKRNILDVRPPSGPRRSQSASDA PLSVRSALLHSGPIYISPNRPYTT RPLCPPPQQQHTLETLLLEEIKAL RERVQAQEQRITALENMLCELV |
| 23217 | 53585 | A | 23351 | 1 | 1898 | MSRKGPRAEVCADCSAPVGPD FALAISELVSPDIFMQSHSENAIS VKEIVTEIESISQGVGQIQLKGDI LPNPCHTPKKNSIHELLLERAQT PENKPGHMEQDEDSCTAQPEL AKDSGMCNPEGCLTTHSSIADL EEGEQLRGNKSSRAQGCTQNS KNDSSVADLAPKGKSDEAPPEH SFVLKEPEMSKGGKYSGSEA GSLSHSEQNATVPAPRVLEFDH LPDPQEGPGPEASNGLKVSQKS EGSQPSSSRSPLEFLKEAGVPNQ TLSSGTPDPYFMALLGPKLNSR RPHLHPVSHTLDLGNPPLPQQ FAKCQRGRKGPEGKYPLHYLV WHNRHRELEKEVRAGQTLITQ TLSQANPTAITAEYFNPNFELG NRDMGRPMELTTKTQKFKAKL WLCEEHPLSLCEQVAPIIDLMA VSNALFAKLRFITLQIPIFHLN ARITFGNLNGCDEPVPSVRGSPS SETPSPGSDSSSVSSSSSTSEAPR ENACPSALPGVASCRGCEISPAL FEAPRGYSMMGGQREAA TRDD DDDLLQFAIQSSLLEAGSEYDQ VTIWEALTNSKPGTHPMSYE/R SPTGQGQVPAATCSG/R YDEQL RLAMELSAQEQEERRRRARQE EEELERILRLSLTEQ |
| 23218 | 53586 | A | 23352 | 341 | 711 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23219 | 53587 | A | 23353 | 57 | 719 | TSDLMAEIIQERIEDRLPELEQL ERIGLFSHAEIKAIKKASDLEY KIQRRTLFKEDFINYVQRIGYSF KKDEIENSIVHRVQGVFQRASA KWKDDVQLWLSYVAFCKKWA TKTRLSKVFSAMLAHNSNKPAL WIMAAKWEMEDRLSSESARQL FLRALRFHPECPKLYKEYFRM ELMHAGKTGGRRRNKLNKKPV WMWRILIILKKSRLRASWHGSST |
| 23220 | 53588 | A | 23354 | 27 | 352 | TESVVTIMSLLNPKSEMTPEE\ REEEEFNTGPLSVLTQSVKNNT QVLINCRNNKLLGRVKAQFDR HCNMVLE\NVKEMLTEG/DRYI SKMFL\AGDPVIVVLRNPLIAGK |
| 23221 | 53589 | A | 23355 | 32 | 575 | STRLDLPKCWDYRSLFNKP\KS EMTP\EELQKREE\EEFNT\GTP LCLTQSVKNNTQSAQSTC\RNN KKLPGAA*RPFDRA\PPCSPPGT CNMVL\ENVK\EMWT*GTQEV GKGKEGSSKP\VNKDRLTSSKM FPGGGGFSSFV\PCGNPFHSAG QIRGPPV\FDKNSHPLVLLKTA CHLVFENY |
| 23222 | 53590 | A | 23356 | 103 | 713 | VTSGCGKKKVWLDPNET\NEIA NANFRSADPGRLIKDGLIIRKPV T\VHSRARLPEKTPLARCKGHG TLGIGKRKGTANA\RMPKEGHH GMRRMRILAPACSRRYRESKKI D\RHMYHSLYLKVKG\NVFKNK ADFSWEHIHKAEGRARPRKEAS WLDQAEA\RRSKDQKGKHKRR EERLPGQRKEEINQRLYSKEGR RPRNKNLTL |
| 23223 | 53591 | A | 23357 | 1 | 2847 | |
| 23224 | 53592 | A | 23358 | 1 | 2823 | |
| 23225 | 53593 | A | 23359 | 3 | 2858 | AMFGFQRRGLGTPRLQLWLLL LEFWEVGSQQLHYSVSEEAKH GTFVGRIAQDLGLELAELVQRL FRVASKTHGDLLEVNLQNGILF VNSRIDREELCGQSAEC\IHLEV IVDRPLQVFHVNV\VEVKDINDNP PVFSLREQLLIAESKQSDSRFP LEGASDADIEENALLTYRLSKN EYFSLDSPTNGKQIKRLSLILKK SLDREKTP\ELNLLL\TATDGGKP ELTGTVRLLVQVLDVNDNDPE FDKSEYKVSLMEN |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23226 | 53594 | A | 23360 | 194 | 931 | NSPVVPVMASGQFVNKLQEEVI CPICLDILQKPVITIDCGHNFCPQ CITQIGETSCGFFKCPLCKTSVR\ RDAIRFNSAVAEIWWEKIQALQ ASEVQSKRK\EAT\CPRHQEMF HYFCEDDGKFLCFVCRESKDH KSHNVSLIEEAAQNYQGGQIQEQ IQVLQQKEKETVQVKAQGVHR VDVFTDQVEHEKQRILTEFELL HQVLEEEKNFLLSRIYWLGHEG TEAGKHYYVEIPLMPTVERSQEA |
| 23227 | 53595 | A | 23361 | 2 | 381 | AINWTSARPVSQCWDP\CPPSQ VVCLAGLPP*RVCQNPVKGP\N CPLAHTSEPTGHCLL*TRGMCF PSLCGQLCP*SGPPDCPSPRALH HTGFCPVALLVAESQVRARAC GPEPHRAGRASRWCLHAG |
| 23228 | 53596 | A | 23362 | 213 | 574 | PQTHGTGNHSERGRQPITRSPEKP EP\CPSKRAPQTQQP\PWAPSLC PPALGPCKGTRRPRVQVHRPTS SQKCPLPAWFHHLPLWPTSAAR SSSTETPTGQQMRKLRHPAAPR SANALSLGE |
| 23229 | 53597 | A | 23363 | 21 | 456 | |
| 23230 | 53598 | A | 23364 | 2 | 98 | |
| 23231 | 53599 | A | 23365 | 64 | 241 | PWPLASNPRGCLP*PSTLN*PTP SSQPGMSLDSLDRHPP*TRETAS GIGGQRP GSDPARTPHFISQTQ |
| 23232 | 53600 | A | 23366 | 209 | 353 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23233 | 53601 | A | 23367 | 1766 | 3292 | SSCPTTRVLIMKGAGHPCYLDK PEEWHTGLLDLFLQGLQLWLMH MQQLMSLAVVSGRLSRGQCGT ERPSRRAAAAAAGQPQRGHF QHIEERLETNVQNCQSPDTLCP THCSPVLNEPCPEVSVVAVAPA SPDRMSGSDGGLEEEPELSITLT LRMLMHGKEVGSIIKKGETV KRIREQSSARITISEGSCPERITI TGSTAAVFHAVSMIAFKLDEDL CAAPANGGNVSRPPVTLRLVIP ASQCGSLIGKAGTKIKEIRETTG AQVQVAGDLLPNSTERA VTVS GVPDAIILCVRQICAVILEGFSV QGQYGAVTPAEVTKLQQLSSH AVPFATPSVVPGLDPGTQTSSQ EFLVPNDVSRGWDGWRLIGCVI GRQGTKINEIRQMSGAHIKIGN QAE GAGERHVITITGSPVSIALA QYLITACLETAKSTSGGTPSSAP ADLPAPFSPPLTALPTASPLAC WAHPMPSPSPTLIGFKAHALLG FTTCFPRAAAGLGGLHRQDGSS |
| 23234 | 53602 | B | 23368 | 1 | 363 | |
| 23235 | 53603 | A | 23369 | 486 | 947 | LDGAGLLAPVKAHLQKKGPRL GTRGCAMPRLGSTPFLKGQCL ANSRNTLEAVSLTESSASRVPP APVLGSRPHSPSPWP/P/YYTP VPPPPRMALVPPNMHGQGTVG LTSVPLACTVAMLGSYKQAGA FGPLANCYGGLGHAQCWGQEF CPTQCP |
| 23236 | 53604 | A | 23370 | 38 | 680 | GSRLRRLQAAAARPALPLPLPP WEWKHLPHVPEAKWWLTAR HSAAYRADPLRVSSRDKLTEM AASSQGNFEGNFESLDLAEFAK KQPWWRKLFQGQESGPSAEKYS VATQLFIGGVGTGWCTGFIFQKV GKLAATAVGGGFFLLQLANHT GYIKVDWQRVEKDMKKAKEQ LKIRKSNQIPTEVRSKAEEVVSF VKKNVLVTGGFFGGFLLGMAS |
| 23237 | 53605 | C | 23371 | 30 | 200 | |
| 23238 | 53606 | A | 23372 | 14 | 161 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23239 | 53607 | A | 23373 | 69 | 715 | APALPGCEHMMMAIRELKVCLL GDTGVGKSSIVWRFVQDHFHDH NISPTIGVASFMTKTVP\WENDFT KFLIWDTAGQERFSFIGLPLYYS RLQLAAVYSCYGYLPSRDFIFIT LKE\W\KRLKELGPE\NIVMAI AGNKCDLSD\REVPPPEGMLKE Y\AESIGAIVVETSAKNAIN\EE LFQGIS\RQIPPLDPPMKNGKQW DHQKLRSQPMQASRRCC |
| 23240 | 53608 | A | 23374 | 3 | 293 | VTSTMAYRAQGQK\QKVMV QPINLIFRYLQNRSRIQVWLYEQ VNMRIEGCIIGFDEYMNVLVDD AEEIHSKTKSRKQLGRIMLKGD NITLLQSVSN |
| 23241 | 53609 | A | 23375 | 3 | 393 | HESCSQRQRAGCALCENSHPW RSRGPVQKSAEGLWCQPICRT SSSRYL\QNRJAGFQVWLYEQV NMRIEGCIIGF\DEYVNLVDD AEEIHSKTKSRK\QLGRIMLK\G DNITLLQTCLPPRMVHGSGEIV |
| 23242 | 53610 | C | 23376 | 129 | 425 | |
| 23243 | 53611 | A | 23377 | 470 | 635 | ENSSSHHIIKPFSSGCSIHGFSGH INVTSVTIL*PIKSCHIRCHF*CA QYMVADN |
| 23244 | 53612 | A | 23378 | 71 | 566 | PLFPPCLSPVVAGWARGHMLG QSHQQVAAPLKHRPITPTELCQ KCLSLIKKTKFLNAYITVSEEVA LKHAEESEKRYKNGQSLGDLD GIPIAEKDNFSTSGIETTACASNM LKGYPYPYNATVDQKLLDQGA LLMGKTKLNDFAMGSGSTDGV FGPVKNPWSYSK |
| 23245 | 53613 | A | 23379 | 255 | 1042 | ILAAARMGKQNSKLRPEVMQDL LESTDFTEHEIQEWYKGFLRDC PSGHLSMEEFKKIYGNFFPYG\D ASKFAEH\VF\RTFDANGDG\TID FREFIIALS\VTSRGKLEQKLLK AFSMYDL\DGNGYISKAEMLEIV QAIYKMVSSVMKMPPEDESTPE KRTEKIFRQMDTNRDGTWVPH LALIYRTAEGGFVQVRASVSFY PPPSAGNAMVNEAAVFLEIPLG SSPGQVSAVCHSGRKLSEEFIR GAKSDPSIVRLLQCDPSSAGQF |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23246 | 53614 | A | 23380 | 1 | 721 | MDGNLRKIRFEKHAITEEFRTT EPGLAALRLPSTWIRGVRTSES KREVGKGGQSQQYENRDTEGE GHVMTKARDWSKAAASQRLP ANHLKLRLCIDGFRSHSLPEEGP KKPCQHHAQQEEPCTRSGRLPQ AHEGSISDCCTSSEQGSMDIGSV EPGTGYNLLVCHLL/STLEKRSI WAGVSRFSRYHLSRLPLARK\G NPLTPCASQLLLPLPSTTQKRQS GHALYSFPYRPQPKNDNLVMP |
| 23247 | 53615 | A | 23381 | 80 | 562 | DRAMWGDWLWLLPPASANPGT GTEAEFEKAAEEVRHLKT/RSPS DEEMLFYGHYKQATVGDINTE RPGMLDF\TGKA\KWD\AWNEL KGTSKGD\AVEA\YLNQV\EELK KKYGD\MERLDLVTVPCVYPKP ETIPFFFSNTVDGWEFRENNPV KPATQRLLTHTGS |
| 23248 | 53616 | A | 23382 | 380 | 1041 | EVTINSGFIFIMLFMEHPEHYTI MHKWILT\WILPTLLYRSCFHIIC LVGTISLACND\MTPEQMATNV NCSSPERHTRS\DYMEGGDIRV RRLFCRTQWYL\RIDKRGKVKG TQEMKNNYNIMEIRTVAVGIVA IKGVESEFY\LAMNKEGKL\YA KKECN\ED\CNFKELILENHNT YASAKL\WTHNGGEMFVALNQ KGIPVRGKKTKEQKTAHFLP MAIT |
| 23249 | 53617 | A | 23383 | 127 | 549 | SSPKMAATMKKAAAEDVNVTF EDQ\QKINKFARNTSRITELKEEI EVKK\KQLQNL\EDACDDIMLA DDD\CL\MIPY\QLGDVFISHSQE ETQEMLEEAKKNLQEEIDALES RVESIQRVLADLKVQLYAKFG SNINLEADES |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23250 | 53618 | A | 23384 | 1 | 2050 | MEYESMVISFDDRVMEKTEYG PIFTVFAMGNRMFTVTEEEGIN VFLKSKKVDFELAVQNIVYRTA SIPKNVFLALHEKLYIMLKGKM GTVNLHQFTGQLTEELHEQLEN LGTHGTMDLNNLVRHLLYPVT VNMLFNKSLFSTNKKKIKEFHQ YFQVYDEDFEYGSQLECLLRN WSKSKKWFLELFEKNIPDIKAC KSAKDNSMDSDEDPVNLQSRS ALVCEMLHVQRSSSDADAIGPH ADHLSNRWEVILADEHGHIAD DMISRYALSEKSQVELSTQVIKS ASSKSVNKSDIDTSVFLNWYNP EKKMIRAYATVIDGPEYFWCQF ADTEKLQCLEVEVQTAGEQVA DRRNCIPCPYIGDPCIVRYREDG HYYRALITNICEDYLVSVRLVD FGNIEDCVDPKALWAIPSELLS VPMQAFPCCLSGFNISEGLCSQ EGNDYFYEIITEDVLEITILEIRR DVCDIPLAIVDLKSKGKSINEK MEKYSKTGIKSALPYENIDSEIK QTLGSYNLDVGLKKLSNKAQV NKIYMEQQTDELAITEKDVNII GTKPSNFRDPKTDNICEGFENP CKDKIDTEELEGVSQKAQESMC TEDMRKSSCVESFDDQRRMSL HLHGADCDPKTQNMNICEEEF VEYKNRDAISALMPFSLRKA VMEASTIMVYQIISQLNYRTPTL |
| 23251 | 53619 | A | 23385 | 3 | 602 | TRPPTRPGLSPDPTSPTEADRGV CERPHRCFLLPQITHPSSGRRCL CLLSPTSFDFSLLYESQSDRAIF GVGTEPDQEPPEPYHEQVPVSV YHPT/PSQTWVATQLTEEEQIRI AQRIGLIQHLPKGVY\DPWRDG SEKKIRECVICMMDFVYGDPIR FLPCVHEWYHLDCIDDWLMRS FTCPSCMEPVDAALLSSYETN |
| 23252 | 53620 | A | 23386 | 33 | 512 | TAARCQGGPTHVPAFVGTACP TRIPGHAPARQCREYYY*YYD F/WKEPRRCHALLPPWAGLEV GMPPSHTQLGMHPAPPPHLEV KAQG\PSNRQRTDGCRWCSGR ASALGGGRQDSRLRERGGGYD H/HCPICRSLKIQLKCHPASGPQ TVGLGRLASVS |
| 23253 | 53621 | A | 23387 | 1 | 1731 | |
| 23254 | 53622 | B | 23388 | 1 | 706 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23255 | 53623 | A | 23389 | 1 | 1986 | MGIGEGPTTSEGCRESVEYSHQ KSELPLSGDSQVPGPIGCNCDP QGSVSSQCDAAGQCQCKAQVE GLTCSHCRPHHFHLSASNPDC LPCFCMGITQQCASSAYTRHLIS THFAP/GDFQ/GFA/LVNPQRNS RLTGEFTVEPVPEGAQLSFGNF AQLGHESFYWQLPETYQGDKG EAYFARMRRAHQNRSLSEEQ LRAAVTAGRIPEPPEGRDWAQR ASQFSLSYEGFSLLPGLYYWQ LPRAFLGDKVAAYGGKLRRTL SYTAGPQGSPLSDPDVQITGNNI MLVASQPALQGPERRSYEIMFR EEFWRRPDGQPATREHLLMAL ADLDELLIRATFSSVPLAASISA VSLEVAQGPSNRPRALEVEEC RCPPGYIGLSCQDCAPGYTRTG SGLYLGHCELCNCHSDLCHP ETGACSQCHNAAGEFCELCA PGYYGDATAAGTPEDCQPCAC LTNPENMFSTRCESLGAGGYRC TACEPGYTGGYCEQCGPGYVG NPSVQGGQCLPESELHFPSVQ PSDAGVYICTCRNLHQSNTSRA ELLVTEAPSKPITVTVEEQRSS VRPGADVTICTAKSKSPAYTL VWTRLHNGKLPTRAMDFNGIL TIRNVQLSDAGTYVCTGSNMF AMDQGTATLHVQGSAAEAGERS MYSISVLLKYTS |
| 23256 | 53624 | A | 23390 | 3 | 13319 | PASGRLRAARSGRRGASERESG AGRAMGWRAPGALLALLH GRLLAVTHGLRAYDGLSLPEDI ETVTASQMRWTHSYLSDDEYM LADISGDDLGSDDLGSDFQM VYFRALVNFTRISIEYSPQLEDA GSREFREVSEAVVDTLESEYLKI PGDQVVSVVFIKELDGWVFE LDVGSEGNADGAQIQEMLLRVI SSGSVASVYTSPQGFQFRRLLGT VPQFPRACTEAEFACHSYNECV ALEYRCRRPDCRDMS |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23257 | 53625 | A | 23391 | 41 | 1323 | HYLVFFLP SLRRYTVSLSPNSTS YQLLVPGPSY/SALPISSAASLY AGA\GGSGSRMSVSHSTSLRDG ISSGGLA/TGMARGLGGMGGIQ NKKETTQSLNDSLAVRVRLET ENRKLESKIREHLEKKGPQVRD WSHYFKTIEDLRAQIFANTVDN VRIFLQIDNARLAADDFRVKYE TELAMRQSVESDIYGLHKVIDD TNVINGCSFFMKKNHGEEVKC LQAQIASSGLTMEVDAPKSQDL AKITADISTRYDELARKNREEL DKYWSQPIEESTTEVTMQSAKV RAAEMTFMELRRTVQSLEIDL LMRNPKASLENSLREVEACYA LQMEQLNLDG/GILLHLESELTQ TRAEGQL\QAQKYKALLNIKNK LEAEIATYCLLEDGKDFNLGD TLDSSNPMQTIQKTTTSRIVDG KVVSETNDTKVWRH |
| 23258 | 53626 | A | 23392 | 1 | 771 | |
| 23259 | 53627 | A | 23393 | 732 | 1656 | SCSWTSPAAWPPNASLHSLCKR RNQDHL LLDWRFLDFPSSMA SKCQSP LLPQKKKPRPLPALGP EKTSASAGLPKKGEKEQETIE HIHEVQNEMDR LNEQAKRSEL ISKIPDFWVTIFVNHPEVSALPG EEDDEALHYL TRVEMTDFDDIK SGYRIDFYFDENPYFENNILAKE FHLNESGDPSSKSTEIKWKY GK DLMKRSSQTQNK AHRKRQHEE PESFFT WFTDHS DVGADDELGEV IKDIWP NPLQYYLVPMDMNEEG EGEEDDDDEEEEGLEDIDEEG DEDEGEDEDEGEKGEDEGE |
| 23260 | 53628 | A | 23394 | 3 | 923 | ARRLVVWFWD FPNSMAPKRQS PLPPQKKKPRPPPALGPEETSAS AGLPKKGEKEQQAIEHIDEVQ NEIDRLNEQASEEILKVEQKYN KLRQPFFQKRSK\LSAGIPNFWV TTFVN\HPQVSALLGEEDEEAL\ HYL\TRVEVTEFEDIKSGYRIDF YFDENPYFENKVL SKEFHLNE\ S GDPSSKSTEIKW KSGKDLTKRS SQTQNKASRKRQHEEPESFTW FTDHS DAGADELGEVIKDDIWP NPLQYYLVPMDMDEEGEGEED DDDEEEEGLEDIDEEGDEDEG EEDEDDDEGEEGEEDGEDD |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23261 | 53629 | A | 23395 | 732 | 1656 | SCSWTSPAAWPPNASLHSLKRR RNQDHLLLDWRFLDFPSSMA SKCQSPLLPQKKKPRPLPALGP EKTSASAGLPKKGEKEQQTIE HIHEVQNEMDRLNEQAKRSEL ISKIPDFWVTIFVNHPEVSALPG EEDEEALHYLTRVEMTDFDDIK SGYRIDFYFDENPYFENNILAKE FHLNESGDPSSKSTEIKWKYK DLMKRSSQTQNKAKHRKRQHEE PESFFTWFTHSDVGADDELGEV IKDIWPNPQYYLVPMDMNEEG EGEEDDDDDDEEEGLEDEDEEG DEDEGEDEDEGEKGEDEGE |
| 23262 | 53630 | A | 23396 | 3 | 924 | ARRLVVWFWDFFNSMAPKRQS PLPPQKKKPRPPALGPEETSAS AGLPKKGEKEQQAIEHIDEVQ NEIDRLNEQASEEILKVEQKYN KLARQPFFQKRSLASAGIPNFW VTTFVNHPQVSALLGEDEEA LHYLTRVEVTEFEDIKSGYRID FYFDENPYFENKVLSEFHLNE SGDPSSKSTEIKWKSGLDLTKR SSQTQNKASRKQHEEPESFFT WFTDHSADAGADELGEVIKDDI WPNPQYYLVPMDMDEEGEGE EDDDDDDEEEGLEDEDEGED EGEEDDDDEGEEGEDEGED |
| 23263 | 53631 | A | 23397 | 1 | 1393 | MKGKQGGGPQAWAEGLGRE WMRMPQEGKGSQRKSTQKQT KREIDAYIVQAKERSYETVLSF GKRGLNIAASPAVQAATKVLW APSPPAAPIPPLRPFGLIQLLCQG AQRWQPGSREVKGRLCQARLA ETSSIAGNLRVQSYERPVDPGV TMDPLLPGRTIVFAAGDHTLW RAPVSSCAQRSGVWSLDNMGV NSGSVPFHGVRIQASQLISLNF FSFCEADLKTPLHGFLLPAGPK EEVTVKKEKRERDRDRQREGH GRGRGRPEVIQSHSIFEQGPAAE MMKKKGNWDKTVDVSDMGPS HIINIKKEKRETEETKQILRML EKDDVDHHLSEHLVTTATFSI GSTGLVVYDYQQVECGGHVRA DLKTQDLYSHAQFGDNNYPGG VDWYRAGGLQSDTEDECWS DTEAVPRAPARPREKPLIRSQSL RVVKRKPPVREGTSRSLKVRTR KKTVPSPDVDS |
| 23264 | 53632 | A | 23398 | 297 | 584 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23265 | 53633 | A | 23399 | 2 | 149 | CMKFGAVTPIGGPPLGDQSPVL LLFAL*KRSTYNLGSSDPPAQGI SHQF |
| 23266 | 53634 | A | 23400 | 1 | 170 | PAGIRHEERSTYDLWSSDRPGQ GTSHQF*IIRFQIPWNSGPRLSE* LLPRSSRLSS |
| 23267 | 53635 | A | 23401 | 1 | 1077 | |
| 23268 | 53636 | B | 23402 | 289 | 1359 | |
| 23269 | 53637 | A | 23403 | 3 | 2233 | |
| 23270 | 53638 | A | 23404 | 1 | 1491 | |
| 23271 | 53639 | B | 23405 | 76 | 511 | |
| 23272 | 53640 | A | 23406 | 1 | 2706 | |
| 23273 | 53641 | A | 23407 | 273 | 862 | |
| 23274 | 53642 | A | 23408 | 1 | 1080 | |
| 23275 | 53643 | A | 23409 | 134 | 675 | MHYFHSSVQIGLPLTRRSQVLIL PQPLLPNPIILLSPLLTPVPAYS FIL/PTSPPPPARQFPLKKVAEAK GIVKQLKTDARSPTKPTGPSQ TLWVTLTVEDLKHAFFTIPLHP SSQPLFAFTWTDPDTHQAQQIT RAVLPQVFTDSPHYFSQAQISS SVTYLGIIILIKTHVLSLLIMSG |
| 23276 | 53644 | A | 23410 | 1 | 895 | MEVHKHPFNTLALRHESGCEL VWAEKHRNQIFPFKSTASPKQ WDTGRHNSDAKQQEPGGREER NTMEMETKETHFIRGPKTLASV TDWEGSLPLVFNHCRGTSIIHP RFKGVRRRDACLGPSPLAASP AFLGKGQHALKGLKPVITRLLQ HGLLKPINSFPFS\PILPVLKPKDK AYKLVQNLRLINQIVLPIHPVVP NPYTLSSIPPSTTHYSVLDLKH AFFTIPLHPSSQPLFAFT*TDPD H*AAQITWAVLPQGFTRQPPLL QLSPNFILICYLSRHNSHKNTRA LPADRV |
| 23277 | 53645 | A | 23411 | 1 | 930 | MIQEHADKQVQRLOGVLLGSIP TAASRARLHPGEINNHVAHTEP VWWSLHMDAYEIWCRGSDRR TSLGRSIPPLPALCSLRRHILRPQ VLRSTSPRNISPISNPGHLSDYTP TFQGCQTMQGRLPWSFTLSGK SRFSGEGATQRQYPIQQALKG LMPAITRLLQHGLLKPINSPYHS PILPVLKPKDKPYKLVQDLRLINQ IVLPIHPMVPNPYTLSSIPASTT HYSV\LYVKHAFFTIPLHPSSQP LSTFTWTDPDTHQAQQIT*AVL PQVFTDSPHYFSQAQISSSVTY LGIILHENTRALPADHV |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23278 | 53646 | A | 23412 | 299 | 1028 | RLGSFSSNHPYLGQRQYPIPQQ ALKGLKPVITCLLQHVLKPVN SPYNSPILPVQKLDMPYRLVQD LCLINQIVLPIHAMVPNPYTLT SIPPSTTHYSVLDLKPAAFTIPLR LSFQPLFTFSWTDPDTHQAQQI TRAVLPQSFTDSPHYFSQAQIS* RLGSFSSNHPYLGQRQYPIPQQ ALKGLKPVITCLLQHVLKPVN SPYNSPILPVQKLDMPYRLVQD LCLINQIVLPIHAMVPNPYTLT SIPPSTTHYSVLDLKPAAFTIPLR LSFQPLFTFSWTDPDTHQAQQI TRAVLPQSFTDSPHYFSQAQISS SSVTYLGIPGFAILTKPLYKLTG GNLADPIDPKSFPHSSFRSLKTA LETAPILALPVSSQPFSLPTAEV WAAQSEFLHKNRDRTE |
| 23279 | 53647 | A | 23413 | 157 | 202 | RSECARWMEK*CPWL |
| 23280 | 53648 | A | 23414 | 184 | 482 | EGVSFVLLSPYQGGPQVSRRC S/RQVSQRCPHRGRGPRCPQVS RSHGPSWVGHPGMPLYGSIEQF YCGAPGLAGPPNGSRGESLKIS VWIFPCRDFGNFN |
| 23281 | 53649 | B | 23415 | 13 | 862 | |
| 23282 | 53650 | A | 23416 | 1 | 11342 | MATRWFYIGHPPRDARVPRIV AEAKEKNLTPGKIIEVDVTIEAQ IRQEFLLDAERDTGGFVKFFRITK KKLQEFFLGEEEEQVPHVSPVE LGAKPTAFNAFIANA VGKTLAV QHASLKAPEPEMTV THERFYG NYAVWITDVDPNRHRIEVIHVI REISGRTSEYVNNLLAQPTPFK VFDWLTETQAKEFVRRNLNTQ GVISVYNKLEDGIPVKVAVKAT EPTNKEKLEAASTKLKAMGAV ATDAYEFHTDLNENE |
| 23283 | 53651 | A | 23417 | 7597 | 7883 | LSSLAWVWQWNHRISVLFHSN SVRTNLVPQFNQLVITESNSCPE FFNQTSAFFKT*VESGCM/CLQD *GIEWFRLRLDVYNSRLVFLTG ATDYCTG |
| 23284 | 53652 | A | 23418 | 3 | 1573 | |
| 23285 | 53653 | A | 23419 | 6692 | 6793 | GASVAPSIGS*STGNAIPSCLFQ QNVIVPIPQS |
| 23286 | 53654 | A | 23420 | 1 | 17727 | |
| 23287 | 53655 | A | 23421 | 6687 | 6785 | VNTGNRTWWEPLFRK*KKTQR EDTTEKKTKGR |
| 23288 | 53656 | A | 23422 | 1 | 2856 | |
| 23289 | 53657 | A | 23423 | 1 | 7194 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23290 | 53658 | A | 23424 | 7460 | 7561 | GASVAPSIGS*STGNAIPSCLFQ QNVIVPIPQS |
| 23291 | 53659 | A | 23425 | 1468 | 1857 | |
| 23292 | 53660 | A | 23426 | 1 | 1985 | MEPVGIDIIAISWIGAPEYDPNV KRAINAKVEATQKTLQREQEIQ QRVAEANMEREQAKGVADAIR LRGEALTENPNVMQLEAINKW NGLVPFITSSPGMGKSAIVRQIA EDFGLKLIDHRLSTSAPEDLSGL PRFKENGRAEFAPFDELFPLEG DAVPEGFNGWLLFLDEFNSAR KEIQAAAYKLVLDGMTGQKKL HPYVAIVCAGNKATDRAITNNL STAMQSRLLHLEMETDFDVFME DVAIPNKWDERVIAFLNANPNK LNDFEPDHQEKTFCCSRTWEFV NKIVSILPPGPINSEMTLLLAGTI TSGVATSFVQFTQVYSNMVSL NEILDNPKKARMPEDNNLLWA VVTSLINNTDEDNHSKIFDYVE RMPFTFKVLYYRSRKTDMSMT DAQLTREYDRCQAKAFMGKTA AFFGSLLC SLKFRWVKDGCOT AQTDGEHLEWNPWFESLLPE SRVTVLMHELWHVGLLHLSVR MGSRDPEVWNYACDIYINNQLI QDGYSGFIENCWKDPKYAGW AEEQIYHDLMSKHPRPPKASGA FGTGSGGDMKPSTSKASLKLSG GSLPGVLP GKMEEVITQFLKPV VPWQVLLERFFNDLQETYYSW QRPNRRYPDMYLPSSMDDDCR LEHLAYFL*NEADLTGLLVLK* TDDGQSVSGQNLLQSDEQLQIY |
| 23293 | 53661 | A | 23427 | 2365 | 2784 | |
| 23294 | 53662 | A | 23428 | 5789 | 5980 | DQNMRFDNFTFETYYWKPTIIVII IRKLLMNDSSKDTLK*LRCWK NWLQILKKHTIHFIMPLQL |
| 23295 | 53663 | A | 23429 | 1 | 6819 | |
| 23296 | 53664 | A | 23430 | 376 | 2052 | SKVCGNDGFADDLKHLIFTGA QSGEDIVPFQLEDGHS LG EVVL LHGGSGVESGQR/CGRTSAGSC Y*SPGKICCCNLLVTKTEGFFAP VPIQLENTNQVTNCS DNW |
| 23297 | 53665 | A | 23431 | 2 | 2189 | |
| 23298 | 53666 | A | 23432 | 2 | 1583 | |
| 23299 | 53667 | A | 23433 | 2142 | 2242 | GASVAPSIGS*STGNAIPSCLFQ QNVIVPIPQS |
| 23300 | 53668 | A | 23434 | 3 | 1188 | |
| 23301 | 53669 | A | 23435 | 470 | 862 | |
| 23302 | 53670 | A | 23436 | 1 | 1352 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23303 | 53671 | A | 23437 | 1837 | 1955 | SKCSIGLYQRYPYNSGC*NSGCI CRVY*CCREHRGYVRN |
| 23304 | 53672 | A | 23438 | 1447 | 1565 | SKCSIGLYQMYPYNSGC*NSGC ICRVY*CCREHRGYVRN |
| 23305 | 53673 | A | 23439 | 773 | 823 | |
| 23306 | 53674 | A | 23440 | 3 | 1529 | |
| 23307 | 53675 | A | 23441 | 1 | 1794 | |
| 23308 | 53676 | A | 23442 | 236 | 427 | DQNMRFDNFTFETYYWKPTIIVII IRKLLMNDSSKDTLK*LRCWK NWLQILKKHTIHFIMPLQL |
| 23309 | 53677 | A | 23443 | 8510 | 8611 | GASVAPSIGS*STGNAIPSCLFQ QNVIVPIPQS |
| 23310 | 53678 | A | 23444 | 516 | 669 | ATSELKRKASLGLMEPDVSRK* ARCSSLPSSSIGDGRYISGYLRL GRCHE |
| 23311 | 53679 | A | 23445 | 410 | 593 | FLNLIQPQGKRKLLLKRCSRLLP KN*CQHSKQHKLSISSVVILNIT NS*PNKVKLMPILAM |
| 23312 | 53680 | B | 23446 | 1 | 2286 | |
| 23313 | 53681 | A | 23447 | 1418 | 1723 | CNTNIIFNCHFPTKLGCKKAMK VVSPLIHNSIVILLNQITIDFFSTL AQICTFICLTYSKQTTTRIASFK KVIEEFLSLAPIEKVELKEHS*YI SISEKV |
| 23314 | 53682 | B | 23448 | 1 | 6167 | |
| 23315 | 53683 | A | 23449 | 1 | 3199 | |
| 23316 | 53684 | A | 23450 | 1 | 5733 | |
| 23317 | 53685 | A | 23451 | 709 | 1099 | |
| 23318 | 53686 | A | 23452 | 5039 | 5230 | DQNMRFDNFTFETYYWKPTIIVII IRKLLMNDSSKDTLK*LRCWK NWLQILKKHTIHFIMPLQL |
| 23319 | 53687 | A | 23453 | 664 | 993 | |
| 23320 | 53688 | A | 23454 | 1 | 19859 | MASIDSI AVCNPRQVRKFVEHC IRSGLV PFITSSPGMGKSAIVRQI AEDFGLKLIDHRLSTSAPEDLSG LPRFKENGRAEFAPFDELFPLEG DAVPEGFNGWLLFLDEFNSAR KEIQAAAYKLVLDRMTGQKKL HPYVAIVCAGNKATDRAITNNL STAMQSR LIHLEMETDFDVFME DVAIPNKWDERVIAFLNANPNK LNDFEPDHQEKTFCCSRTWEFV NKIVSILPPGPINSEMTLLLAGTI TSGVATSFV |
| 23321 | 53689 | B | 23455 | 74 | 240 | |
| 23322 | 53690 | A | 23456 | 143 | 384 | |
| 23323 | 53691 | A | 23457 | 1 | 3267 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23324 | 53692 | A | 23458 | 2 | 550 | KRSSEHIQRIDRDVSGTLRKHIF FRDRYGTKQRELLHILLAYEEY NPEVGYCRDLSHIAALFLLYLP EEDAFWALVQLLASERHSLQG FHSPNGGTVQGLQDQQEHVVA TSQPKTMGHQDKKDLCGQCSP LGCLIRILIDGISLGLTLR\LWDV YLVEGEQAFMPITRIAFKVQQK RLTKTSR |
| 23325 | 53693 | A | 23459 | 72 | 630 | |
| 23326 | 53694 | A | 23460 | 1 | 2835 | MDALMLALGALMLALGLGDP KSAQVSDPDGAEPGPGRATGT DPLVQIHWKLGISEALSIPGGRL YRDLWSLTPVCLHIPGIAHHGP FTLGRMDVVEVAGSWWAQER EDIIMKYEKGHRAGLPEDKGPK SFGSYNNNVNDHLGIVHETELPP LTAREVKQIRREISRKSKWVKM LGEWDTYKNSRKLIDRAYQGIP MNIRGPMWSVLLNIEEIKLKNP GRYQVRSARAQPTGQAVSGAQ VSSWRERQDHPGELGVKI |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23327 | 53695 | A | 23461 | 1 | 832 | MGWRARWLMPVISALWEAED PIPELTRLLQQSQDPLLMGLFP TNPKEKTQEPPGQSRAVLT VSKFKVLAGLLHLGNIQFAASE DEAQCQPMDDAKCEGQGVG WAGPVRKASLEQLLQVLHSTT PHYIRCIPNSQQGAQTFLQEE AGAGRRRQRRRQKQQRRRRQ LGGGGDGGNGSVGDDGATRG RGCALEKECVATPRRGLLFSRP HKLAFVGGSVTSVGPKPAP MDVVEVAGSWWAQEREDIM KYEKGHRAGLPEDKGPKPFRS YNNNVDDLGLVQDFADFGTTIK QDFRLLGQTSVDRLLQLSQGQ AVKGNQLLPVSLVKRKTTLAP NTQTASPRALADSLMQLARQV SRLESGHFYDAHNPFLPPPSMS KQAKKTGVPSEGLCRPGGEGQ SAVARLTGEKKNHPGAQYANR LSPRVGRFINAAGTTGFPTGKR AVSATQLIGLQLILLGEVLQKV LTASYPAQSSVPLTSGPVRQIM KEKGKRSSEHIQRIDRDISGTLR KHMFFRDYGTQRELLHILLA YEEYNPEVGYCMDLSHIAALFL LYLPEEDAFWALVQLLASERHS LQAARAPAAIGAHERADQAQIS LGLTLRLWDVYLVEGEQALMP ITRIAFKVQKRLTKTSRCGPW ARFCNRFVDTWARDEDTVLKH LRASMKKLTRKQGDLPAPAKPE |
| 23328 | 53696 | A | 23462 | 3 | 497 | SSECLTMAWIPLLLPLLILCTVS VASYELTQPASVSVSPGQTASIT CSGDVLAKKKYARWFQKPG QAPVLVIYKDSERPSGIPERFSG SSSGTTVTLTISGAQVEDEADY YCYSAADNNGWVFGGGVTKLT VLSQPKAAPSVTLFPPSSEELQ ANKAHTGVSQ |
| 23329 | 53697 | A | 23463 | 1 | 393 | FRSGSELVKAGLRAFFENAAED LEKTSNENLKLKGFTHSRTQIKG VSQNINYTTVALLPILTSIFEHV TQHQFGMDLLLDVQISCYHIL CSLYSLGTGKNIVVEILGMPDT VEDMCPDIPQLECLMKEIN |
| 23330 | 53698 | A | 23464 | 319 | 508 | |
| 23331 | 53699 | C | 23465 | 94 | 222 | |
| 23332 | 53700 | A | 23466 | 1 | 636 | |
| 23333 | 53701 | A | 23467 | 1 | 483 | |
| 23334 | 53702 | A | 23468 | 1 | 1797 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23335 | 53703 | A | 23469 | 1 | 4275 | |
| 23336 | 53704 | A | 23470 | 1 | 1848 | |
| 23337 | 53705 | A | 23471 | 122 | 14928 | ARSWRRRWRTTRTKRRRRKSAA AVSARRAAAGGSRGAGGWGT ADASGAMAEGGEGGEDEIQFL RTEDEVVLQCIATIHKEQRKFC LAAEGLGNRLCFLEPTSEAKYIP PDLVCNCFVLEQSLSVRALQEM LANTGENGGEGAAQGGGHRTL LYGHAVLLRHSFSGMYLTCLTT SRSQTDKLAFDVGLREHATGE ACWWTIHPASKQRSEGEKVRIG DDLILVSVSSERYLHLSVSNNGNI QVDASFMQTLWNVHPTC |
| 23338 | 53706 | A | 23472 | 134 | 1063 | RPPGLTRSPSPAPARSPTRRQS TRRRSGATTSCSQRLWATWNG CD/VCLNQLSREIPTDDKGFTAI HFAAQWGKLACLQVLVEEYKF PVDLLTNNSQTPLHLVIHRDNT TVALPCIYYLLEKGADLNAQTC NGSTPLHLAARDGLLDCVKVL VQSGANVHAQDAMGYKPIDFC KIWNHRACARFLKDAMWKKD KKDFAREMTKMKMFKSQLTL MEHNYLIEYQKEHKILREAAIR KWLHGKLLHPGHSLVSN TKQAR ATALSKTPEQRESQRSRSFHPVS DARLQCIPQPTMPKPIYRKPTV KRPHNVEC |
| 23339 | 53707 | A | 23473 | 1 | 1280 | MAGLGFWGHAPGPLLLLLLLV LPPRALPEGPLVFVALVFRHGD RAPLASYPMDPHKEVASTLWP RGLGQLTTEGVRRQLELGRFLR SRYEAFLSPEYRREEVYIRSTDF DRTLESAQANLAGLFPEAAPGS PEARWRPIPVHTVPVAEDKLLR FPMRSCPRYHELLREATEAAEY QEALEGWTGFLSRLENFTGLSL VGEPLRRAWKVLDTLMCQQA HGLPLPAWASPDVLRTLAQISA LDIGAHSVGPRAAEKAQLTGGI LLNAILANFSRVQRLGLPLKMV MYSAHDSTLLALQGALGLYDG HTPPYAACLGFEFKHLGNPAK DGGNVTVSLFYRNDSAHLPLPL SLPGCPAP\CPLGRFYQLTAPAR PPAHGVTCHGPYEA AIPPAPVV PLLAGAVAVLVALSGLGLLA WRPGCLRALGGPV |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23340 | 53708 | A | 23474 | 133 | 672 | AVGWESGKWDSGRGQGGGQE QMWSCQSDMLYPPDQVGAWG LPGPTGPKGDAGSRGPMGMRG PPGECQCCPTAPLAIPSTRWAL PCSWPPGPPGPPGPPAPVGPPHA \GSPSMVSPPGIPAGGGGGGVAI STVPATIKTRRQEVSPELPRP/PG PAPPPGPDVRPWLLRPPGPMGK LSPGQG |
| 23341 | 53709 | A | 23475 | 135 | 677 | AVGWESGKWDSGWGQGGGQE QMWSCQSDMLYPPDQVGAWG LPGPTGPKGDAGSRGPMGMRG PPGECQCCPTAPLAIPSTRWAL PCSGPPGPPGPPGPPAPVGPPHA \GSPSMVSPPGIPAGGGGGGVAI STVPATKKTRRQEVSPELPRP/P GPAPPPGPDVRPWLLGPPGPMG KLSPGQG |
| 23342 | 53710 | A | 23476 | 220 | 745 | TVIQR TGLHSVGPDPQQGLRE AKLGTMVRLVLLPTPRRTTEVR TGPERELSMVLEAILGSLL ETAC DHRQTPPSSKPQA/GSSRLREGT SAGQPCS/LRLRLGPRAGGRRC CRDIERSSSSSVCGRKCKRKKR KRGMCQSRHKHGCRRPQEGPR CNDGRALCSPRPQTTPGPLSTA |
| 23343 | 53711 | A | 23477 | 1 | 2433 | |
| 23344 | 53712 | A | 23478 | 3 | 803 | FPGRFRVRACVAGGSHCLFNS CCCCTASLPARERHEWPGPAA AAAAAAAAAARRSQTQREGLFA GWGGGFAMSDDDSRASTSSSSS SSSNQQTEKETNTPKKKESKVS MSKNSKLL\SPRAKGIQKEL\AD ITLDPPPNCSAGPKGDNIYEW STILGPPGSVYEGGVFFLDITFTP EYPFKPPKVTFRTRIYHCNINSQ \GVICLDILKDNWSPALTISKVL LSICSLLTDCNPADPLVGSIA TQYMTNRAEHDRMARQWTKRYA T |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23345 | 53713 | A | 23479 | 372 | 1839 | GEAGGTEAEPENGAGGPRVPG WWGWSSTSSPRGCWDSGRSAA AIMDFLWDKRTGLAARKMPHP RRYHSSERGSRGSYCEHYRS/R K/HKQRRSRWSSSSDRTRRRR REDSYHVRRRCRSTFSRSSSQH SSRKAKSVEDDTEGHLYHVGD WLQERYEIVSTLGKGTfGRVV QCVDHRRRGARVALKIIKNVE KYKEAARLEIKVLEKINEKDPG KNLCVQMFDWFDYHGHMCISL ELLGLSTFDLKDNNHLPYPIH QVHHMASQLCQAVKFLHDNK LTHDLDKPENILFVNSDYELTY NLEKKRHERSVKSTAVRVGDF GSATFDHEHHSTIVSTRHYRAP EVILELGWSQPCDVWSIGCIIFE YYVGFTLFQTHDNRQHLATME RILGPIPSRMIRKTRKQKYFYRG RLDWDENTSAGRYVRENCKPL RQYLTSEAEEDHQLFDLIESML EYEPAQRLTLGEALQHPFFSRL WAEPNKLWDSSQDISP |
| 23346 | 53714 | A | 23480 | 28 | 941 | QSARPSLKRARSQRGRPLPSRA LVFLFLFFFFFFNFLPIHTQPSAH KDMTTNAGPLHPYGPQHLARLD NFVFNDRPTWAYTGLGLFSVT GGLRSWTTWAVVQGRAAGCPI GDFGRATVPCCWVLQCVGFIH LVIEGLVPFSNYERPCFGDQSL NLKLWKEYGQGETARLHPGG DKFHSVALGTITSFA\WGEPFSL WVVI\FLLQHPLRFIL\QLVVS VG\QIYG\DV\FYFLKEHPRRDS KHGKPGPTPLLLPGFSFVFHEM PLWLVPAGSPLCLDA\VKAPS THAPEHAWNAKGPKPKSKKN |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23347 | 53715 | A | 23481 | 1 | 1386 | MWRNLKLPRDLLNGFDQNADS DMDNEVQAEVVTGDEELIGN WSKGHSCYILAKRLAAFFPCPK DLWKFELERDDLGYLAEEISS EAFKSVSYEKAAHWNPLESTC RHASLALAVVLQRRDWENPVG VTQL\NRLAAHPPFASW\RNSEE ARTDRPSQQLRSLNGEWRLMR YFLLTHLCETLVKVKDAEDQL GARVCVLERQIFDFLG YQWAPI LANFVHIIIVILGLFGTIQYRPRY ITGILSFPHKHQESLSLKFTCLTEA ERDTDALLHLENACRESTATQR IQGFFLKDKKRKKQQPQQQKQ QQWAKVQLGPWLQRVQAPSL GSFHGVLRLVHRSKELRFRNC CLDFRGCMEMPGCPGRGV LQA QNPRGEPLLGQCRREMC GGSP YIVPTGALPSGAVRRRPPSSRPH NGRPTDSLHCVP GKAA DTQH PLKAARRAAVPCKATGSELPK |
| 23348 | 53716 | A | 23482 | 3 | 732 | SPLTPTATSGNPSKASSPGGLGS LVSTASSLPAGEKNSPRTGPGP RRAG\AGIPNSGPD TVEGPYNL CGRQGRWGGLIISLASEMKLQT LQTSVTTAKATLLELFVPLGGL VASLASEVRLQIFPRGGHLQSA KCGLLLHFSLPTSRSRRKANR PMAVTVLLVLIRDCADLLAVK AVIH CYQDQWPLRGSSRPANTP PPKASVSRPPGHRGVRRGSPL LQVGARRVGAEAPALLELQSPS |
| 23349 | 53717 | A | 23483 | 1 | 234 | |
| 23350 | 53718 | A | 23484 | 1 | 256 | MLNLQGKEWLELEEDAQKAYI MGLLDRLEVVSRRRLKVARA VLYLAQDGEKFCPKRDCTNNS/ RY/NSI*MIQMMRFGTLELMRL |
| 23351 | 53719 | A | 23485 | 1 | 3333 | |
| 23352 | 53720 | A | 23486 | 1 | 2661 | |
| 23353 | 53721 | A | 23488 | 3 | 433 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23354 | 53722 | A | 23489 | 3 | 990 | EKMNTADQARVGPADDGPAPS GEEEGEGGGEAGGKEPAADAA PGPSAAFRLMVTRREPAVKLQ YAVSGLEPLAWSEDHRVSVST ARSI AVL ELICDVHNP GQDLVIH RTSV P AP L NSCL L K V GSKTEVA ECKE KFAASKDPTVSQTFMLDR VFNPEGKALPPMRGFKYTSWSP MGCDANGRCLLAALTMDNRL TIQANLNLRLQWVQLVDL TEIYG ERLYETSYRLSKNEAPEGNLGD FAEFQRRHSMQTPVRMEWSGI CTTQQVKHNNESRDVGSVLLA VLFENGNI AVWQFQLPFVGKES ISSCNTIESGITSPSVLFWWEYE HNNRKMSG L I V GSAFGPIKILPV NLKAVKGYFTLRQPVILWKEM DQLPVHSIKCVPLYHPYQKCSC SLVVAARGSYVFWRLLLISKAG LNLHNSHVTGLHSLPIVSMTAD KQNGTVYTCSSDGKVRQVIPIF TDVALKFEHQLIKLSDVFGSVR THGIAVKPCGAYLAIITTEGMIN GLHPVNKNYQVQFVTLKTFEE AAAQLLESSVQNLFKQVDLIDL VRWKILKDKHIPQFLQEALEKK IESSGVTYFWRFKLFLRLIYQS MQKTPSEALWKPTHEDESKILLV DSPG\MGNADDEQEEGTSSKQ VVKQGLQERSKEGDVEEPTD\D SLPTTG\DAG\GREPMGRNSW GNSK GKIRSCWEMRLTREHMK |
| 23355 | 53723 | A | 23490 | 1218 | 1446 | RCTDSQVRSPTPLHLAAQACSL ETTVCLLCSKADYTLSEKRGW MPIHF AAFYDNVCIIALCRKDP SLLEAEATAE |
| 23356 | 53724 | A | 23491 | 2 | 632 | NMAKTYDYLFKLLLIGDSGVG KTCVL\FRFSEDAFNSTFIFTIRI DFKIRTIELDGKRIKLQIWDTAG QERFRTITTAYYRGAMGIMLVY DITNEKSFDNIRNWIRNTEEHAS ADVEKMILGNKCDVNDKRQVS KGS/GENKLALDYGIKFMETSA KANINVENAFFTLARDIKAKMD KKLDGNSPIQGSNQG VKITPDQ QKRSSFFRCVLL |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23357 | 53725 | A | 23492 | 1 | 1018 | MVFYHVGQAGLELLTSGPHCP DSQAADKAESATLLSRARLGA YCACASLERRWPHFPSGRECN MAKTYDYLFKLLL\IGDSGVGK TCVLF RFSEDAFNSTFISTIGIDF KIRTIELDGKRIK\LQIWDTAGQ ERFRTDHNRP TYRGAMGI\ML VYDITNE\KSFADNIRN\W\RNIE EHASAD\VEK\MILGNKCDVND KRQVSKERGEKLALD\YGIKFM ETSAKANINVENAFTLARDIK AKMDKKLGPARPHGTLLGKGE EFAGVAGASASGSASLGTLPKQ TRPCPVNPQASREHTAFSIPKQ QKDNMEGNSPQGSNQG VKITP DQQKRSSFRCVLL |
| 23358 | 53726 | A | 23493 | 1 | 130 | |
| 23359 | 53727 | A | 23494 | 1 | 1392 | |
| 23360 | 53728 | A | 23495 | 445 | 649 | YPSLTNSKLLVHH\FMELC\WD KCVEKPQGIALDSRTENCL\SC \VDRFID\TLAITSRFAQIVQKG GQ |
| 23361 | 53729 | A | 23496 | 210 | 397 | VIYAPGKKAQRTQK/APKTKTK KPHLSPCPSP/WRSRSCQPMQQS WSGAQVHIPQPPHTTCITWA |
| 23362 | 53730 | A | 23497 | 55 | 286 | QASSSPPISSVTCKALPPGQTK KGLVASGDPEPVSMGTSSPTPS LAPEHSSRASLEPSSSA*PSLAT* SRAGGSQA |
| 23363 | 53731 | A | 23498 | 780 | 1022 | QAMHGRSPGVTVRASGLRNEG DGPLGSVPTQARATGAPGHSAT PSPA WRAW\SSSSKAS/WLPDA AGPPTPPWSGPSPTSW |
| 23364 | 53732 | A | 23499 | 1 | 782 | |
| 23365 | 53733 | A | 23500 | 275 | 688 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23366 | 53734 | A | 23501 | 1166 | 2271 | LRCILTLISRWCS*VSTVANLPP GISKWGANWQRCMKE*CWSP AVTWCITCAQRSG/IGDSSPYPG ATSFNEYVKANLTWRGPVEQH PLVNYLDHERGTLSNPTARHYL PVLVYLRAILWARTPLPIPGRRT VSKVKMKKRILRAMRQKQQVL PLLVLGLGLDELSMSAPSIPAAK ARMAQLDSRECRKLLNQAMA CRTSLEVEHLLAQFRMTQQDA PLVTAECITLES DWSKEEV LK GMTDNL LLAGRCRYPRKLEAD LWAREAVFSTGLGFSFAIPHSK SEHIEQSTISVARLQAPVRWGD DEAQFIIMLT LNKHAAGDQHM RIFSR LARRIMHEEF RNALVNA ASADA IASLLNMNWT VKEHHE |
| 23367 | 53735 | A | 23502 | 1 | 2604 | |
| 23368 | 53736 | A | 23503 | 306 | 468 | TRHCDRRQPRRGHRRAGT/CNQ I*KGCCCVRTKQPLSSVLISPNF CPCSSFLKNS |
| 23369 | 53737 | A | 23504 | 102 | 509 | AAQQGTMARSLLLPLQILLLSL ALETAGEEAQGDKIIDGAPCAR GSHPWQVALLSGNQLHCGGVL VNERWVLTAAHCKMNEYTVH LGSDTL/E/ADRKAQRIKPSKSF RHPGYFTQTHVNDLMLVKLNS QARLSSMVK |
| 23370 | 53738 | A | 23505 | 1 | 1032 | MMQATVGFEDGDAATSQVSPS VNKVHSSYFLDFFEEYIVIAFKI LRRGPDISCSQIINGEDCSPHSQP WQAALVMENE/LFCSGVLVHP QWVLSAAPVSRKYNRPLAND LMLIKLDES VSESDTIRSISIASQ CPTAGNSCLVSGWGLLANDPT SRLPPPLECRNPVPQLLLPPEKP RTAPDTLGSSPVPKSRTGSSGSS FLLPAPPSPFPRPHHGTPPTSCG QDVDVPALAGGSLGSPAGEAL PRLAAPERLSRHHGKIPSPAPAD LTAILALETAGEEVPFPLTSCA WMSSSSPPGLHEGLQGLTGKFH AVRWHPR LQEKRLQSVSPDSR IPGARRPAAR |
| 23371 | 53739 | A | 23506 | 303 | 393 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23372 | 53740 | A | 23507 | 391 | 1170 | GSFFFFFFKYFAYSPMPKNSKVV KREDDDDVTESVKDLLSNEDA ADDAFKTSELIVDQGEEKDTDV EGK\SEVEDERPAWNSKLQYIL AQVGFSVGLGNVWRFYLCQK NGGVVEPECEQSSATYYWYR EALNISSSISESGGLNWKMTICL LAAWVMVCLAMIKGIQSSGKV N'TYDRVTMSATVLAALQEQQWT FSPIRSGNGHLTGSGAQRTPCRI RRGGSQLRVCDGGKQQWWTV SQSSARAITNTDQKSVQLQDLIE |
| 23373 | 53741 | A | 23508 | 45 | 546 | EGGGSRSLSWFRELIGQPVSFIE PVAAGGAVALNVQ/RSCGVVS AAPACL*SRPHSWRWGGPACW RTPGG/LASRSSSSASILMSSSRA SFTRSLSLSTHKDQGLVCSGSS GATGAGSC/LWPPTSHTVKLMF LYSTVSTLKPMVGMVVTISPSL SL*RIVVFPAASRPT/YEDAHFFF CQKGP*RGSWSSLQHPGPP |
| 23374 | 53742 | A | 23509 | 1367 | 2142 | VRRPQGCLGKRSLLSRVCALVP WGIWP/WSLAVGPQYSSLGSQP ILCASIPGLVPKQLRFCRNYVEI MPSVAEGIKIGIQECQHQRGR RWNCTTVHDSLAIIFGPVLDKG YFGYLETITVPSDSVVSTKAETP DKGVCGRELGFRGGWLPELQS LDEISMGWALCSRLQIKATRES AFVHAIASAGVAFVTRSCAEG TAAICGCSSRHQGSPPGKWKW GGCSEDIEFGGMVSREFADARE NRPDARSAMNRHNNEAGRQV GSPPARVLGKKEPPQQGVCPGS LGHMARSLAVGPQYSSLGSQPI LCASIPGLVPKQLRFCRNYVEI MPSVAEGIKIGIQECQHQRGR RWNCTTVHDSLAIIFGPVLDKG YFGYLETITVPSDSVVSTKAETP DKGVCGRELGFRGGWLPELQS LDEISMGWALCSRLQIKATRES AFVHAIASAGVAFVTRSCAEG TAAICGCSSRHQGSPPGKWKW GGCSEDIEFGGMVSREFADARE NRPDARSAMNRHNNEAGRQ |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23375 | 53743 | A | 23510 | 2094 | 2619 | ASPASPAPCSGIPRT*SPYPSPSR TQ\APRARGPAIHHPGP/RGCT ALPRQGPPTPGSARAPPRIPAHR APTSPTLNFCLASSRQSMPPAPR PPPVPATNPVTPGCGRPPPTLGC RNPQTLRPPPGLPSPALLRRPLP PPARVGMPPHQPLPTTPACWR PVDWARAEGAGRAVC |
| 23376 | 53744 | A | 23511 | 3050 | 3317 | PARTSPSASGPP**DLISALWTPS QPRAPTRQSLNSLSSSAPSSSTIG PSPSPAPGPAPPLPWLPSPSSL PRLSQVSRRPHSHLHPQ |
| 23377 | 53745 | A | 23512 | 862 | 2954 | AEHTLLVCFNLNTSLTTTSTHVES FGGQLRGSQIGHPRRPNKMPYA WSIPQDPPLKPERDPGGPLGVS LSLPVNQYGESEEPMGDDDDYD EYSKELNQYRRSKDSRGRGLSR GRGRGSRGRGKGMGRGRGRG GSRGGMNKGGMNDDEDFYDE DMGDGGGGSYRSRDHDKPHQ QSDKKGKVICKYFVEGRCTWL YHTTGNCINGDDCMFSDPLTE ETRELLDKVEMTGSSVFDYIHP GDHSEVLEQLGLRTPPTPGPPTPP SVSSSSSSSSSLADTPEIEASLTK VPPSSLVQERSFFVRMKSTLTK RGLHVKASGYKVIHVTGRLRA HALGLVALGHTLPPAPLAELPL HGHMIVFRLSLGLTILACESRVS DHMDLGPSELVGRSCYQFVHG QDATRIRQSHVDCETHLHPPSL PTTPQTRASHSLVPGSPSSGLPT VPPAAPTAPGTPFSIGRAARRLS DASGLLDKGQVMTGYRWLQ RAGGFVWLQSVATVAGSGKSP GEHHVLWVSHVLSQAEGGQTP LDAFQLPASVACEEASSPGPEPT EPEPTEGKQAAPAEAEAPQTQ GKRIKVEPGPRETKGSEDSGDE DPSSHPATPRPEFTSVIRAGVLK QDPVRPWGLAPPDPPPTLLHA GFLPPVVRGLCTPGTIRYGPAEL GLVYPHLQRLGPGPALPEAFYP PLGLPYPGPAGTRLPRKGD |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23378 | 53746 | A | 23513 | 1319 | 2211 | GSKVYGSLFHINHGPNPFNMEVL VDSWPEYQMVIIRPQ/ETVRGE EKVQGNDLTFHHPTQEMTDDM DSYTNVYRVFSKDPQKSQEV KNSEIINWKQKLQIQGFQESLG EGIRAAAFSNSVKVEHSRALLF VTEDILKLYATNKS KLGSWAET GHPDDELESETPNFKYAQLNVS YSGLVNDNWKLGMNKRSLRYI KRCLGALPAACMLGPEGVPVS WVTMDPSCEIGMGYSVEKYRR RGNGTRLIMRCMKYLCQKNIPF YGSVLEENQGVIRKTSALGFLE ASCQWHQWNCYPQNLVPL |
| 23379 | 53747 | A | 23514 | 234 | 858 | SVPLQESPLPPPPTHQADC*SPC GAQGGWVTLAVASASS*AHTA SPLPRSPQAQGRAPSPAPPQIHL TTPSSFSSQGT/SHGGLGSTPGA DDPNTSSS\PPPGGSTPRWSAGD SAHSGGEVDGWS*SFP*SVPSY GT*SPFCWPSSGQRSFHGIASG WEPDGIPDGSSRWPCGKPQES ETGVEGRQHFPKQLCLGSCRA VASPRVARA |
| 23380 | 53748 | A | 23515 | 1 | 3582 | |
| 23381 | 53749 | A | 23516 | 628 | 4254 | RLPESRAHDVAGADERPWPVH AGIFKSPAAGAAMSPAAAAAG AGERRRPIASVRDGRGRGCGGP AGAALLGLSLVGLLLYLVPAA AALAWLAVGTAAWWGLSRE PRGSRPLSSFVQKARHRRTLFA SPPAKSTANGNLLPRTLLEGP DPAELLLMGSYLGKPGPPQAP APEGQDLRNRPGRRPPARPAPR STPPSPPTH RVHFFYPSLPTPLL RPSGRPSPRDRGTLPDRFVITPR RRYPIHQTQYSCPGVL |
| 23382 | 53750 | A | 23517 | 1 | 392 | KVHMNGRLRYALYIMGPALTRG CHQVLIMLCCEVIERILT/VMM KEAYFGEVDIMDDLPTGNISA NVTGRLYKCGVINHTVDLRRM KT/EKWQNNLLPSRQFGFIVLTT SAGIMDHEEARRKHTGGKILGF |
| 23383 | 53751 | A | 23518 | 227 | 352 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23384 | 53752 | A | 23519 | 3 | 507 | SFRAATMVRMNVLADALKSIN NAEKRGRQVLIRPCSKVIVRF LTVMMKHGYIGEFEIIDDHRAG KIVVNLTGRLNKVGVQWRDLG YCNLCPLGSSDSSASASLVAEIT \\CGVISPRFDVQLKDLEKWQNN LLPSRQFGFIVLTTSAGIMDHEE ARRKHTGGKILGFFF |
| 23385 | 53753 | A | 23520 | 279 | 653 | ARAQRFSSQVDVFYLIQSVIFCR LALAEFEIIDDPQSLGKLL*TLT GRLKQ/CLGVISPRFDVQLKRP WKKWHEIIL/PSNPAKFGFIVLT TSAGLHG/HHEGRQDRKHTGG KILGILLYRDVIHIFT |
| 23386 | 53754 | A | 23521 | 1 | 392 | KVHMNGLRYALYIMGPALTRG CHQVLMCLCCEVIERILT/VMM KEAYFGEVDIMDDLPTGNISA NVTGRLYKCGVINHTVDL/PPY ENGKWQNNLLPSRQFGFIVLT SAGIMDHEEARRKHTGGKILGF |
| 23387 | 53755 | A | 23522 | 108 | 371 | LSYIGKFEIIDDHRAGKIVVNLT GGLNKCGVISLRFDVQLKDLEK WQNNLLPSCQFGFIALTTAGI MDHKEAR*KHTAGKILEFFF |
| 23388 | 53756 | A | 23523 | 252 | 378 | |
| 23389 | 53757 | A | 23524 | 3 | 518 | HASAFRAATMVRMNVLADAL KSINNAEKRGRQVLIRPCSKVI VRFLTVMKHHGYIGEFEIIDDH RAGKIVVNLTGRLNKVGVQWR DLGYCNLCPLGSSDSSASASLV AEIT\\CGVISPRFDVQLKDLEK\\ WQNNLLPSRQFGFIVLTTSAGI MDHEEARRKHTGGKILGFFF |
| 23390 | 53758 | A | 23525 | 279 | 709 | ARAQRFSSQVDVFYLIQSVIFCR LALAEF*NPLMTHQSLGKFVVN PHRAGLNKCG\\VISPQILTVQLQ RPWKKWAGLILL/PSRQVLGFI VLTTSAGI\\MDHEEARPKTPRR GKSWGFFFLGDVNYILFYKLKC LMDSGASTWSF |
| 23391 | 53759 | A | 23526 | 207 | 564 | SMAKEAISINRSLWAGPAKISSP AETEVIESLISLFQKYVGKGGYN CTLSKTEFLSFMNAELAAFTKN QKDPGVLHRMMKKLGTNNDG QLDFSEFLNLIGGLAMACHDSF LKAVPSQKRT |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23392 | 53760 | A | 23527 | 1 | 407 | FREKQSQELSQYGAMGAGQSF NSQFLQHGGPRGPSVPAGMNP TGIGGVMGPSGLSPLAMNPTRA AGMTPLYAGQRLPQHGYPGPP QAQP/PAPTGGQENLL*GVSRA AVSARSLPGPFRAIPVSHLAGNP TPPMNPH |
| 23393 | 53761 | A | 23528 | 3 | 315 | |
| 23394 | 53762 | A | 23529 | 1 | 763 | DYEEITIDPTCSWKVPVPKPD HIKEEPDGPALKRCRTVSPA LMPSVMEMIAALGPGAAPFAPL QPPSVPAUSDYPGQGSSFLGPGT FPESFPPTTPSTPTLAFTPGPPPI CYQSDIPSSLLTSEKST/SLPLQA RR/PPAGHLDPTHNPGLHTS NLGAPPGPQLHHSNPPASRQS LGQASLGPTGELAFSPATGVMG PPMSGAGEAPEALDLLPELT NPDELLSYLGPPDLPTNNDDL LSLFENN |
| 23395 | 53763 | A | 23530 | 1 | 2901 | MERRGPGAATARGRARPGGGP SVGLLATGSSLNPSFHGVARI GFIRIARPRDGSFAYESVPWQ ATQPAGSLSVTTVWGVGNAT QSQVLGNPMGPAGSPSGSSMM PGVAGGSSALTSPQCLGQQAFA EGGANKGYVQQGVYSRGGYP GAPGFTTGYAGGPGGLGLPSH AARPSTDFTQAAAAA ATATATATATVAALQEKQS LSQYGAMGAGQSFNSQFLQHG GPRGPSVPAGMNP TGIGGVM |
| 23396 | 53764 | A | 23531 | 80 | 412 | KPGNGACAGREWCDGGGA NWRDPGLPVGDGSDVDRV LLGPRSPRPLDVGGPAAGTPGV LSR/HLPVDCGLGPEALLCSSAP AARRPSLCGGHGRVMRGFR LCGFRP |
| 23397 | 53765 | A | 23532 | 1 | 192 | RPLDVGGPAAGTPGVLSR/HLP VDCGLGPEALLCSSAPAARRPS LCGGHGRVMRGFRGCGFRP |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23398 | 53766 | A | 23533 | 1 | 2094 | RPLDVGGPAAGTPGVLSRPCPS TAALAPKPFCAAPRPQPDAPAC AGATGGSCADFDGSGVDFVRRR SSGLWGPQPPLFPVKNYTEMFQ DPVAFKDVAVNFTQEEWALLD ISQKNLYREVMMLDTFWNLTSIG KKWKDQNIIEYEQNPRRNFRS VTEEKVNEIKEDSHCGETFTPV PDDRLNFQKKKASPEVKSCDSF VCGEVGLGNSSFNMNIRGDIGH KAYEYQEYGPCKCQPKKA FRYRPSFRTQERDHTGEKPYAL LKNDGKKPLFYHSSIQRHMVV HSGDGPYKCKFCGKAFHWLSL YLIHERHTTGEKPYECKQCGKS FSYSATHRIHERTHIGEKPYECQ ECGKAFHSPRSCHRHHERSHMGE KAYQCKECKGAFMCPRYVRRH ERTHSRKKLYECKQCGKALSSL TSFQTHIR\MHSGERPYECKTCG KGFYSAKSFQRHEKTHSGEKPY KCKQCGKAFTRSFSRYHERTH TGEKPYECKQCGKAHERHTTG EKPYECKLYGKALSRLISFRRH MRMHTGERPHKCKICGKAFSS PSSFQRHERSHTGEKPYCKQC GKAFTCFHF\FQYHERHTTGEK PDGCKQCGKAFRSAKYIRIHGR THTGEKPYECKQCGKAFHWVS SFHRHERTHAGEKPYECKHCG KAFTCSIYIRIHERIHTGEKPYQ CKECKGAFIRSSYCRKHERTHTI |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23399 | 53767 | A | 23534 | 48 | 1317 | CGLMDELVHDLTSALEQTSEQ NKLGELEWEEMALSPRQRRQL RKRRGRKRRSDFTHLAHTCC YSEASESSLDEATKDCREVAPV TNFSDSDDTMVAKRHPALNAI VKSKQHSWHESDSFTENAPCRP LRRRR\KVKRVTS EVAASLQKK LKVSDWSYERGC RFKS AKKQR LSRWKENTPWTSSGHGLCESA ENRTFLSKTGRKERM ECETDEQ KQGS DENMSECETSSVCSSSDT GLFTNDEGRQGDDEQSDWFYE GECVPGFTV PNLLPKWAPDHCS EVERMDSGLDKFSDSTFLLPSR PAQRGYHTRLNRLPGAAARCL RKGRRRLVGKETSINTLGTERIS HIISDPRQKDFWLP SAGKRERN QFNPLSPLYSLDVLADASHRRC SPAHC SARQANVHWGPPCSRDI KQEAETSGHSIFV |
| 23400 | 53768 | A | 23535 | 225 | 403 | |
| 23401 | 53769 | A | 23536 | 1 | 403 | REQEFLHMAPGEV TITVR LIRS LEHR\NFKPVVYHGVNLDQTV KEFIVFLKQDIPLRTNLP PFRN YKYDALKIIHQAHKSKTNELVL SLEDDERLLLKEDSTLKAAGIA SETEIGIFREEDYRNYKANPISS |
| 23402 | 53770 | A | 23537 | 2 | 239 | |
| 23403 | 53771 | A | 23538 | 2 | 214 | |
| 23404 | 53772 | A | 23539 | 1 | 1341 | |
| 23405 | 53773 | A | 23540 | 1 | 1677 | |
| 23406 | 53774 | A | 23541 | 1010 | 1509 | |
| 23407 | 53775 | A | 23542 | 1 | 6355 | |
| 23408 | 53776 | A | 23543 | 223 | 10504 | VKMPIGSKERPTFFEIFKTRCNK ADLGPI SLNWFEELSSEAPPYNS EPAE ESEHKNNNYEPNLFKTPQ RKPSYNQLASTPIIFKEQGLTLP LYQSPVKELDKFKLDLGRNVP NSRHKSLRTVKT KMDQADDVS CPLLNSCLS\ESPVVLQ\CTHVTP QRDKSVVCGSLFHTPKFVKGR QTPKHISESLGAEVD PDMSWSS SLATPPTLSSTVLIVRNEEASET VFPHDTTANVKSYSFNHDESLK KNDRFIASVT |
| 23409 | 53777 | B | 23544 | 137 | 709 | |
| 23410 | 53778 | A | 23545 | 1 | 1974 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23411 | 53779 | A | 23546 | 207 | 1622 | MACCL\SDEVKESKRINAEIEKA AAAETRRDARREL/RRLLLLT GESGKSTFIK\QMRIHGAGYSE EDKRGFTKL VYQNIFTAMQAM IRAM\ETL\KILYKVRSTRANA L\LIRGGGTLEKVTTFGAFSYVQ LPLKDLFGRDPGIQE/CAYERQP RSYQLSDSAKYLTVDVRIATL GYLPTQQ\DVPA GSRVPTT\GHI EY PFDLENII FARMVDVGG\QRS\ E RRKWIHCFENVTSIMFLValse YDQVLVESDNENRMEESKALF RTIITYPWF\QNSSVILFLNKKDL LEDKILYSHLVDYFPRSSMGPO R\DAKAAREFILKMFVDLNPNS DKII/YTSHFTCPHRHRRTSRFV FPAVKDTILQLNLEEKPGLSAP GPGRRDGDTGQDLPSTEPAAA RAGGAAESGPGLPAGGDDFFF IFLTNGFYFTVIRGCTSLPPYTSR TFSPFVNGKGSFLALTYGSLFS KKKKKKKE |
| 23412 | 53780 | A | 23547 | 1 | 401 | KKVPGRLSEMSFSLNFTLPANT TSSPVT\DCGPSLGLAAGIPLL VATALLVALLFTLIHRRRSSIEAM EESDRPCEISEIDDPKISENPRR SPTHEKNTMGAQEAHIYVKTV AGSEEPVHdryRPTIEMERRR |
| 23413 | 53781 | A | 23548 | 584 | 1071 | PCRLPLHLILVEDLSFSLNFTLP ANTVSTAAPIHQAT/PEKTSAEF TDCGPSLGLAAGIPLL VATALL VALLFTLIHRRRSSIEAMEESDR PCEISEIDDPKISENPRRSPTHE KNTMGAQEAHIYVKTVAGSEE PVHdryRPTIEMERRRGLWWL VPRLSLE |
| 23414 | 53782 | A | 23549 | 25 | 654 | LFLQMKDTSPIIFVRKELTIRQC TKKVPGRLEMSFSLNFTLPAN TTSSPVTGGKETDCGPSLGLAA GIPLL VATALLVALLFTLIHRR RSSIEAMEESDRPCEISEIDDPKI SENPRRSPTHEKNTMGAQEAHI Y\VKTVT\KSEEPVHdryRPTIE MERRRGLWWLVPRLSLGMMP TSNQGSHTWHLGTGLKTQGF VLGEERCQAAS |
| 23415 | 53783 | A | 23550 | 108 | 413 | RRSGSMALWRAYQRALAAHP WKVQVLTA/GLLGRKAALLAP CQ*LYLPTQASWTEGHASCS SLQEATSCPSAFCA*NSKATKQLV ERRGLQEHQGRGRTLT MVS |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23416 | 53784 | A | 23551 | 1 | 146 | |
| 23417 | 53785 | A | 23552 | 2 | 442 | GREARRSRSMALWRAYQRALA AHPWKVQVLTAA\ASGEEGSTA GMPVAIPADPGLLD*RTRFLLL TPRSHFLPLCLLRMKLKSHKRS LMGLGDIISQQLVERRGLQEHQ RGRTLTMVSLGCGFVGPVVG WYKVLDRFIPGTTKVDA |
| 23418 | 53786 | A | 23553 | 3 | 675 | RHSRFGAQGSMA\WRAYQ\RT LFA\LPWK\QVLTAGSLMGLG DIISQQLVERRGLQEHQ\RGRTL E/TMVSLGCGFVGPVVGWYK VLDRFIPGTTKVDA\ALKKMLLD QGGFAPSFLGCFLPLVGALNGL SAQDNWGQTTAGELG/RDYPD ALITNYYLWPAVQ\LANFYLP LHYRV\AVVQCVAVIWNYSLS WKAHRALSLPHSIVSTLQVMQ LDPWNGSDNPPQKWA |
| 23419 | 53787 | A | 23554 | 512 | 1227 | LQGHLMGIMAASRPLSRFWEW GKNIVCVGRNYADHVREMRSA /VWLSEPVFLFKPSTGVRAQRA RPILMPAYTRNLHHELEL\ALVI GQ\RCRAVPE\AAAMDYVGG\Y ALCL\DMTAWDVQ\ASARKKG LAWDSGE/DAFTASCPVQRVSL PKEKIPDPSQ\KALGFKVNGEL RQEGETSSMIF\SIPYIISYVSKIIT LEEGDIILTGTGPKGVGPVKEND EIEAGHTRAGQYDHLKVEKAQ |
| 23420 | 53788 | A | 23555 | 192 | 436 | RTSDHECFREGQICSVCLRERL NLNPEEACLLSQAPCMLFVLQY LNTVIPYEKKASPPSV\EDLQML VTNILFAMKEDNEKVP |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23421 | 53789 | A | 23556 | 94 | 1252 | ARMEAPLVSLDEEFEDLRPSCS EDPEEKPCFYGSSPHHLEDPSL SELENFSSEIISFKSMEDLVNEF DEKLNVCFRNYNAKTENLAPV KNQLQIQEEEEETLQDEEVWDA LTDNYIPSLSEDWRDPNIEALN GNCSDTIEHEKEEEEFNEKSEN DSGINEEPLLTADQVIEEIEEMM QNSPDPEEEEEVLEEEDGGETSS QADSVLLQEMQALTQTFNNNW SYEGLRHMSGSELTELLDQVEG AIRDFWE\ELVQQLARRDELEF EKEVKNSFF\TVL\IEVQNKQK\E QRELMKKRRKEKGLSLQSSRIE KGNQMP\LRFSMEGISNILQSG IRQTFGSSGTDKQY\NTVIPYEK K\AYPPSVE\DLQMLTNILFA\M KEDNEKVPYFA |
| 23422 | 53790 | A | 23557 | 391 | 1169 | GSFFFFFFKYFAYSPMPKNSKV KRELD DDVTESVKDLLSNEDA ADDAFKTSELIVDGQEEKD TDV EGK\SEVEDERPAWNSKLQYIL AQVGFSVGLGNVWRFYLCQK NGGVVEPECEQSSATTYYWYR EALNISSSISESGGLNWKMTICL LAAWVMVCLAMIKGIQSSGKV NTYDRVTMSATVLA\QEQQWQT FSPIRSGNGHLTGSGAQRTPCRI RRGGSQLRVCDGGKQQWWTV SQSSARAITNTDQKSVQLQDLIE |
| 23423 | 53791 | A | 23558 | 321 | 568 | CLWCGASWPRRHSSPGRPAGD HRGDRP/EGPDTQGPGRPEPSTE PAFNPQSSLDQGGGPAAPAVD DDTRRGHGGVCGDGGAGEA |
| 23424 | 53792 | A | 23559 | 510 | 690 | LRSPQ\RGVAAPPFLGSPVPFGG FRVQGGMAGQPSAPPALQTDD PYSKAHSVTPKSTPRVT |
| 23425 | 53793 | A | 23560 | 25 | 480 | |
| 23426 | 53794 | A | 23561 | 84 | 292 | VRAVQSLHFHFPWRR/ISCPSES TRSIHVDR\PRRNSASLSL\SAFP VSAGALINGEAWVRMGQVPIPI KAP |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23427 | 53795 | A | 23562 | 1138 | 1924 | CRSSATWTPWTTTGCRGDLTK TYSLEAYDNWFNCLSM LVATE VCRLLLSPGSAMLRSPATFQVV KKKHRTRMLEFFIDVARECFNI GNFNSMMAIISGMNLSVARLK KTWSKVKTAKFDVLEHHMDPS SNFCNYRTALQGATQRSQMAN SSREKIVIPVFNLFVKDIYFLPQ NP\SNHLPNGHINFKKFWEISRQ IHEFMTWTQVECPFEKDKKIP\S YLLTAPHPTARKLSSSPSESEG PENHMEKDSWKTLRRTLLNRA |
| 23428 | 53796 | A | 23563 | 3 | 260 | |
| 23429 | 53797 | A | 23564 | 1 | 1386 | |
| 23430 | 53798 | A | 23565 | 137 | 611 | MKVNLGDSQNLACVFCRKHD DCPNKYGEKKTKEKWNLT VH YYCLLMSSGIWQRGKEEGVY GFLIEDIRKEVNRASKLKCCVC KKNGAFIGCVAPRCKRSYHFP CGLQRECIFQFTGNFASFCWDH RPVQIITSNNYRESLPWHLLG NLFEPIPSY |
| 23431 | 53799 | A | 23566 | 181 | 486 | DPQGEAKGAAPAEAGGGGPV*W N\GLQGPAGVPGRDGGSPGANGI PGTPGIPGRDGFKEKGECLRE SFEESWTPNYKQCSWSSLNYGI DLGKIAECTFTKMRS |
| 23432 | 53800 | A | 23567 | 600 | 888 | QYNGMCSPGPAGVPGR\EGSPG ANGIPGTPGIPGRDGFKEKGE CLRESFEESWTPNYKQCSWSSL NYGIDLGKIAGRNCWHILAPVP NIVSLYFGS |
| 23433 | 53801 | A | 23568 | 91 | 1170 | ISLHRRPGPTCSMESPASSQPAS MPQSKGKSKRKKDLRISCM SKP PAPNPTPPRNLDSTFITIGDRN FEVEADDLVTISELGRGAYGVV EKVRHAQSGTIMAVKRIRATV NSQEQKRLLMDLDINMRTVDC FYTVTFYGFALFREGDVWICME LMDTSLDKFYRKVLDKNMTIP EDILGEIAVSIVRALEHLH SKLS VIHRDVKPSNVLINKEGHVKM CDFGISGYLVDSVAKTINAGCK VKHGHESLN\PD LN RK GCDVKS HVWSLGITMIEMAFLRFPYESW GTPFQQLKQVVEHPSPQLPAGR FSPEFVDFTAQCLRK NPAERMS YLELMEHPFFTLHKTKETDIA\A FVKEILGEDS |
| 23434 | 53802 | B | 23569 | 111 | 193 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23435 | 53803 | A | 23570 | 312 | 696 | RP*SAHPEPGDCSPPHPPRCGG VAQTAQVPDAPAPV*AG\QHSR SYMEDHLKKNRLEKEWEALC AYQAEPNSSFVAQREENVPKN RSLAVLTSQPTRNQCLPFLQHG PGDICTPVSISSIVLCHRVT |
| 23436 | 53804 | A | 23571 | 1 | 2974 | QAAGMGPPPLLLLLLLLLLPPR VLPAAPSSVPRGRQLPGRLGCL LEEGLCGASEACVNDGVFGRC QKVPAMDFYRYEVSVALQRL RVALQKLSGTGFTWQDDYTQY VMDQELADLPKTYLRRPEASSP ARPSKHSVGSERRYSREGGAAL ANALRRHLPFLEALSQAPASDV LARTHATAQDRPPAEGDDRFSES ILTYVAHTSALTYPGPRTQLH EDLLPRTLGLQLQPDELSPKVDS GVDRHHLMAALSAYAA |
| 23437 | 53805 | A | 23572 | 1 | 3202 | ASRRLPRGHGLSAAGQAAGMG PPLLLLLLLLLLPPRVLPAAPSS VPRGRQLPGRLGCLLEEGLCGA SEACVNDGVFGRCQKVPAMDF YRYEVSVALQRLRVALQKLS GTGFTWQDDYTQYVMDQELA DLPKTYLRRPEASSPARPSKHS VGSERRYSREGGAALANALRR HLPFLEALSQAPASDVLARTH AQDRPPAEGDDRFSESILTYVA HTSALTYPGSRRTLREDLLPR TLGQLQPDELSPKVDSG |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23438 | 53806 | A | 23573 | 1 | 1459 | MPLTSQDQVDQKTA A W V P T N R D STVPSDPWDCKRRPWPLLVLRP LAPGTKAPPGGQNGRGRQKGS PCSRRLLEPAGPLGPASVRCIR TTTPQLLIITTSRFPSEAAVGY GSNTCIFANACQMVFIMITWPY LQCIPYSVLLKDLEMRNLRELE DLIIEAVYTDIIQGKLDQRNQLL EVDFCIGRDIRKKDINNIVKTLH EWCDGCEA\ALLGIEQQVLRAN QYKENHNR/TLQQQVEAEDVYI LPQSGNDCRGLRFVSSLIGGVR CVHLKHKGDV V WEAIEEGEA LPGKYRLKGGRSVWAAAVRA VCMDQVTNIKKTLKATASSA QEMEQQLAERECPPHAEQRQP TKKMSKVKGLVSSSPLGPAGA AGTHQAWVRWGGDTKGPFPL STCSEFQTCPSPHQRLPTLLVLF QKNCYSPSPTSPFSCSLQTQGL HQCHPKTGSDTAQLPSRRFLSL CKGLVSLPVFLLLPRHFVRLVIK |
| 23439 | 53807 | A | 23574 | 2 | 396 | |
| 23440 | 53808 | A | 23575 | 1 | 1014 | |
| 23441 | 53809 | A | 23576 | 110 | 212 | |
| 23442 | 53810 | A | 23577 | 1 | 747 | |
| 23443 | 53811 | A | 23578 | 323 | 495 | GRAGK W H T Q P E * S L R K A M * M F Q I L M M K M I V A L A R A T S G T E A V A G R S W A S G L R R S G R V |
| 23444 | 53812 | A | 23579 | 26 | 229 | |
| 23445 | 53813 | A | 23580 | 1 | 574 | |
| 23446 | 53814 | A | 23581 | 889 | 1189 | |
| 23447 | 53815 | A | 23582 | 170 | 625 | G A A V A L V R P N G G T A A S H V V C R E M R P L R P L Q S R R C S R R R T G I S N M R A L E N D F F N S P P R K T V R F G G T V T E V L L K Y K K G E T N D F E L L K N Q L L D P D I K D D \ Q I I N W \ L L E F R S S V M Y L T K \ D F E \ Q L I S I I L R L P \ W L N R S Q \ T V V E E Y L A F L G N L V S A |
| 23448 | 53816 | A | 23583 | 166 | 455 | R W K P S G T W P R N P M E R P G H * E S V P K P G D * A K K S G G E T \ R G R K E G N E H R E T F S Q I P D C H L N K K S Q T G V K P C K C S V C G K V F L R H S F L D R H M R A H A G H K R S |
| 23449 | 53817 | A | 23584 | 3 | 3706 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23450 | 53818 | A | 23585 | 1 | 1970 | MVTDKAAAGTHGEARPCWG SGSRVHTYRGAGERAMRVHRP MPREDSERVREADGGKHEQRS FGDLHPTAAPAPAAASGCGTQPG RVKQPGEWQHREAPQQRQPPV RPHGSHQLVTVRYERRPGGKE RARLRPGLGCPSGRTPQGRAPQ GTALPTAAAAAIFPSAALTSGQ RNASLPKFYFRGGTWTGTSQSEA LCGKLSNQFLGEPLVPRIRLILS CGTCSGCSSPRKDPGHPEAGNG PSRDFQPLPSEERDSVAFEDVA VNFTQEEWALLSPSQKNLYRD VTLETFRNLASVGIQWKDQDIE NLYQNLGIKLRSLVERLCGRKE GNEHRETFSSQIPDCHLNKKSQT GVKPCCKSCVCGKVFLRHSFLDR HMRAHAGHKRSECGGEWRETP RKQKQHGKASISPSSGARRTVT PTSMRPYE\TKVCGKA\FIS\PIYF QIHQRTPTTEKRSYKCREIVRAFT VSSFFRKHGKMHTGEKRYECK YCGKPIDYPSLFQIHVRTHTGE KPYKCKQFGKAFISAGYLRTHE IRSHALEKSHQCQECGKKLSVCS SSLHRHERTHSGGKLYECQKC AKVFRCPSTSLQAHERAHTGERP YECNKCCKTFNYPSCFRRHKKKT HSGEKPYECTRCGKAFGWCSSL RRHEMTHTGEKPFDCQWVKS |
| 23451 | 53819 | A | 23586 | 86 | 390 | LGSGDLPEWINPLSSCSLLREKD PPTTSGPQTTSRPNISPISNPELA THAGNLATGPRNARSPGFLLSR VPSVWDPTENRTVQLTWQPLP ELLELPKVL |
| 23452 | 53820 | A | 23587 | 1 | 502 | MLLTQSLFGGLFTRTHMKFGA VTQIRGPPLGDKSPVLLLFALER QRRHVLSMDPKLRCWSRTGKA AFPWCLIIAEMPDISPTFQRCQ TTQGRLPWSFTLSSKSRFSGEG ARACYKCQKSDHQAKECPQPG IPPKPCPICAGPTGNRTVQLTW QPLPEPELELPKAL |
| 23453 | 53821 | B | 23588 | 1 | 663 | |
| 23454 | 53822 | A | 23589 | 233 | 496 | |
| 23455 | 53823 | A | 23590 | 2 | 378 | ERQRRHVLSMDPKLRCWSRTG KAAPWCLIIAEMPDISPTFQR CQTTQGRLPWSFTLSSKSRFSG EGARACYKCQKSDHQAKECPQ PGIPPKPCPICAGPTGNRTVQLT WQPLPEPELELPKAL |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23456 | 53824 | A | 23591 | 3 | 452 | VRPRRDACLGPSPLAASPAFLG KGQVPQPLISLCPDPLFPHPNLIS LRPNPLCPHPDLVSLCPDPFPAF LEAHKNFQTPEPQQPGIPPEPPP PGACYKC/HEI*PPGQGMCAAQ DSS*AMS/LSVRDPTGNQTVQL TWQPLPEPLELWPKAL |
| 23457 | 53825 | A | 23592 | 1352 | 1540 | |
| 23458 | 53826 | A | 23593 | 177 | 383 | EAMEPWKGVPLGRVNTEQIAP FSEAEGPREIH*GSRKVRKAAQ GLNEGPRELFWQPLPEPLELWP KAL |
| 23459 | 53827 | A | 23594 | 1478 | 1744 | |
| 23460 | 53828 | A | 23595 | 23 | 178 | SCLEVCDEQGPEK\TRQRALRG VSSVTEDTLNICRLCWQPLPEPL ELWPKAL |
| 23461 | 53829 | A | 23596 | 1 | 282 | |
| 23462 | 53830 | A | 23597 | 34 | 241 | SGDLPWEINPPSSCSLLREKDPP MTSGPQT\TSRNPISNPDPDTG NRTVQLTWQPLPEPLELLPKAL |
| 23463 | 53831 | A | 23598 | 121 | 286 | AASFYSSPTSLTIPQPLSPFNLG VTLQSLPSLNFNSFLFWQPLPEPL ELWPKAL |
| 23464 | 53832 | A | 23599 | 144 | 488 | GYEIWCRRSDQGTFPWEINPPS SCSLLREKDPPTSGPQT\TRPR NISPISNLVSGLFLLSSPPLTIPQ PLSPFNLGATLQSLPSLNFNSFH FLVETKETRFIRGAKIPAPVTD |
| 23465 | 53833 | A | 23600 | 471 | 677 | |
| 23466 | 53834 | B | 23601 | 67 | 555 | |
| 23467 | 53835 | A | 23602 | 1 | 1440 | |
| 23468 | 53836 | A | 23603 | 860 | 1209 | IPGNCRDSSGVGIKERETNAGS QMH/IKNSSVHGYPRLCVEDE DAYKKQFSQYIKNSVTPDMM EMEYKKAHAAVPENPVYEKKPK KEVKKRWNRSKMSLAQKKD WVAQKKASFLRA |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23469 | 53837 | A | 23604 | 1 | 966 | MGFVKVVKNKAYFKRYQVKF RRRREGKTDYYARKRLVIQDK NKYNTPKYRMIVRVNTRDMICQ IANARIEGDMIVCAPYAHLP KIWV*RVGLTNYAAA\YCTGLL AGPAGFFHFRGMDQIYE\GQVIE LTGDEYNVESIDGQPGCLHPAY WDARPLPTYPLAIKVFGCP*R GA\VDGGLVLFPHSTKTIPPGY DS\ESK\EFNAES/IHRKPHPWAQ NVARLHAPTLMEEDEDA/YTK KQFSQYIKNSVTPDMMMEEMV/Y RKAHAAIRENP\VYEKKPKKEV KRKRWNRPKMSLAQKKDRVA PKKASFLQSSRSGLLES\TPAIFP |
| 23470 | 53838 | A | 23605 | 1 | 644 | ANSSPVNPVFFDVSIGGQEVG RMKIELFADVVPKTAENFRQFC TGEF/RVSFRCV*LLCLLQRGVL GLQ*GYR*TTCWP*MIAGDSDR RKDGVPYIGYKGSTFHRVIKDF MIQGGDFVNGDGTGVASIYRG PFADENFKLRHSAPGLLSMANS GPSTNGCQFFITCSKCDWLDGK HVVFGKIIDGLLVMRKIENVPT GPNNKPKLPVVISQCGEM |
| 23471 | 53839 | A | 23606 | 638 | 1391 | CPAYKGAHQICQVYCTLPPLL QTTRRVRRNPTLPTSASGSEPW RLANSSPVNPVFFDVSIGGQE VGRMKIELFADVVPNTAENFR QFCTGEFRKDGVPYIGYKGSTFH RVIKDFMIQGGDFVNGDGTGV ASIYRGPFADENFKLRHSAPGL LSMLTWPGKLTAGIFGFHQANS GPSTNGCQFFITCSKCDWLDGK HVVFGKIIDGLLVMRKIE\GMPC IFQPTWTHFLPVITTACSALGSM LAAERGTKN |
| 23472 | 53840 | A | 23607 | 2 | 591 | ARAEFGTSRVGAMAVANSSPV NP\VVFFDVSIGGQEVGRMKIEL FADVVPKTAENFRQFCTGEFRK DGVPYIGYKGSTF\HRVIKGF\MI QGGDFV\NGDGTGSRPVFTRGP ILQMKIFKL\RHSA\GLLSMAN SGP\STNGC\QFFITC\SKCDW/V WDGKHVVFGK\IIDGLLVMRKI E\NVPTGPNNKPKLPVVISQCG |
| 23473 | 53841 | A | 23608 | 6 | 424 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23474 | 53842 | A | 23609 | 3 | 470 | DAWVSGRLTELPSSCFFPPIFRQ LLPVMPEPSKSAPAPKKGSKKA VTKAQKKDGGKKRKRSRKESYS VYVYKVLKQVHV\PD\TGISSKAM GIMNSF\VNDIFE\RIAGEASRLA HYNKRSTITSREIQTAVRLLLPG \ELCKHAV\SEGTNA\VTKYTSS |
| 23475 | 53843 | A | 23610 | 93 | 421 | |
| 23476 | 53844 | A | 23611 | 2 | 1173 | DHAAPRRRSRASVATVTRAGR CPTMSVRVARVAWVRGLGASY RRGASSFPVPPPGAQGV AELLR DATGAEEEEAPWAATERRMPGQ CSVLLFPQGQSQVVGMRGRL NYPRVRELYAAARRVLGYDLL ELSLHGPQETLDRTSQVQSPGT GIPRRVRAHVLHLSPQVIENC/V VS/AGLAFSPFCALIFPNALL/F WPGLYAVKIRAEAMQEASEAV PSGMLSVLGQPQSKFNFACLEA REHCKSLGPVNGQICKGGFLGH CSAETSFLPQALRFLQKNSSKF HFRTRMLPVSGAFHTRLMEP AVEPLTQALKAVDIKKPLVSVY SNVHAHRYRHPGHIHKLLAQQ LVSPVKWEQTMHAIYERKKGR GFPQTFEVGPRQLGAILKSCN |
| 23477 | 53845 | A | 23612 | 187 | 425 | |
| 23478 | 53846 | A | 23613 | 1 | 1258 | MKAYLLLGAAPPLPWFPQAV FRPCPPAGLWRTAQLVELEHG PVPREDLIPCSRPFISFLGPERV DGLAFPRIQALGIAAARGMEPK GAPGKSDSGNSRSAGGRVLGC QGAALEVECSAGRGGPVRLAV GCVLLRAPERGWRREGGAARG IPAGRSES LGALSPQVGVRSDI GINGNIWHPGVQTD FSSLKRSQ GLYAVKIRAEAMQEASEAVPS GMLSVLGQPQSKFNFACLEARE HCKSLGIENPVCEVSNYLPDC RVISGHQEALRFLQKNSSKFHF RRTRMLPVSGAFHTRLMEPAV EPLTQALKAVDIKKPLVSVYSN VHAHQIQIPGHIHKLLAQQLV SPVKWEQTMHAIYERKKGRGF PQTFEVGPRQLGAILKSCNMQ AWKSYSADVLTLEHVDLDP |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23479 | 53847 | A | 23614 | 2 | 1050 | GRCPTMSVRVARVAWVRGLG ASYRRGASSFPVPPPGAQGVAE LLRDATGAEEEEAPWAATERRM PGQCSVLLFPQGGSQVVGMR GLLNYPRVRELYAAARRVLGY DLLELSLHGPQETLDRTVHCQP AIFVASLAAVEKLHHLQPSVIE NCVAAAGFSVGEFAALVFAGA MEFAEG\LRFLQKNSSKFHFR TRMLPVSGAFHTRLMEPAVEP LERKLLKAVDIKKPLVSVYSQR PTRIRLQAFPGNIQQSCLAQQLG LPK*KWEQ\TMHAIYERKKGR RGFPQTFEVGP\GRQLG\AILKS CNMQAWKSYS\AVDVLQTLEH \DLDPQEPPKMTGRGLKCNDP LCPPEERL |
| 23480 | 53848 | A | 23615 | 600 | 905 | QAPASGSPWLSGGPQQVEDAG AGYGFAPGQPPPPRTQPRSAC SRRAAG/TPVPRAPPAPSAG\PK ARAPRSLGCGSLGRFSTGVRPD KCIFPPETENAAGCF |
| 23481 | 53849 | A | 23616 | 390 | 722 | QAPASGSPWLSGGPQQVEDAG AGYGFAPGQPPPPRTQPRSAC SRRAAG/TPVPRAPPAPSAG\PR AAPRSLGCGSLGRFSTGVRPD KCIFPPETEMSYLLFRNTVSR C |
| 23482 | 53850 | A | 23617 | 1 | 673 | MGQVKGHKLCLDFTLLSPDGG AAEGRCLELGWQAKEVEETIE GMLLRLEEFCSLADLIRS DTSQILEENIPVLKA\KLT KMRGIYAKVDRIKAFVK MVGHHVAFLEANVLQA ERDHGAFPPQALRRWLGS AGLPSFRNDPTAPLRQVFE ASPDRLARTVTIQTQQPV RVSGPLSGQRKEKSLQKGA QVFQTNVPE TLLEGAAIS PACGGPLTSGDGFRHVRK |
| 23483 | 53851 | A | 23618 | 1 | 651 | |
| 23484 | 53852 | A | 23619 | 195 | 497 | DQFLENTKKCDGLNQLSFDPA NNNKPLEFGRARGPLVTEGLIE NGGESSKKRRRTNSSADNSRT LNVDSTAMTLPMSDPTAWATA MNNFGMAPVRIVGH |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23485 | 53853 | A | 23620 | 241 | 1823 | NDDRAKFTVEDHTMQRD FRWLWVYEIGYAADNSRTL NVDSTAMTLPMSDPTAWA TAMNNLGMAPLGIAGQP ILPDFDPALGMMTGIP PITPMMPLGLIVPPPIP PDM PVVKEIIHCKSCT LFPPNPNLPPPATRER PPGCKTVFVGGLPENGT EQIIVEVFEEQCGEIIA IRKSKKNFCHIRFAE EYMVDKALYLSGNREL KKFLNKEDNYFRKINLT ALYKTVLEERCEKRRGG YRIRLGSS TDKKDTGR LHVDFFAQARD DLY EWECKQRMLAREERH RRRMEEERLRPPSPPP VVHYSDHECSIVAEK LKDDSKFSEAVQTLLT WIERGEVNRRSANNFY SMIQSANS HVRLVNEK AAHEKDMEEAKEKFK QALSGILIQFEQIVAV YHSASKQKAWDHFTKA QRKNISVWC KQAE EIRNIHNDEL MGIR REEE MEMSDDEIEEM TETKETESEL KKLE GIVDGSVEVSAEALR KLL NEYERQVKEEQK VG YRIWGTI HNKGE GKKEEFAEELEKSS SER |
| 23486 | 53854 | A | 23621 | 996 | 1512 | RPVHLASPAKEQQGTR KGRRAPARLPVPTTGR GLEKG PESQAPPSFR QATGRFSRSGSSGGPT PSK NSRDCSHTPOLP TPRGNPYVFPS PGH PEPSRPVEMPAPG\EP RTRQLCRERTRKACPP KPRPPLGLPG DPTG PVTHHAPPVSPTGASG QERRAEPGAVSYAHAS ATK |
| 23487 | 53855 | A | 23622 | 293 | 1140 | PRGILHQDKNLVVINK \PYGLPVHGWPWG\Q LCITDVLPIAKML HGHKAEPHLHLCHRL DKETTGMVLAWDKDMA HQVQELFRTR QVV KKYWAITVHVPMPSA GVVDIPIVEKEAQGGQ QH HKMTLSPSYRMDD GKMVKVRRSRNAQV AVTQYQVLSSTLSSA LVELQPITGIKHQLRV HLSFGLDCPILGDH KYS DWNRLAPQKLS VGT LKKL GLEQSKA RYIPLHLHARQLILP A LGS GKEELNLVCK LPRFFVHSL HRLR LEMPNEDQNENNEA KCL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23488 | 53856 | A | 23623 | 1 | 1328 | MAVDLGSHTPGSSGVTAATFR GRRLLVNTREESVVLGAGGEVL SGVPGTWDALGPGASFGIKGM FPKGTVMSTSPMCEGPVPRRK PCASSVGQQNSRSRKAGRKT TLAGRHPVKIKKEAIQQKPLP ASSFSPALTRSGAIFGPCALTS APVLEYPLQKVVENEAFKVFN NRDEESKRQKQAEFRMLTSAIR GPAGPRGHSSTRKPPSNPPPPGA CFKCGNEGHRSRQCPNPGTTSQ EAELIALTRALTLAAGQQINIYS NSHYVFHIVHSHSSIWKERGILT AKNTPAINGSLINKLLKAARLP QKVAIIHCRGHQTPDNPILAGN VLADQVAKQVALQPVQQQFLS LSLFSPLYSSEKEDFRAQNLQ KQGPW/LQSQGARLLVPAACAS KVAEAGRKPAGRHVPLKIQKE AIWSSPFSVPMATRAAASTSPT |
| 23489 | 53857 | A | 23624 | 475 | 622 | IHSKVLFSASSSSC*NTNNSWFR ASIKKNPEKQKNMQSAIPQHG LWKI |
| 23490 | 53858 | A | 23625 | 17 | 992 | GRGEVLRGRGRGQLDAVLSRE HCGGSRQSEQPWSRRSSSSSR RRLRSAEPAMALSMPLNGLK EEDKEPLIELFVKAGSDGESIGN CPFSQG\FMILWLKG\VFVS TVALKRKPADCQNLVPGTPPP\ LILFSSEVKTDVKNIEEFSEEV\ CPPKYLKLSPK\HPRSNTAGMDI FA\KFSAY\IKNSRPEANEALER GLLKTLLQKLDEY\LNS\PLP\DEI DENSMEDIKFSTRKFLDGNEMT LADCNLLPKLHIVKVVAKKYR NFDIPKEMTGIWRYLTNAYS RDEFTNTCPSDKEVEIAYS DVAKR LHQVKSRLLEKVSFMSSP |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23491 | 53859 | A | 23626 | 1 | 1128 | MALASGEGLPVALSHGRRGNG QERVPLYKLKRDTCAYRVAWRC NRLARAKVKRTSYRSGYGNGF EPGVEPDCVVLLALGVENDLV RISSKAEKYSLYEFSFPLRVSR CEEECRKEPWFNPGQKPSVLIT SGQILGQEEQKTLFLPGLLSLVF QFNVENSCLRCLSLAENLEISAL LSLSCSSVIRLILINLEVTISPPITI LKHAPPLTSLEASSSSSGIEKKIH NNFRQGPFPSSATRSTFLMNHT SFDSYVVVSNIPLRLNLYPQVL DVLQSLHKIHLASNAKWTIQG PAKPDGLGELGLHRYPDWEKE ERKKKRKRSVSPEKSITTHNKP TSSGIFY/RPRRCGCDLGRPPAP GPHPSPPHSPQPSPRCPPV |
| 23492 | 53860 | A | 23627 | 3 | 453 | SLGKDIRPRSARAACKGVGLWS GCFGKMAGSGVRQVTSTASTF VKPIFSRDMNEAKRRVRELYRA WYREVPNTGER*RLVRPAVLK HSYVANRSF |
| 23493 | 53861 | A | 23628 | 3 | 695 | PYASRRKFRVDPRVRAWSGCF DKMAGSGVRQATS\TASTFVKA HFSVGDME\AKREGARVLTAP WYR\ EVPNT\VRVHQFQLD\TV KMGRDKVREMFMKNAHV\TDP RVVDL\LVIKGK\IE\LEETIKVL KQ\RTHVMRFFH\ETEAPRPKDF LSKF\YV\GHDPLKSFSGKDAR WILFLGAQIKLTIQWSLCDRIPL MNQFSAASFCLSKWGPWVLHI TCSFPFSWKCGVCKLD |
| 23494 | 53862 | A | 23629 | 82 | 441 | SLPINPVPTACTLQAGLLRPPG SDVRTPMLPPSAPSQPSYPTSRP PLWPTWPAGPVFRRSQPLAQPN LPRSYHQQAPGGQTPVALGLE\ CPKATNQPFGLTQRDPKSPAKV PPFEFSL |
| 23495 | 53863 | A | 23630 | 3 | 504 | DRSSSSTMSTGGDFGNPLRKFK LVFLGEQSVGKTSITRFMYDS FDNTYQATIGIDFLSKTMYLED R/TNVNSFQQTTKWIDDVTER GSDVIIMLVGNKTDLADKRQVS IEEGERKAKELNVMFIETS/KA GYNVKQLFRRVAAALPGIMPS VLFQIIPSQALTRYLC |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23496 | 53864 | A | 23631 | 416 | 1239 | GGGRSSSSTMSTGGDFGNPLRK FKLVFLGEQSSIGKTSLITRFMY DSFDNTYQATIGIDFLSKTMYL EDRTIRLQLWDTAGQERFRSLIP SYIARDSAAVVVYDITNVNSFQ ANYKSGIDDVRTERG\SDV\IM LVGNKTDLADKRQVSIEGERK AK\ELNV\ILMETSAG\YNVK QLLSTCKQPALPGMESTQDRSR EDMIDIKLEKPQE\QPVSEGLF LTNLPCHLQPPFQKLTGFWPPY SFIDCSVNIGLMPFPFSNNVLRFI IAACPAWR |
| 23497 | 53865 | A | 23632 | 1 | 493 | PKPATAPPPPSL/RARFLCPQRRP ERAR/PRARGASPRPEKTAGAR KRRRGSCERPHPGG/RPPAPG*I SSRPTLGFFWILNFFFLKKLGR KDVPWQDSTKEHLSVCRGLRG TWSVPSASDPLHPAWRRTCFRV PPTTGAREWWLHLPALQRP DSRQCHRIPC |
| 23498 | 53866 | A | 23633 | 1 | 560 | MESIWAGLWTAQDTTVLADDF EFILWTLKRRPERAR/PRARGAS PRPEKTAGARKRRRGSCERPH GGLRRLPGARDQRAPPSDAG RSPGRLRRLPALLCAGPLSPGRE PRRWEPRAGVARPAGQQWGFF WPGNQQGASICSLILWFLLECG SRSTGGPCSGTELGHFSRERPTV LLSRLGTVKRP |
| 23499 | 53867 | A | 23634 | 32 | 327 | LTQRLFGLFTRTHMKFGALTR IG\DLPWE\INPLSS\CSLLPEKDP PMTSGPQTDQPEHLTNFKSAA RRSSRTSSHRNLLHVLEIWQLD QGMPAARDF |
| 23500 | 53868 | A | 23635 | 2 | 424 | LTPFSDSAHLHPGEINSPVAHTK PVGGLFTRMRVTFGAKTQDRS TPQETSPLSSPS\PTSGPQTNQ PKEHLTNFKLGKQSFHSSHASL ATLQSSSLATLQSPCPSNSNSFS SLVETRRRPGAVARLQSQLSGR LRGGRIA |
| 23501 | 53869 | A | 23636 | 31 | 246 | TALLLTQSLFGGLFTRTHMKFG AVTRIG\DLPWGINPLSSCSLLR EKDPLTISGPQTHQPEHLTNF KSGPH |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23502 | 53870 | A | 23637 | 125 | 464 | TAVFLTQSLFGGLFTRTRMKFG TMTRI/RGDLPEINPLSSCSLL HEKDPPTTSGPQTNQPKKHLTN FKSRKVERTKGLLKTHLTKLSH QLKKAWTILLPLSLLRIQACPR NAT |
| 23503 | 53871 | A | 23638 | 1064 | 1304 | TAMLLTQSLFGGLFTQMCMKF GAVTRIG\DLPEINPLSSCSLL HEKDPPTTSGPQTDPRKEHLIN KSGACYTCRKSGH |
| 23504 | 53872 | A | 23639 | 539 | 747 | TAMLLTQSLFGGLLTRTRMKF GALTRIG\DLPEINPLSSCSLL HEKDPHTPSRKIHIRPQGNHESQ KGL |
| 23505 | 53873 | A | 23640 | 709 | 950 | TALLTQSLFGGLFTRTHMKFG AVTQIG\DLPEINQSPVLLCSLL REKDPPTTSGPQTDQPKHLTN FKSGKWSFHSSPAF |
| 23506 | 53874 | A | 23641 | 1 | 1257 | MGKKVLGIASQLLGAVRCEPD GRRVLPEDWPECLSLVTHGTW FTRQGDKNIQMADNSFSDGVPS DFVEAAKNASKTEKLTQVMQ NPGVLAALQERLDNAPHTPSSY IETLPKAVKRRINALKQIQVRC AHIEAKFYEEVHDLERKYAAL YQPLFDERREFITGDVEPTSDM ESEWHRENEEEKLAGDRKNK VVITEKAAATAEPPNPKGIPEF WFTIFRNVDMLSELVQEYDEPI LKYLQDIKFHFQPNDCFANSVL TKTCKMKSEPKADPFSAFAGPE IMDCDGCTIDWKKGKNVTVK IKKKQKRKGPGTVRTITKQVSN ESFFNFFNPLKASGDGESLDKD SEF/ASDFEIGHFFRER\PQAVLY FAGEALKDDDNFDEGEEDEDEL EGDEEGEDEDEVEINPNKEPSQ |
| 23507 | 53875 | A | 23642 | 132 | 1277 | |
| 23508 | 53876 | A | 23643 | 1 | 515 | RVRHRSVSVGSTHASAHAYGE GSLRIIPVTRSPVLTNMHIVQTF SPVNSGQP\PNYEMLKEEQEV MLGAPHNPAPPTST\VIHIRSET SV\PDHVV\WSLFNT\LFMNTCC LGFIAYAYS\VKSRDRKMVGDV TGAQAYASTAKCLNIWALILGI FMTILLIIPVLVVAQR |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23509 | 53877 | A | 23644 | 243 | 643 | NHTVQTFFSPVNSGQPPQRMRCIKEEHEVAVAGGPHNPAPPTS TVIHIRSETSV\DHVVWSRVQ TPSSMNP\C\LGFIARLTP*SLR DRKMVGDTV\GAQA\YAST\AK CLN\IWAHDSGASVMTILLIVIPS |
| 23510 | 53878 | A | 23645 | 3 | 1498 | RCNFLRSSRIRVHPTPAASTMPPKFDPNKVVYL\RCTGGEVGA TSALAPKIGPLGLSPKKVGDDIA KAMGDWKGLRITVKLTIQNRQ AQIEVVPASAMIIKALKEPPRD RKKQKNIKHSGNITFDENGNIC STDNR\HRSLSRELSGTTKEILG TAQSVGCNVDGRHPHDIIIDDIN SENDKQPRKSKMRTSFSPQIPG HEHFHYLLLLQHVCQLALT LARKEGSSTHHQKLSTYYFKEG NSKEPKKIQRNTELKKEEG GSGKAPGSEIKLESPACSGASL GEMTAWTMGARGLDKRG SFF KGPLPNTCGHFWEMVWEQKSR GVVMLNRVMEKGSVVEFVTEL FFYVALPKMFPVHYIVILLASKL EEVTFNFPPPPDLCTPFLQNYLR VAFQEVNSGCTGKTLVLRPYIT TEDVCQICVEKFKVGDPEEYSL FLFVDETWQQLAEDTYPQKIK A ELHSRPQPHIFHFVYKRIKNDPY GIIFQNGEEDLTTS |
| 23511 | 53879 | A | 23646 | 361 | 918 | GCTGSRGTVPLSALGPQRIGPP GSCLQIKSWNDICQRQPG\DW KGP*GFTVKLTHSRTGQAPDCT RVP/VLPSCP*FIQSPSREPPKRPE KKPEKTFKHQLGIFTFLNEICST LLRQMR\HRSLSPEKLSWNPT* RDSWGIAQFSGAVNVDG\RH\ P HDNDDIQQWVLWKCPRLST KENIFNKGII |
| 23512 | 53880 | A | 23647 | 1 | 642 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23513 | 53881 | A | 23648 | 894 | 2438 | VETKRIQPQPPDEDGDHSDKED EQPQVVVLKKGDLSEVEVMKI KAEIKAAKADEEPTPADGRIIY RKPVKHPSDEKYSGLTASSKK KKPNEDEVYQDSVKKNSQKLI NSSLLSFDNEDENDTEKSMENL TGKIRKLQLRIVDPTFLPKLSNK GKDPVAVARLETGKGNGGAFR VLRDISRWATLCTSPQHSSEA KNIIPYQATQFQNEVHKWYKK KGGLKISKRKALFFLTQDIQKK LQKLALGPNTPTPDILKIASLVF YNQDQEEKERAQQNERQKEKL YWLSYKSASPFQVALRILSQET THKDELPTDLPNNPEVQAPGIP GNTIMAMPVAIQLKDPSSYPGR IHKVPEIASWIHRTQVKLWKSPE TSELEPTPSVIEYTREALEDLKF LFKQKDNSSAKTPGRAYAASPR DWTSEIAELHIFYQWDPNLKG MFKPASLLAKVKQDFPDHKEK PIFRAIFSNITLMGIAPICVTGKTI KKRTRQHHHTPKSNLREQASQ GSLNWEKN |
| 23514 | 53882 | A | 23649 | 200 | 1727 | RTATSLDSVLYKSDYMTWKYR VSFFYILSCRLKK/QCTDNEHV YMELSKKLYKYPKEWKKEAS KVRQYEVTWVVS KR GKDYILK HIPNMHKDQFALTASEAHLKYI KEAVRLDDVAVHYRLYKDK REIEASLTGLTMRGIQIFQNL EEKQLLYDFPWTNVGKLVFVG KKFEILPDGLPSARKLIYYTGCP MRSRHLLQLLSNSHRLYMNQ PVL RHIRKLEENEEKKYRESYI SDNLDLMDQLEKRSRASGSS AGSMKHKRLSRHSTASHSSHT SGIEADTKPRDTGPEDSYSSAI HRKLKTCSSMTSHGSSHTSGVE SGGKDRLEEDLQDDEIEMLV DPRDLEQMNEESLEVSPDMCIY ITEDMLMSRKLNGHSGSLIVKEI GSSTSSSETVVKLRGQSTDSLP QTICRKPKTSTDRLSLDDIRL YQKDFLRIAGLCQDTAQS YTFG CGHELDEEGLYCNSCLAQQCIN IQDAFPVKRTSKYFSLDLTHDE |
| 23515 | 53883 | A | 23650 | 182 | 423 | RLSIMASSLNEDPEGSRITYVKG DLFACPKTDSL AHCISED CRM GAGIAVLFFKKKFGGVQELLNQ HYKEKGLRTSQLYG |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23516 | 53884 | A | 23651 | 1 | 249 | |
| 23517 | 53885 | A | 23652 | 435 | 494 | |
| 23518 | 53886 | A | 23653 | 163 | 578 | RVTWLKKHLNSGNSDSVCMAS SLNEDPEGSRITYVKGS\LFEGP KTDFLAPCISED CRMGAGITVL FKKKF\GGVQELLNQKKK\GE V\AVLKRRWGRLYIFTWITKRK RAFAQSPLYENL TEEFRGQLKS HLSEEW SH |
| 23519 | 53887 | A | 23654 | 1 | 2238 | |
| 23520 | 53888 | A | 23655 | 26 | 1941 | RDAGTKWQRLGHL SCHCRKQA AREIINMHFQAFWLCLGLLFISI NAEFMDDDDVETEDFEENSEEID VNESELSS EIIYKTPQPIGEVYFA ETFD SGRLAGWVLSKAK\KVD MDEEIS IYDGRWEIEELKENQV PGDRGLVLKSRAKHHAISAVLA KPFIFADKPLIVQYEVNFQDGDID CGGAYIKLLADTDDLILENFYD KTSYIIMFGPDKCGEDYKLHFIF RHKHPKTGVFEKHA KPPDVD LKKFFTDRKTHLYTLVMNPDD TFEVLVDQTVVNKGS LLEDVV PPIKPPKEIEDPNDKKPEE WDER AKIPDPSAVKPEDWDESEPAQI EDSSVVKPAGWLDDEPKFIPDP NAEKPDDWNEDTDGEWEAIPQ ILNPACRIGCGEWKPPMIDNPK YKGVWIPPLVDNPNYQGIWSPR KIPNPDYFEDDH\PILLTSFSALG LELWSMTSDIYFDNFICSEKEV ADHWAADGWRWKIMIANANK PGVLKQLMAAAEGHPWLWLIY LVTAGVPIALITSFCWPTKVKD\ RHSDLEYIIPDICIPQTKGVLEQE EKVEKA ALEKPM DLEEEKKQ\N DGEMLEKEEESEPEEKSEEEIIEI EGQEESNQSNKSGSEDEMKEA DESTGSGDGP IKS LRKRRVRKD |
| 23521 | 53889 | A | 23656 | 297 | 398 | |
| 23522 | 53890 | A | 23657 | 286 | 430 | TAGARCSSRTSSPGSCFNCQKS GHWAR\NARSPGFLLSRVPSVN WIHI |
| 23523 | 53891 | A | 23658 | 405 | 524 | ARMSVACLPG LFFICLRGDFKQ NLTA YCWKCYQL* RSLGTHS |
| 23524 | 53892 | A | 23659 | 1 | 657 | |
| 23525 | 53893 | A | 23660 | 22 | 334 | ALKHFCLCSLIFS VTTMKFLAV LVLLGV SIFLVSAQNPTTAAPA DTVSSLLVLLMMKPLDAETTA AATTATTAAPT TATTAASTTAR KDIPVLPKWVGDL PNR |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23526 | 53894 | A | 23661 | 1 | 270 | |
| 23527 | 53895 | A | 23662 | 1 | 284 | |
| 23528 | 53896 | A | 23663 | 111 | 281 | |
| 23529 | 53897 | A | 23664 | 229 | 363 | |
| 23530 | 53898 | A | 23665 | 250 | 586 | PVRHGAFQDKSSDKKVQTKG KRGAKGKQA\EVANQETKEDL PAENGETKTEESPA\ASDEAGEKE CQCLINNHIPCLISGPCLP\PSCTIQ RNIFINYFVNASFLVALETFLKK |
| 23531 | 53899 | A | 23666 | 3 | 478 | APAVGLSSSGGGRSGSGKAARF REGCRRAAARMQQA\PGTRLPR RHPARAFPAATMPKRKVSSAE GAAKEPKRRSARLST\KLPK V\EA\KPKKAAAKDKSSDKKV\Q TKGKRGAKGKQA\EVANQETK\ EDLPAENGETERLEEESLLIEA GEKEPKS |
| 23532 | 53900 | A | 23667 | 1 | 252 | |
| 23533 | 53901 | A | 23668 | 328 | 414 | |
| 23534 | 53902 | A | 23669 | 1 | 3156 | |
| 23535 | 53903 | A | 23670 | 1887 | 2036 | |
| 23536 | 53904 | A | 23671 | 3 | 212 | |
| 23537 | 53905 | A | 23672 | 22 | 539 | YEGIVMKPLIIVNPADCIGC\RT CE\VACVVAHPSEQELNADVFL PRLKVQPIWTA\VSAAR*CCPFSS ENAP\CVGA\CPVGA\LTMG\EQV VQ\TNSARCIGCQSCV\SACPF\GM ITIQSLPGDTRQQIVKCDLCEQR EEGPACVESCPTQALQLLTERK LRRVRQQRIVVSGENPL |
| 23538 | 53906 | A | 23673 | 135 | 302 | PIHMKTRQPRDQFSADCVFLQS TCPVPC*RNRL*TPGGYWRTRR DYLRCDRSVHV |
| 23539 | 53907 | A | 23674 | 175 | 794 | LSTHSQPIADAADPPPHLHTGEL LCSAHQADFAVSAEPARPANN NAATTAPVHAVAITPPAYPDCF RTLPSKLSHQDSTQRLYGIARL LLRISTSGPPPSRLKVQRLDSISA PV/MCHQCENAPCVGACP/VGA LTMG\EQVVQ\TNSARC/IGCQSC VSACPF\GMITI/QSLPGDTRQQI VKCDL\CGALRDCVA\VLQR\RN SRV\LD\ACTRA |
| 23540 | 53908 | A | 23675 | 2 | 434 | LISLPFPDSL\AHRPPSSAPTEPQ GLFTVAAPT\PGAPSPPATLAHL LPTPAMYSLLETELKNPVGTPT QAAGTGGPAAPG/GRKMALEN PKMHNSEISKRLGADWKLLTD AEKRPFIDEAKRLRAVHMKEYP DYKYRPRRKT\CTL |
| 23541 | 53909 | A | 23676 | 3 | 264 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23542 | 53910 | A | 23677 | 1 | 2377 | MDDTFLNYKYKNKCGPKHIKK KEEEEEDNNSNDSKNKDKTLT TGSSGSAKIFLMRGRRQLLLP TSLCLLSVQRSPGSHEGPPQS MNPRLSPQGKYLKNDFLDVIG MCDIACHLVVELLVGNNGNFL AHAFAHVEVVAQQNQRENAA RPNGGSVMIGQGASLRTCQSRV LRVARGGPSPNPGESEQGLFTV AAPAPGAPSPPATLAHLLPAPA MYSLLETTELKNPVGTPTQAAGT GGPAAPGGAGKSSANAAGGAN SGGGSSGGASGGGGGTDQDR VKRPMNAFMVWSRGQRRKM APENPKMHNSEISKRLGADWK LLTDAEKRPFIDEAKRLRAVHM KEYPDYKYRPRRKTTLKKD KYSLPSGLLPPGAAAAAAAAA AAAAAASSPVGVGQRLDTYTH VNGWANGAYSLVQEQLGYAQ PPSMSSPPPPALPPMHRYDMA GLQYSPMMPPGAQSYMNVAA AAAAAAGYGGMAPSATAAAA AAYGQQPATAAAAAAAAAAAM SLGPMGSVVKSEPSSPPPAIASH SQRACLDLRDMISITGRENIFV VGDPAACLLPIEMEETFLPWPL GFEDRLHLEGPRPVQEIPSFLRK VPNCGQWLLQTPSVEPADPWE NPQAFPPSLQQEQPCLSLIVGIF VEAFGGRGRWGSKGKKPKRYR TVEWMRIHQPSICCLQETHLTR |
| 23543 | 53911 | A | 23678 | 1 | 399 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23544 | 53912 | A | 23679 | 3 | 1216 | LGNKRAGLRRADGEAPSALPY CYFLQKDAEAPWLSKPAYDSA ECRHHAAEALRVAWCLEAASL SHRPGPRSGLSVSSLRPTRKMA TTFLAHEKIWFDFKFKYDDAERR FYEQMNGPVAGASRQENGA\T VILRDIARARENIHKS LAGSSGP\ GAS\SGTSGDHGELVVRIASLEV ENQSLRGVVQELQQAISKLEAR LNVLGKELRLAHRGTAPQTQH VSPMR\QVEPP\AKKPATPAEDD EDDDDIDL VGRDNEEEDKEAA QL\REER\LR\HYAEKKAQESLP LGGQVPPSLLDVK\PWDDSDM AQLEACVRSIQ/LGTGRSWGAS QMVAVGYG\IRKLQIQCVVEDD KVGTDLLEEEITKFEEARARSV DIASFSTRSEALKCVYVAHVRE GPCTRSKDLRPAKKKKKK |
| 23545 | 53913 | A | 23680 | 1 | 2066 | MAAALRAPTVSAASSRPPLPS PPETEGRVKGFLQPGPHCPAQC LCSGDDGSNEDLEQKREVIFPR PHEAPVAEHRQQT VGLRELVAI PKRKEETTAIVQVFVAFEDVAI YFSQEEWELLEDQMRLLYRDV MLENFAVMASLGCWCGAVDE GTPSAESVSVEELSQGRTPKAD TSTDKSHPCICTPVLRDILQMI ELHASPCGQKLYLGASRDFW MSSNLHQLQKLDNGEKLKFKVD GDQASFMMNCRFHVSGKPFTF GEVGRDFSATSGLLQHQTPTI ERPHSRIRHLRVPTGRKPLKYT ESRKSFREKSVFIQHQRADSGE RPYKCSECGKSFSQSSGFLRHR KAHGRTRTHECSECGKSF SRK THLTQHQRVHTGERPYDCSEC GKSFQVSVLIQHQRVHTGERP YECSECGKSFSHSTNLYRHRS HTSTRPYECSECGKSFSHSTNLF RHWRVHTGVRPYECSECGKAF SCNIYLIHHQRFHTGERPYVCSE CGKSFGQKSVLIQHQRVHTGER PYECSECGKVFSQSSGLFRHRR AHTKTKPYECSECEKSF SCKTD LIRHQT VHTGERPYEC SVCGKS FIRKTHLIRHQT VHTNERPYEC DECGKSYSQSSALLQHRRVHT GERPYECRECGKSFT RKNHLIQ HKTVHTGERPYECSECGKSFSQ |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23546 | 53914 | A | 23681 | 1 | 468 | MAAQVGAVRVVRAVAHEEP DKEGKEKPHAGVSPRGVKRQR RSSSGGSQEKGRPSQEPPLAPP HRRRSQPPTSWAAA VNDM/PAP TVPGPVEPLLLPPPPPSLAPAG PADDAPLPAPSTSGLFTFSPLTA SAAGPKHKGTQGAAQAPSPPRP RW |
| 23547 | 53915 | A | 23682 | 950 | 1326 | RPESQRANGVDSGPNLKTVPQP DTRKGSVLK WISKRGKPLAVEI EESHCL\CLPLRTECLGIKP\IVH LFSCTRPVIVPSLELN YD VDSIA HMFVADLLL MITLPSYDIPFYC LVFQNL LVLEFYLY |
| 23548 | 53916 | A | 23683 | 271 | 918 | NQGLRDLGLCRICLVNKMFTSS ILGKGHRHSLVSIKQEHSALRK AAG\PLPLKVGYC\QGFSPCDSL KYG\SWDEKDLTPQPDTHKGS VLRWISKRGKPLAVEIEEG\HCL PELPPGELECPG\ILKHGLYHWS SSEMGE\NRPMVG\ARHVYSNA ALLFF TALRIFGQRRNINLGLRA HPG\IVPPLELN YDIDSSAHM/FF LADLLLITLPSYIIPFC |
| 23549 | 53917 | A | 23684 | 1 | 942 | |
| 23550 | 53918 | A | 23685 | 346 | 1753 | TWIPLSRTGRRFPVFSCSSSRVY AAISFHKRWKEGRCFGRTRGE MGWEGRSRSLKELNTRNDWNP GERELDFWRKITRFKEAASWTL EAL EEAGSTARRRVWLEDGRR TCEILSVLCTSSLSSNCASLDCV TYKALSTTRYDSVYWNKKPE RSSSPATEQSWTENDFDKLREE GFRR\IN YSELKEEARTHGKEVI NLEKK\LDERLTRITNAEKSLKD LMELKTMARELRDECTSFSSQF DPLEERVSVMEDQMNMK\QE EKFREKRIKRN/EKQSLQEIWYD VKRPNLHLIGVPESDRENGTKL ENTLQEIIQENFPNLARQANIQI QEIQRT PQRYSSRGATPRHIIVR FTKVEMKEKMLRAAREKGRVT HKGKPIRLTADLLAETLQARRE WGPIFNILKEKNFQPRIAYPAKL SFISEGEIQYFADKQMLRDFVTT RPALKELLKEALNMERNN WYQ PLQKHAKW |
| 23551 | 53919 | A | 23686 | 73 | 327 | GALQPTAALWEPLSGLAKAAA RSLSLQGGVEGDARAGTGAAR GACGPAGVPGGRGLGPPALGA AGRPGP*LPSRGAGLGTAARHA |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23552 | 53920 | A | 23687 | 322 | 402 | DQEPTNSGHIGNLEQCLGHGYQR*LFP |
| 23553 | 53921 | B | 23688 | 545 | 3063 | |
| 23554 | 53922 | A | 23689 | 1 | 579 | MKHEKRDRCAELTAILLNEQAS PMCTIVLGYTGTSTITLPRTSCH FAPRLSNSQQHSSYQVGHPES YCVRNWWVLGLTDFKNEAAD PHNSGGQLASPSGSRGTGAAGG\ VPASPAPCARTPQPLGGRWDW AP\GTGGGIRRGSGCTGTHGG GGRLRHGGLQSGGLPRGKAAK ARREIESSAGYSNSSSKCSII |
| 23555 | 53923 | A | 23690 | 399 | 592 | KCIHFPGPTPKFVCGVIVVTAVP /TFGM*TVYV**LPFSILAQNVG *RDDCDPGWKLNLFYAKKKK |
| 23556 | 53924 | A | 23691 | 3 | 268 | DRV/RPLRKNFQRNDQTAAFTV HENPLLCSYRCWYPGKQEKK IKPQRGGKNRAEKLETLSRAP LLFQRNAVPHQQRNKAGWRM TLTS |
| 23557 | 53925 | A | 23692 | 29 | 484 | CSFFLVSMVFTFWHDFAAAGTS CSFPCLVLSFRSSFRAGLVVTKS LSICLSVKYFISSSLMKLSLAGY EIVG*KFFSLRMLNIGPHSLLAC RVSAERSAVSLMGFSLRVTRPF SLAALNIFSISTLVNLTIMCLG VALLEKYLCGILCVS |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23558 | 53926 | A | 23693 | 182 | 2076 | MQEWLRLTARKTELSRDSRSC GQLKTSLLISLLVESTQGRH*SF L/VWTQTHSGGDGWRVAKAW RPKYHDTQLGGEKEEPQGHHA SDCRWRAQPHCRTLSAAVVNV AGFTVTFELRCLTLMKMREKD HHLCDNDIVLFPPDTAFPLDCL LSCIHSTVHGLLRWNAIQYLAS RSESHPERSEGGTPDRNGHPAL SLASFNGAQQDRRTVQSLGEKP GLPEEMAAFMAGTEKEQNELG IEFFQLIIPASKRTHSENAFSSH GDDTECSRSGQGSPPSYSRGPP RRTFILATQPLCSKEAQTSPHEQ PTRTEKNRGSHLYHKSPCDHAS PGMSVTMSGMQQALPRQLTTL TFYPPAFRSIKIFRIMILKTEMLH THARSQEALLKDSSKTMHLSTL PSCVRKSNYHHRERKIKTKEAF PAKIHRSRNQGMKVEVAPLTIT SSDPLAEFLLPVTVTLCASLEV LAPEGGMLSPGDATMIPLNWK LTLP PGHSGLLLPLSQQVKKRV PVLVGVIDLDYQDEIDYSSMK ERSSSPATEQSWMENDFDELRE EGFRRSNYSELREEIQTKGKEV ENFEKNLEECITRITNTEKCLKE LMELKTKVRELREECRSLRSRC DQLEERVSAMEDEMNEK |
| 23559 | 53927 | A | 23694 | 933 | 1118 | RVERRRLQTIKLLRATGGNSNQ RQRS*KL*KKFRMYN*NNQY REVLKGADGAESQGSRTT |
| 23560 | 53928 | A | 23695 | 2 | 250 | WCHTKLDGLSLFGESVALEEA GGQTALWLMRFLSRKANYVD KITTREVGHRE*LMSSRLHSR* WAASSVCSSCVLLPSSH |
| 23561 | 53929 | A | 23696 | 1017 | 1230 | |
| 23562 | 53930 | B | 23697 | 62 | 1069 | |
| 23563 | 53931 | A | 23698 | 216 | 582 | ILVPTLFWLGEFLLRDPLL*W ASI*G*PD/AFSLAALNIFSISTL/ RESDNYSVWSCSSRGVSL*RSL YFLNLNVGLPCQIGEVLLDNIL QSVFQLGSILPVTFGYTQMQI WFHFIFHH |
| 23564 | 53932 | A | 23699 | 434 | 681 | TLACLARLGKFSWIISCRVFSNL VPFSLSLSGTPIRRRFGLFT*SHI SWRLCSFLFILFSLNFPSPRFISV SSSITDTLSS |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23565 | 53933 | A | 23700 | 290 | 1231 | RSFRAIGEVSIRGWGGGYAAQ LQSPSRPLVGLGGGKKGSRGV GQGSSRAEVGLGSQRERSGTG AEAAAAAAQLIAGTGSSLPYQG PGQNQTAIAPTCAPLSPCKAAA VIMGNIFGNLLKSLIGKKEMRIL MVGLDAAGKTTILYKLKLGEIV TTIPTIGFNVETVEYKNISFTVW GCGVARDK\IRPL\WRH\YFQN\T QGF DILWSDSN\DR\ERVNEA\R EEL\MKNAGAETSLRDAVLPFL/ FGNKTDLRNAMNAAG\IQDKL G\HSLRHRNWY\I\QATCATRG NGLYEGHLHWLANSVPKQEVES RTALT KHPNRP |
| 23566 | 53934 | C | 23701 | 164 | 208 | |
| 23567 | 53935 | C | 23702 | 1 | 381 | |
| 23568 | 53936 | C | 23703 | 43 | 276 | |
| 23569 | 53937 | C | 23704 | 1 | 462 | |
| 23570 | 53938 | C | 23705 | 38 | 121 | |
| 23571 | 53939 | A | 23706 | 77 | 202 | QKNYTQRPLPLHGLLELEVTCR CWSWQPLLEPLELR\RLSD |
| 23572 | 53940 | A | 23707 | 123 | 209 | |
| 23573 | 53941 | C | 23708 | 1 | 411 | |
| 23574 | 53942 | A | 23709 | 1400 | 1809 | SSNPLSRPPLPTVTPCPLLRLSL LRACCCCLFLPLRFFSCPLLCL LCFFFSVCSPAHNKMPKPQW SGIPTGPPPSGSCFKCQKSGHW A\RNACSPGFLLSHVPSVWDPT GNQTVQLAWQPLLEPLEL*P\RLSD |
| 23575 | 53943 | B | 23710 | 76 | 358 | |
| 23576 | 53944 | B | 23711 | 1 | 606 | |
| 23577 | 53945 | C | 23712 | 272 | 388 | |
| 23578 | 53946 | A | 23713 | 1 | 259 | PGVRGAQGGPSIPRQCEESAIGP KFAWIISSFWKQGMFNMEAP SSLFFVNMCAVKKQTTWGRPD RGFIWQPLPEPLEL*P\RLSD |
| 23579 | 53947 | A | 23714 | 684 | 917 | GDFGLRQWGFLNIQSCHLQTGT I*LPLFLIEYPLFLSPA*LPWPELP TLCCIGVVREGISVLCQFSKGM LPVFAHSV |
| 23580 | 53948 | A | 23715 | 618 | 683 | |
| 23581 | 53949 | A | 23716 | 306 | 710 | DRVSLLT PRLGVQWPDPSLQ RPPGFKRFYCLSLPSS*DYRHEP LLPAYFFPYRIIGWSRL |
| 23582 | 53950 | A | 23717 | 2 | 88 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23583 | 53951 | A | 23718 | 972 | 1967 | FPPGRGRGPGRPAGCSRGRARA CPKPVDPVHVKRPMNAFMVWSR AQRKMAQENP\QMHNSEISKR LGAEWKLLTESEKRPFIIDEAKR LRAMHMKEHPDYKYRPRRKPK TLLKKDKFAFPVPYGLGGVAD AEHPALKAGAGLHAGAGGGLV PESLLANPEKAAAAAAAAAAR VFFPQSAAAAAAAAAAAAAGS PYSLLDLGSKMAEISSSSSGLPV LNMPNMHINSLGKNLALNLFV YNDANSMLDLCYDGVGDKGPI CFCATQGYEDIFKAGYGSVVD YYNDGSDLTTPLEIATVIPTFSN HPLMSQRPSTWRQNPLAKRLP LTEDSDGDDH |
| 23584 | 53952 | A | 23719 | 2 | 144 | RPQRRP/LPPPTGSPLKHPGGAS GAAGAPIGEPQHPGAVVSVRA WSLCS |
| 23585 | 53953 | A | 23720 | 219 | 897 | PGRAGGTLGLGSRRDGTREKG VEETPHRLHARTDTPAGCCGS PIGAPAAPEAPPGCFEG\PRWVE GVKKASPPLPAELIGWLVNFPL ARPVRPPSLSPGPPRRPPEGVCG SWPGRSEGERGKAKNTAESTPR QNLHRKYTIIVTHYQRNRKGQ NISFSLVCEFHPSLADWTTVTA LTWTSPKDNSLTEESWLREGN VHRGMDEYVRAQSFLILMTLE NSGGSVVSK |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23586 | 53954 | A | 23721 | 937 | 2730 | TNPHCCHDHYHHHHHHCHHCH HHHHHCHHHHYHHHHHCRDH HYHHHHHCHHCHHHHHHCHH HHYHHHYHHHCHDHHYHHHH HCHDHHYHYHHHHCHDHHYH HHHHCHDHHYHYHHHCHDHH YHHHHHCHDHHYHHHHHCHD HHYHHHHHCHDHHYHYHHHC HHHRYHHHHHCHHCHHHHH/P HHHHHHHCHHHHYHHHHHC HHHHYHHHHHCHHHHYHYHC HHHHYHHHHHCHHCHHHHYH HHHHCHDHHYHHHCHHCHHH HYHHHHHYHDHHYHHHHHCH HCHHHHHHHHDHHHHHLCHH HYHHHHHHHHHHHYHHHHHH HLCHHHHYHHHHHHHHHHY HHHCHHCYHHHYHHHHYHCH HHYHHHHHYHPYHYHQHHHH YHPHHYHHHYHCHHHHDYH HPHHCHHHHHYHQHHYYPITII TTTITTTITTTITVTTFTTTTNT TAPTTPVTAITTTTTTTTITTT TPITITTNITTTVTTVIITTF TTTIHPYHHHHHHHPVTITTTIT TATIITTTTSITTTITTTIVTTII TTTAATHHHYHPYHHHYHHHH HHHHTHSYHYHHHHHHHCF HYHHHHYHHH |
| 23587 | 53955 | A | 23722 | 2348 | 2571 | |
| 23588 | 53956 | A | 23723 | 4919 | 5142 | |
| 23589 | 53957 | A | 23724 | 2 | 370 | |
| 23590 | 53958 | A | 23725 | 588 | 701 | |
| 23591 | 53959 | A | 23726 | 295 | 521 | |
| 23592 | 53960 | A | 23727 | 2837 | 3061 | |
| 23593 | 53961 | A | 23728 | 272 | 436 | |
| 23594 | 53962 | A | 23729 | 239 | 514 | |
| 23595 | 53963 | A | 23730 | 105 | 367 | TGRPPELLHLRSLSPPLL/CSSP/ TPPPQLPPPVSLASGYPLLHPL ARYPACPLPPRRARTEQRGGEQ PGVGASPLPIGRWPGTEAT |
| 23596 | 53964 | A | 23731 | 999 | 1145 | |
| 23597 | 53965 | A | 23732 | 1084 | 1893 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23598 | 53966 | A | 23733 | 1605 | 2296 | HSIHSSVDHPENRIYRRKIEELS KRFTAIRKTKGDGNCFYRALAI PYLESLLGKSREIFKFKERVLT PNDLLAAGFEEHKFRNFFNALR AGRAQFYVVELVEKDGSVSSL LKVFNDP\GASDHIVQFLR/LCF TSAFIRNRADFFRHFIDEEMDIK DFCTHEVEPMATECDHIQMTA LLQALSIALQVEYVD\GWIPALT QHVFLAATPSVYMLYKTSQY NILYAADKH |
| 23599 | 53967 | A | 23734 | 529 | 1830 | AGYGDRTMLARKSIIPEEYVLA RIAAENLRKPRIRDRLPKARFIA KSGACNLAKHNIREQGRFLQDI FTTLVDLKWRHTLVIFTMSFLC SWLLFAIMWWLVAFAGDIYA YMEKSGMEKSGLESTVCVTNV RSFTSAFLFSIEVQVTIGFGRM MTEECPLAITVLILQNVGLIINA VMLGCIFMKTAQAHRAETLIF SRHAVIAVRNGKLCFMFRVGD LRKSMIISASVRIQVVKKTTTPE GEVVPQHLDIPVDNPIESNNIFL VAPLIICHVIDKRSPLYDISATDL ANQDLEVIVILEGVVETTGITTQ ARTSYIAEEIQWGHFVSIVTEE EGVYSVDYSKFGNTVKVAAPR CSARELDEKPLPSLFRPSQKSEL SHQNSLRKRNS\HRRNNFHRRN N\SIRRN\SSLMVPKVQFMTPE GNQNTSES |
| 23600 | 53968 | A | 23735 | 968 | 1243 | |
| 23601 | 53969 | A | 23736 | 541 | 1010 | SVTSCLKVTSVCLTSAAASCRH RRSVEEYLV*KLPM/WSRRRK AAALTES/V/CIVFWLASWMMS RWLHYPDWVTIIAQQVLMNVV SVMQADCRMNLLIFLRWLMR KIFHNILRHFSQLLNVPITRPF WILRPF |
| 23602 | 53970 | A | 23737 | 766 | 1910 | LLTARLTWVSARLMSYVLLMC *LFPRLLSCLTTPPHCSFSICFVI CSRTLILKGSSLMYVFCLPNTAI GGSSRVDRCAATSRGSSRVDL TL*KYSLVGPSVPLVSSV**SDW PLKLLMTMMS |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|---|
| 23603 | 53971 | A | 23738 | 581 | 1434 | KLPMGVAVVKLLHLPKVIIVFW LASWMMSRWLHYPDWVTHAQ QVLMNVVSVMQADCRMNLEI FLRWLMRRASDICSSIHGD*EPL L/YAVFGKQNTYIRLEPFKINV EQITKHIEKLQCGGVVKQLSRR GNNQHISSTYDINRADTQVRR VNNYDIIVMSNSFNGQSEHQV WIDRKAGECLLHEYEDLVPIRD TLRLFPGGRYLPRAKHVAPSEP DPEQDEQKLRFCKRHLYGKQP RSPVERVWDHGPTRIVGLIISLG PRSHSYRRSDNQGTGTVPLVSS |
| 23604 | 53972 | A | 23739 | 515 | 774 | LFPRLLSCLTTPPHCSFSICFVIC SRTLILKGSSLMYVFCLPNTAIS GTTVPLVSSV*LLVWDHGPTRI VGLIIRLGPRSHSYRRS |
| 23605 | 53973 | A | 23740 | 322 | 763 | CRMC*LFPRLLSCLTTPPHCSFSI CFVICSRRTLILKGSSLMYVFCLP NTAIVMALSPRGWRSKFGMPV EDTSLSTPAAPMVDSLIARVGV MARGNAITLPCGRDVKSTLE VLRGDSVEKTSRVWSGNERDQ ELLTEDALDDL |
| 23606 | 53974 | A | 23741 | 1 | 127 | MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEK*RRL SPLHSLMMTARKRGK*PGAGE |
| 23607 | 53975 | A | 23742 | 9 | 437 | WLGLGNWKERLGTQTRMIWS QKTARRLCRTFSGIPAYSMCI/CI GMAERMWCDNRNRHTVSSSG GNRLPNPDWAPGPPRIVGLNIS LGPTVPTRIVGLIISLGPRSHSYR RSDNQGTGTVPTRIVGLILVLGP WSHSYRRSDY |
| 23608 | 53976 | A | 23743 | 766 | 767 | LLTARLTWVSARLMSYVLLMC *LFPRLLSCLTTPPHCSFSICFVI CSRTLILKGSSLMYVFCLPNTAI GGSSRVDRCAATSRGSSRVDL TL*KYSLVGPSVPLVSSV**SDW PLKLLMTMMS |
| 23609 | 53977 | A | 23744 | 573 | 1085 | VCHQILTHLPALLSGARMWWD QLWRGRP*RRCQQPQCGG*WH CFWATAHHSPLDSTLNHLHCLP RGP |
| 23610 | 53978 | A | 23745 | 2 | 379 | WLTRSSCSWRLPPRRKKKGAL V*PVWLPPGGVAVLLQLGCCV LQDVSCKRLCYNRKQGQSEIVL MS*ITMWKLFPRPPLLPFSTCIC *KTCGKGRSK*KVDILVLSIRF SAIKLEPLDCHENAWL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23611 | 53979 | A | 23746 | 575 | 576 | TGIDSDQLNGRDWRRALSVSPA PDSGFPRCNGDEQAGI*LLGTG WAEKCHRLAFPPAGSTAGR |
| 23612 | 53980 | A | 23747 | 1 | 723 | MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGRRLRAEDVFPPVI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVCSWKERPPGNSL NVSRMVWDHDPTRVVGLIIGL GPRSHLYCRSDYQQRS\TSVCG CMPAVDCCCVLLIHNILRTVM WTKYLVTAQVPA*PGCIRCKC |
| 23613 | 53981 | A | 23748 | 1 | 1101 | |
| 23614 | 53982 | A | 23749 | 5 | 205 | YCSSLSTAAITSRAFLPDRRITT PPATSPSPFSSAMPRIISGPIWTF ATSRR*TGTPFSLAFKTM |
| 23615 | 53983 | A | 23750 | 1 | 761 | |
| 23616 | 53984 | B | 23751 | 56 | 2188 | |
| 23617 | 53985 | A | 23752 | 627 | 1272 | |
| 23618 | 53986 | A | 23753 | 448 | 2218 | VRRQRSDPERSDARMVRFNCN YI*RKNPFILH*LFR*TLRQTKPD NSAGKCVKI |
| 23619 | 53987 | A | 23754 | 171 | 959 | AASRGPDAPGLEMAGNCWEA HPGNRNKMCPLSEAPELYRR GFLTIEQIAMLPPAVMNYIFLL LCLCGLVGNGLVLWFFGFSIKR NPFSIYFLHLASADVGYLFSKA LFSILNTGGFMGTFFADYIRSVCR VLGLCMLLTGVLLMPAGWDE RGVRSERAWCTVETGRVHRSR VRVSRNTARDPANGLGHLLQS LGMPALEPGPTLGSALRWEFLQ TASPQLPVQPLHPAAATPQRS RGRGRGPKARALGLGPRSTSYR |
| 23620 | 53988 | A | 23755 | 664 | 838 | |
| 23621 | 53989 | A | 23756 | 2732 | 3007 | |
| 23622 | 53990 | A | 23757 | 1522 | 1706 | CHYFACMWSGCEVYS*SAPG** C*EDLSGLVRCRCLHSNAETPI* FAANADTSPRGPFLLCR |
| 23623 | 53991 | A | 23758 | 537 | 795 | ADCPHLMGRPCLID*GPCRTE*P RCAVVCLLWIAAVSCLSTT/SLR TGI/DGPKYLVTAQVPA*PGCI RCKCVAVDELASSDMRLPCS |
| 23624 | 53992 | A | 23759 | 2074 | 2276 | |
| 23625 | 53993 | A | 23760 | 36 | 206 | ECWIWCELGAELHHQP*ASSH WKSSYRQQSSLPCRASQRTLH LLLQGWAVLGPLE |
| 23626 | 53994 | A | 23761 | 444 | 725 | |
| 23627 | 53995 | B | 23762 | 1 | 1212 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23628 | 53996 | A | 23763 | 11 | 972 | RFSKSLDSGVQLASPSGSRTG ATGGAHSPARAPALHSPWAV DGTRGRLAGTAGLWSPRPAFH FKVLSLPFSCVSSPFGPPLGPS PRKHQMADDAGAGVGGRRPR GPRMG/NRGGFRRGFGSGIRHQ GCGCGQGQGQGRGVRGGKAE YKEWMTVTKLGHLVKDIKIS LEEIYLSFFKTSSSLKDEVLKI MLVQKQTHTSQCTRFKAFVAT GDYNHISLGIKCSKEVATAIC GAILAKLSIVACRGYWGNKIS KPHTIPCKVAGCCGSVLVCLIS VPRGTGIVLAPCEGDRGLRKSS PASLSPESCKDGSHSRSF |
| 23629 | 53997 | A | 23764 | 2 | 260 | LLEECRSLRSRCDQLEERV SAM EDEMNEMK*EGKFREKRISPKR APERSAKHGKEQVPAAAKSC QNVNTIETRKKLHQLTSKITS |
| 23630 | 53998 | A | 23765 | 3 | 1150 | |
| 23631 | 53999 | A | 23766 | 1 | 1521 | |
| 23632 | 54000 | A | 23767 | 1 | 753 | |
| 23633 | 54001 | A | 23768 | 1 | 3351 | |
| 23634 | 54002 | A | 23769 | 1 | 1740 | |
| 23635 | 54003 | A | 23770 | 1 | 1353 | |
| 23636 | 54004 | A | 23771 | 1 | 1932 | |
| 23637 | 54005 | A | 23772 | 1 | 1221 | |
| 23638 | 54006 | A | 23773 | 1 | 1214 | MAKKQNRKTGNSKKQRASPPP KECSSSPATEENWTENDFDEL EEGFRQSNYSELWEDIQTKGKE VENFEKTLEECITRITNTEKCLK ELMELKTKAQELRKECRSLRSR CDQQQERASVLEVLEVLAR\QL GRKRK*RVFN*EKRSNCPCLQ TT*LYI*KTPLSQPKISLS**ATS AKSQDTKSMYKNHKHSYTPPT DKQRAKS*VNSHSQLLQRE*NT *ESNLQES*NWISSHLHIQKSIQD GLKT*TLDLKPSKP*KKT*ALPF RT*AWARTSCLKHQKQWQQR KLTNWI*LN*RASA/PAKESTV/S SEQATYNMGENFHNLLI*QRAN IQNLQ*TQTNLQEKKNKQPHQKV GEGHQQTLLKRRHLCSQKTHE KMSIITGHQRNANQNHNEIPSH TSYNGNH |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23639 | 54007 | A | 23774 | 1157 | 2085 | QGRPTDFADFGTTIKQDFRLLG QTSVDRLLQLSQGQAVKGNQL LPVSLVKRKTTLAPNTQTASPR ALADSLIAAGTTGFPTGKRAVS ATQLMTQFSPAREQSWRKN/DF DELRKE/GFARSNYS\EKCLKEL MELKTKARELREECRSLRSRCD QLEERVVSAMEDEMNMKREG KFREKRIKRNEQSLQEIWYVVK RPNLRLIGVPESDAENGTKLEN TLQDIIQENFPNLARQANVQIQE IQRTSQRYSSRRATPRHIIVRFT KVEMKENMLRAAREKGWVTL KGKPIRLTADLVAETLQARRE WGPIFEFP |
| 23640 | 54008 | A | 23775 | 1 | 1707 | |
| 23641 | 54009 | A | 23776 | 1 | 1899 | |
| 23642 | 54010 | A | 23777 | 1 | 2781 | |
| 23643 | 54011 | A | 23778 | 1 | 831 | |
| 23644 | 54012 | A | 23779 | 1 | 3264 | |
| 23645 | 54013 | A | 23780 | 1 | 882 | |
| 23646 | 54014 | A | 23781 | 1 | 1853 | |
| 23647 | 54015 | A | 23782 | 1 | 550 | |
| 23648 | 54016 | A | 23783 | 1 | 831 | |
| 23649 | 54017 | B | 23784 | 64 | 3436 | |
| 23650 | 54018 | A | 23785 | 1 | 1422 | |
| 23651 | 54019 | A | 23786 | 1 | 773 | MGKKQSRKTGNSKKQSATPPP KERSSSPATEQSWTENDFDEL EEGFRRSNYSELQEETQTKGRE VENFEKNLDECITRTTNTTEKCL KELMELKAKAWELREECRSLR SRCNQLEERVSVMEDEMNMK REGKFREKRIKRNEQSPQVIRD YVKRPNLRLIGVPESDGKNGTK LENTLQDIIQENFPNLARQANIQ IQEIPRTS/QRYSSSEHSIIGLIGR FPS*RTDMFRAPKKREQKRNNR KIQKEEGGRTAPTGI |
| 23652 | 54020 | A | 23787 | 1 | 2775 | |
| 23653 | 54021 | A | 23788 | 1 | 2712 | |
| 23654 | 54022 | A | 23789 | 1 | 1590 | |
| 23655 | 54023 | A | 23790 | 1 | 547 | MGKKQNRKTGNSKKQSASPPP KECSSSPATEQSWTENDFDEL EEGFRRSNYSELREDIQTGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELREECRSLSSR CNQLEERVPADEDEMNMKE D/GNRYDDRRQ/RKEEIMIKSW RFCCRHLIRVVRGWGPSKYLWI TMVVTLAGNPQ |
| 23656 | 54024 | A | 23791 | 1 | 710 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23657 | 54025 | A | 23792 | 1 | 895 | |
| 23658 | 54026 | A | 23793 | 1 | 1938 | |
| 23659 | 54027 | A | 23794 | 1 | 1413 | |
| 23660 | 54028 | A | 23795 | 985 | 1219 | LCSGSVERCTESYLHSSHCLVQ QAGVTGDEGGSCY*DPPSHHRS HPRKLKKLC EQEFSVTSAPWRK CRSLHGRFPGLP |
| 23661 | 54029 | A | 23796 | 1 | 3570 | |
| 23662 | 54030 | A | 23797 | 1 | 634 | |
| 23663 | 54031 | A | 23798 | 1 | 4551 | |
| 23664 | 54032 | A | 23799 | 1 | 4721 | MHPSQRTPYQSRSPATIFATVST FKSHKSNLETKHPQQVPLSSLG LAANISSEDI ESEAEDNGKWES VDRTSFFPALTSFQQSMIHKKI MTVFKSVEPEDGLGRPTLAFHE DRCQLSIQNSLDAGGGCPSMA APPAEVHELASGLISAAALLLSP AASGRVSKHQHIPTGFDPDKA LHKGKLTTRKDIYTENPSVHHH HQRPKVDKTTKMGKKQNRKT GNSKTQSASPPPKECSSSPATEQ SWMENDFDELREE |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23665 | 54033 | A | 23800 | 1 | 2152 | MDILGWASRAHKWKGRATGT HVFNLMMREYLISLQCCASEQAA SPEHGASFRVWKS LGFQKLILS LICPQCLQSLTRETWMRFKSKK TKGPDLRLVMDANKWEFRRH ALRPALTFFNEGDDLGV EALPV ALPPEAHVGGVVLPAALVRGA HGEQLPAIPGPEEFALPAVQAR AARPERQVVVIVVNEAGVDP GVEGLAPVPVLPVLRLEATAPK QPPRLPARLRAPLPSGRKLNK CPRLRWGFFVQDGDGTELACL SEGDDGGCCQEAPLDHRPRLRG LAGSAGAREAREPRLRPGDWG NRIARVRAPEEAAAALSRPARV AAALAKTHRREHRARSQKLVM SSVQOGKLTTRKDIYTENPSVH HHHQRPKVDKTTKMGKKQNR KTGNSKKQSAF\PPPKECSSPA MEQWTW\DNDFDELREEGFRGS NYSELREDIQTGKEVENFEKD LEECITRITNTEKCLKERMELKT KARELREECRSLRSRCDQLEER VSAMEDENEMKREGKFREK RIKRNEQSLQEIWDYVVRPNLR LIGVPESDVENGTKLENTLQDII QENFPNLRQANVQIQEIERMP QRYSSRRATPRHIVRFTKVEM KEKMLRAAREKGRVTLKGKPI RLTAVLSAETLQARREWGPIFN ILKEKNFQPRISYPAKLSFISEGE IKYFIEKQMLRDFVTTRPALKE |
| 23666 | 54034 | A | 23801 | 1 | 2109 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23667 | 54035 | A | 23802 | 1 | 2544 | MSVHSWKPSWIRPIRSLSPKRPL GTQGTSEVPPDTHICQTKFHSLS SGPLLLSVHPVGKLSAVVGRVF IHLSQRERRRRRVISAFPSEVPG SSHQGVPDSCGRSVGAHPVREP KQGEALPHSGSPREGKLTNRKD IHTKNPSVHHHHQRPKVDKTT KIGKKQNRKTGNSKTQSASPPP KECSSSPATEQSWMENDFDEL EEGFRQSNYSELRKDIQTKGKE VENFEKNLEECKTRITNTEKCL KELMELKTKARELCEECSRLRS RCNQLEERSVMEDEMNEMK REGKFREKIRIKRNEQSLQEIWD YVKRPNLRLLIGVPESDVENGTK LENTLQDIIQENFPNLARQANV QIQEIQRTPQRYSSRRATPRHIIV RFTKVEMKEKMLRAAREKDRS TRQKVNKDTQELNSALHQADL IDIYRTLHPKSTEYTFFSAPHHT YSKIDHIVGSKALLSKCKRTEII TNYLSDHSAIKLELRIKNTQSR STTWKLNNLLLNDYWVHNEM KAEIKMFFETNENKDTTYQNL WDALKA VCRGKFIALNAHKGK QERSEIDTLTSQLELEKQEQT HSKASRRQEITKIRAELEKETQ KTLQKINESRSWFFERINKIDRP LARLIKKKREKNQIDTIKNDKG DITTDPTIEIQTIREYYKHL YAN KLENLEEMDTFLDTYTL PRLNQ EEVESLNR PITGSEIVAINSLPT |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23668 | 54036 | A | 23803 | 1 | 1886 | MKENFKHRHVVAFISSQEAQE DSREEEDRLESRFYFLFLELSY KTTGLNREPTVSLNSKSGTPMD QNEHSHWGPBAGKQGCASRSEL RIILVGKTGTGKSAAGNSILRKQ AFESKLGSQTLTKTCSKSQGSW GNREIVIIDTPDMFSWKDHCEA LYKEVQRCYLLSAPGPHVLLLV TQLGRYTSQDQQAQRVKEIF GEDAMGHTIVLFTHKEDLNNG SLMDYMHDSDNKALSKLVAA CGGRICAFNNRAEGSNQDDQV KELMDCIEDLLMEKNGDHYTN GLYSLIQRSKCGPVGSDERVKE FKQSLIKYMETQRSYALAEAN CLKGALIKTQLPKVDKTTKIGK KQSRKTGNSKKQSTSPPPKERS SSPAMEQSWTENDFDELREEGF RRSHYSELPEDIQTEGREVENFE KSLEECITRITHTEKCLKELMEL KTKARELREECRLRSQCDQLE ERVSAEMEDMNEMKREGKFKE K\RIKRNEQSLQEIWVYVVRPN LRLIGVPESDAENGTKLENTLQ DRIQENFPNLRQANGFCRFRN HHQTGFSPAGANQRGPLAATLS GPGGEGQSAVARLTGEKKNHP GAQYANRLSPRVGRFINRSWH DRFPDWKAGTGLKSAIFAW |
| 23669 | 54037 | A | 23804 | 1 | 4134 | |
| 23670 | 54038 | A | 23805 | 1815 | 1849 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23671 | 54039 | A | 23806 | 1 | 4016 | MGKKQNRKTGNS\KTQSAFP\ PKECSSSPATEQSWMENDFDKL REEGFRRSNYSELRI\EDIQTKGK EVENFEK\NLEECITRITNTEKC LKELMELKTKGSRNYVKECR\ S LRSRCDQLEERVVSAMEDEMNE MK*EGKFREKRIKRNEQSLQEI W\DYVK\RPNLRPIGVSESDGEN GTKLENTLQDIIPENFPNLARQA NVQIQEIQRTPQRYSSRRATPRH ILVRFTKVEMKEKMLRAAREK GQVTLKGKPIRLTADLSAETLQ ARREWGPIFNILKEKNFQPRISY PAKLSFISEGEIKYFIDKQMLRD FVTTRPALKELLKESLNMERNN WTSKQIIQEDGYSEEGWLCRA VIYSHTLQAIMAIVKATGNLQT DFANPFHTDDARQQFAMS\TV VGQGALPEDLSRCHLQTEAVQ RHPESLGCPLDLLHGMPVSSCF GYPQDTSSTV |
| 23672 | 54040 | A | 23807 | 2059 | 3153 | |
| 23673 | 54041 | A | 23808 | 6 | 188 | |
| 23674 | 54042 | A | 23809 | 3 | 1014 | VACRPLPRRRAQPATFIPRVAV KMALVASVRVPARVLLRAGAR LPGAAFGRTERAAGGGDGA\RP \FGSQRVLVEPDAGAGVAVMK FKNPPVNSLSLEFLTELVIS\LEK LENDKSFRDVILTSD\RPGVFSA GLD\LTEMCG\RSPAHYAWVLE RPVQELWLRLYQSQL\VLVSAI NGA\CPAGG\CLVALTCDYTIL\ AGNPRYCIGLNETQ\LGIIAPF\ WLKDNPWRTPIGHRAAESALQ LGLPLPPPAEALQVGIVDQ\VVP \EEQVQSTALSAIAQWMAIPKP MAHK\LTKAIMRKGQGP\AWS RKG\YADVQNF\VSFISKDSIQKS LQMYLERLKEEKG |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23675 | 54043 | A | 23810 | 1 | 2665 | MTTSIRQFTSSSSIKGSSGLGGG SSRTSCQLSGGLGAGSCRPGSA GGLGSALGGSSYSSCYSFGSGG GYGSSSFEGVDGLLVGGEKAT MQNLNDRLASYLDKVRALLEA DTELEVKIRDWYQRQAPGPAR DYSQYYRIIEELQNKPPPSDDL TLPSPLILTATVDNANILLQNDN AHLAAADFRTKFETEALCLSV EADINGPCRVLDELTLARADPE MHLENLKEELAYLKKNHEEMN APRGQVGGEINVMGAAPGVD LSRILNEMREQYEKMAEKNRK DAEDWFFSKTEELNREVATNSE LVQSGKSEISELRCMQALEIEL QSQLSMKASLEGNAETENRY CMQLSQIQLIGSVEERLAQLL CEMEQQNQEYKILLDMKMRLE LEITTYHRLLEGEDAQTVQHTP GSPCVPEWAHDCSLPAQLDE WSCQAQRGICGHRRENCWERIP SQSCFYRPTARSLTSLGTMST CSHQFTSSRSMKGSIGSGSIGG GSSRISSVLAGGSCHAPSTYGG ASCGLGGGYGGGFGSSSFASG FGGGYGGGLGAGFGGGLGAGL GGGFAGGDGLLVGSEKVTMQH LGDRLASYLKVRALLEANAD LEVKIRDWYQRQRPSEIKDYSP YFKTIEDLRHKIIAATIENAQPIL QIDNARLAADDFTNYEHELAL QQTVEAGVNGLCREMLALRGQ |
| 23676 | 54044 | A | 23811 | 222 | 548 | TLPCGDHHSQDPARLPSWHD LLQERSEKCGSQDWQRDSVQP GVSQYQFCCVPWPAGRSPQPRH CWGCCGTEASYDSGI*SLSTPG GGQLQGSV*GPDGAGLQNSHR |
| 23677 | 54045 | A | 23812 | 2 | 165 | |
| 23678 | 54046 | A | 23813 | 1 | 665 | |
| 23679 | 54047 | B | 23814 | 1 | 1673 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 23680 | 54048 | A | 23815 | 1 | 331 | ARQLRTSAMTMPVNGAHKDA DLWSSHDKMLAQPLKDSDEV YNIKKESNRQRVGLELIASENF ASRAVLEALGSCLNKNKYSEGYP GQRYYYGGTEFIDELETLCQKRA LQAYKLDPPQCWGVNVQPYSGS PANFAVYTALVEPHGRIMGLDL PDGGHLTHGFMTDKKKISATSI FFESMPYKVNPD TGYINYDQLE ENARLFHPKLIAGTSCYSRNLE YARLRKIADENGAYLMADMA HISGLVAAGVVPSPFEHCHVVT TTTHKTLRGCRAGMIFYRKGV KSVDPKTGKEILYNLESINSV FPGLQGGPHNHAIGVAVALK QAMTLEFKVYQHQQVVANCRA LSEALTELGKIVTGGG/CVISG GAGKPG*FSHQDGTGTSQDGG RRPFLHHTLSY |
| 23681 | 54049 | A | 23816 | 3 | 1709 | SHPTPRETPTGVEGQATPSVLG AAPASQAKATPTLGRPHASDR GEVAQLDEWSCQAQRGICGHR RENCWERIPSCFYRPTARSLT SLLGTMSTCSHQFTSSRSMKGS CSIGGSIGGGSSRISSVLGGSC HAPSTY/GGGLCVSFSRFSFGGA CGLGGGYGGGFGSSTNFWG\GF GGGYGAGLGAGFGGGLGAGL GGGFAGGDGLLVGSEKVTMQH LGDRLASYLDKVRAL E EANAD LEVKIRDWYQRQRPSEIKDYSP YFKTIEDLRHKIIAATIENAQPIL QIDNARLAADDFRTKYE\HELA LRQTVEADVNGLRRLDELTL ARTDLEMQIEGLKEELAYLRKN HEEEMLALRGQTGGDVNVEM DAAPGVDLSRILNEMRDQYEQ MAEKNRRDAETWFLSKTEELN KEVASNSELVQSSRSEVTELRR VLQGLEIELQSLSMKASLENQ L\EETKGRYCMQLSQIQGLIGSV EE\QLAQLRCEMEQQSQEYQIL LDVKTRLEQKYCHPTAALLEG EDAHLSSQQASGQSYSSREVF SSSSSSSRQTRPILKEQSSSSFSQ |
| 23682 | 54050 | A | 23817 | 2 | 365 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 23683 | 54051 | A | 23818 | 1 | 464 | RRWRICSTWTRSFATAWLPPAP SANFPRTDRSQGDRGAPAGFAL APILEFFLWDTSQKFLQKPHCF MHGRERAKMGRRAQQESAQA ENHLNGKNSSLTLTGETSSAKL PRCR/QGGWAGDSVKASKFRR KASEEIEDFRLRPQSLNGSDYG GDIP |
| 23684 | 54052 | A | 23819 | 384 | 805 | |
| 23685 | 54053 | A | 23820 | 3 | 392 | MKYSAIQTLDGEIDLKLLTKVL APEHEVR*VQWWQFPGLSTL AIPINPAELPGLALCLP*RPWNG REKVSLQLREKALSLSYPAPKF L\EDDVGDWDHDLFTEVSSEV LTE\WDPLQTEKEDPAGQARHT |
| 23686 | 54054 | A | 23821 | 63 | 785 | GPIRGPWGPGFGGWGGATPPAP TSLRRLRAAGLAPRRRAKMGR RAQQESAQAENHLNGKNSSLT LTGETSSAKLPRCRQGGWAGD SVKASKFRRKASEEIE\DFR\LRP QSLNGS\DYGGDIP\MPDLEEVQ EEDFVLQVAAAPPSI\QIKRVMT YRDL\DNLM\KYSAIQTLDGE D\IDLKLLTQK/VLAPEHEVRER NPSWQDDVGLGTWGPICSTEV SLRRSFTEWDP\QTEKEDPGG Q\ARHT |
| 23687 | 54055 | A | 23822 | 1 | 441 | MSFNCSTRNCSSRPIGGRCIVPV AQVTTTSTTDADCLGGICLPSSF QTGSWLLDHCQETC/CGCQPLG GISSVCQPVGGISTVCQPVGGV STVCQPACGVSRITYQQSCVSSC RR\PAKCVGASERIKTPRPASCF QDLPACCLSLNSSS |
| 23688 | 54056 | A | 23823 | 1 | 538 | PTRPLQQATCSPLSDIMSFNCST RNCSSRPIGGRCIVPVAQVTTTS TTDADCLGGICLPSSFQTGSWL LDHCQETCCEPTACQPTCYRRT SCVSNPCQVTCRQTTCISNPCS TPTAGRSP/CVSSGSQPLGGISS VCQPVGGISTVCQPVGGVSTVC QPACGVSRITYQQSCVSSCRRTC |